

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 12:21:38 ; Search time 13284 Seconds
(without alignments)

10154.434 Million cell updates/sec

Title: US-09-927-112-1

Sequence: 1 tcgcgactctagaactagtgg.....ggtaacggyggccacagccocg 4635

Scoring table: IDENTITY_NUC
Gapcod 10.0 Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pac.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
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- 11: gb.ste.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
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- 31: em.hc.in.v.*
- 32: em.hc.other.*
- 33: em.hc.mus.*
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- 35: em.hc.rod.*
- 36: em.hc.mam.*
- 37: em.hc.vrt.*
- 38: em.sv.*
- 39: em.hcgo.hum.*
- 40: em.hcgo.mus.*
- 41: em.hcgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score												
1	3684.6	79.5	4237	6	AX304472	AX304472	Sequence						
2	2838.4	61.2	6551	6	AX392826	AX392826	Sequence						
3	2527.4	54.5	4411	6	AK074149	AK074149	Homo sapi						
4	2161.4	46.6	2243	6	AX402958	AX402958	Sequence						
5	1540.4	33.2	6946	6	AB007919	AB007919	Homo sapi						
6	1540.4	33.2	154736	6	AL139246	AL139246	Human DNA						
7	1127	24.3	3283	6	AK096620	AK096620	Homo sapi						
8	861	18.6	2480	6	BC019679	BC019679	Homo sapi						
9	780	16.8	5551	6	AX411647	AX411647	Sequence						
10	780	16.8	5551	9	AB028692	AB028692	Homo sapi						
11	545.2	11.8	1977	9	AK026110	AK026110	Homo sapi						
12	328	7.1	646	6	AX411650	AX411650	Sequence						
13	323.4	7.0	3263	6	AK023083	AK023083	Homo sapi						
14	314.4	6.8	3113	4	AF498759	AF498759	Sus scrofa						
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18	308.6	6.7	2629	6	AX420077	AX420077	Sequence						
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Accession	Sequence	Length	Source	Patent	Accession
AX304472	10	4237 bp	From Patent	PAT 30-NOV-2001	
AX304472		WO0185956			
AX304472.1	GI:17383843				

REFERENCE
AUTHORS

1. Das, D., Reddy, R., Yao, M. G., Nguyen, D. B., Lu, Y., Tribouley, C. M., Yue, H., Khan, F. A., Gandhi, A. R., Au-Yang, J., Lal, P., Kearney, L., Elliott, V. S., Ding, L. and Thornton, M.

Db 4227 AGAAGGTTG 4235
RESULT 2
AX392826
LOCUS AX392826 6551 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 12 from Patent WO0216597.
ACCESSION AX392826
VERSION AX392826.1 GI:19700922
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1
Griffin, J.A., Paterson, C., Gandhi, A.R., Lu, Y., Yao, M.G.,
Baughn, M.R., Wallis, N.K., Hafealia, A.J., Ding, L., Tribouley, C.M.,
Das, D., Thomson, M. and Lal, P.
TITLE Lipid metabolism enzymes
JOURNAL Patent: WO 0216597-A 12 28-FEB-2002;
Incyte Genomics, Inc. (US)
FEATURES
source
1. 6551
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 72023748CB1"
BASE COUNT 1230 a 2108 c 2172 g 1041 t
ORIGIN
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Best Local Similarity 87.7%; Pred. No. 0;
Matches 3342; Conservative 0; Mismatches 11; Indels 457; Gaps 4;
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QY 937 -----AGTGGCTGAAGCAAGCTTTGACAGAGGCC 965
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QY 966 GACAAAGAGGGGATGGAGCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTC 1025
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Db 3028 GAGGACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087
QY 1947 AATCGAAAGGCTGATGAAACATCTGCTAAGAGGAACTGATTCCTCTCAATCAAGAGTGC 2006
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RESULT 3

AK074149 4411 bp mRNA linear PRI 15-FEB-2002

LOCUS AK074149 4411 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00222 protein.

ACCESSION AK074149

VERSION AK074149.1 GI:18676645

KEYWORDS fis (full insert sequence).

SOURCE Homo sapiens adult spleen cDNA to mRNA, clone: FLJ00222.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1

Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O. The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

2 (bases 1 to 4411)

REFERENCE Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O. Direct Submission

AUTHORS Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, URL: http://www.kazusa.or.jp/NEDO, Tel: 81-438-52-3913, Fax: 81-438-52-3914)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert and 5'- & 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

FEATURES

source

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BASE COUNT 740 a 1528 c 1438 g 705 t

ORIGIN

Query Match 54.5%; Score 2527.4; DB 9; Length 4411;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2542; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy 2147 CGTCGAGGAGACCTTCAGGCGGCAAGAGAGGCGACGACGTCGAGAGAGGCGGCGAC 2206

Db 61 CGTCGAGGAGACCTTCAGGCGGCAAGAGAGGCGACGACGTCGAGAGAGGCGGCGAC 120

Qy 2207 CGTCGAGGAGGAGATGAGGTCAGGACTCCCGGAGGCGCAAGCCGAGGCGGACCCG 2266

Db 121 CGTGAGAGGAGGAGATGAGGTCAGGACTCCCGGAGGCGCAAGCCGAGGCGGACCCG 180

Qy 2267 GCAGAGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2326

Db 181 GCAGAGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 240

Qy 2327 CGTGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2386

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Db 421 GCAGGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 480

Qy 2567 GATGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2626

Db 481 GATGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 540

Qy 2627 GCCTGAGGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2686

Db 541 GCCTGAGGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 600

Qy 2687 GCTCAAGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2746

Db 601 GCTCAAGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 660

Qy 2747 CTCGATGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2806

Db 661 CTCGATGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 720

Qy 2807 GCTCCCTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2866

Db 721 GCTCCCTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 780

Qy 2867 CACTGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2926

Db 781 CACTGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 840

Qy 2927 CTTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 2986

Db 841 CTTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 900

Qy 2987 CAGCAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3046

Db 901 CAGCAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 960

Qy 3047 CTTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3106

Db 961 CTTGTCGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 1020

Qy 3107 AGGCTCTTCTCTCGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3166

Db 1021 AGGCTCTTCTCTCGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 1080

Qy 3167 CCGGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3226

Db 1081 CCGGAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 1140

Qy 3227 GAGCAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3286

Db 1141 GAGCAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 1200

Qy 3287 CTCGAAGGAGGAGGAGGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTC 3346

Dp	1201	CTCCAAAGGGGTGGCAGACGATGTGGTGTGCCCCCGGGGCCCGGACCTGGCTCGGAAAGCCCC	1260
Qy	3347	AGCCCAAGAGGGGACCCGGCAGCCGCAAGCCCCGAGGTTAAAGTCGCCAAGCTGGGTGGCAGA	3406
Dp	1261	AGCCCAAGAGGGGACCCGGCAGCCGCAAGCCCCCGAGGTTAAAGGCCACAGCTGGGTGGCAGA	1320
Qy	3407	GAAGAGCCCTGTGCGAGTGTGGGCCCCCGGTGCTCGAAGCCGCCCGGGACCTGGCTGGGAT	3466
Dp	1321	GAAAGCCCTGTGCGAGTGTGGGCCCCCGGTGCTCGAAGCCGCCCGGGACCTGGCTGGGAT	1380
Qy	3467	GGCCGCACATGCATGCATGAAGTGTGTGGATCTGTGCGCGGGCTGAACAACCGGGGAGCTT	3526
Dp	1381	GGCCGCACATGCATGAAGTGTGTGGATCTGTGCGCGGGCTGAACAACCGGGGAGCTT	1440
Qy	3527	GCAAGGGGACCGGCAACCCAGCCCCGGGGGCTGTGAACAGAGGACGACGCATTCGGCAGCA	3586
Dp	1441	GCAAGGGGAGGGGCAACCCAGCCCCGGGGGCTGTGAACAGAGGACGACGCATTCGGCAGCA	1500
Qy	3587	GGCCGGGGCCGGGCTGACTCATCTGGGGGGCCCCCTGTGTGGCTTGAACCTCAGCTAT	3646
Dp	1501	GGCCGGGGCCCGGGCTGACTCATCTGGGGGGCCCCCTGTGTGGCTTGAACCTCAGCTAT	1566
Qy	3647	CCCGGGGAGAAAGCAGAGAGGCCCCCAAGGATCTTGGGGCTTGAAGCAGGGTCTCAGCGG	3706
Dp	1561	CCCGGGGAGAAAGCAGAGAGGCCCCCAAGGATCTTGGGGCTTGAAGCAGGGTCTCAGCGG	1620
Qy	3707	TAGGGGCTCCATGTCTCTGGAACTTCAGAGCCAGCAGCGGGGATCCCGGAAAGGTC	3766
Dp	1621	TAGGGGCTCCATGTCTCTGGAACTTCAGAGCCAGCAGCGGGGATCCCGGAAAGGTC	1680
Qy	3767	CCCCGGCTGGCTTGAAGGATGCTTGCAGAGCAACCGGGGGCTCTGCAGAGAGATGATGTC	3826
Dp	1681	CCCCGGCTGGCTTGAAGGATGCTTGCAGAGCAACCGGGGGCTCTGCAGAGAGATGATGTC	1740
Qy	3827	CTTGTATTGCTCAAAAGCTGAGAGAGATCAGAGATTAATCCCCCATGTTCTCCGCGGGTAA	3886
Dp	1741	CTTGTATTGCTCAAAAGCTGAGAGAGATCAGAGATTAATCCCCCATGTTCTCCGCGGGTAA	1800
Qy	3887	GGCCCTCTTGGCCCTGAGTGTCTCCCGCAGCGCCCTGGGATGGCTGGGCTTGGGATCC	3946
Dp	1801	GGCCCTCTTGGCCCTGAGTGTCTCCCGCAGCGCCCTGGGATGGCTGGGCTTGGGATCC	1866
Qy	3947	TGCTGTGCTTCTGCGGTGGAAGGATGTGCTGCTGTGTGCTGTGCTGTGTATTC	4006
Dp	1861	TGCTGTGCTTCTGCGGTGGAAGGATGTGCTGCTGTGTGCTGTGTGCTGTGTATTC	1920
Qy	4007	GTGGGACGTCTCCGTGAGCACTGCTGCCCTTGAAGCTTGGTGGCCCAATGAGCCAGGC	4066
Dp	1921	GTGGGACGTCTCCGTGAGCACTGCTGCCCTTGAAGCTTGGTGGCCCAATGAGCCAGGC	1986
Qy	4067	CTCTGTGTGAAGCTTGAAGCCCTTGGGACTTGGGTTGAAGGCTTGAAGGCCCGGACAAGCT	4126
Dp	1981	CTCTGTGTGAAGCTTGAAGCCCTTGGGACTTGGGTTGAAGGCTTGAAGGCCCGGACAAGCT	2040
Qy	4127	GGGAAAGAACAGGCTGCTTGTCTGAAGGATCTGGGGCCGGGACCTGTGACATGTCTGG	4186
Dp	2041	GGGAAAGAACAGGCTGCTTGTCTGAAGGATCTGGGGCCGGGACCTGTGACATGTCTGG	2106
Qy	4187	GGCCCTCCGGGTGGGCGCTTCCCAAACTCACTCTGGGCGGCTGGCGACTGCATGATGGC	4246
Dp	2101	GGCCCTCCGGGTGGGCGCTTCCCAAACTCACTCTGGGCGGCTGGCGACTGCATGATGGC	2166
Qy	4247	CCCTGATGCTTTTCTGTGGGATCTGGGGGCACTATGACATTCACACTCCCTCTTAG	4306
Dp	2161	CCCTGATGCTTTTCTGTGGGATCTGGGGGCACTATGACATTCACACTCCCTCTTAG	2220
Qy	4307	GCAAGCTCAGAGGGTCCCTTACTGGGAAGTCTGATGTGGGACAGGTATGTGACGTCTGGGC	4366
Dp	2221	GCAAGCTCAGAGGGTCCCTTACTGGGAAGTCTGATGTGGGACAGGTATGTGACGTCTGGGC	2286
Qy	4367	GTCTCTGCGCCCTCGGAGCGCTTGAAGCTTGTGAATGCTGCTGGAGTGAATTCCTTG	4426

Db	2281	GTCTCTGGCGCCCTCGGGAGCGCTTGAGACCTTGCTGAGTGCTGCGTGAAGTATTCCTCG	2340
QY	4427	GGCCCCCAGGCTTTGGCTGTCTTTGGGGCTGGAACACCCCACTTGAAGGGTGTCTCTTTAACC	4486
Db	2341	GGCCCCCAGGGGCTTGCTGTCTTTGGGCTTGGAACACCCCAATGTGAAGGGTGTCTCTTTAACC	2400
QY	4487	TGGAGGGAGGGACATPACCGGAGGCCGCCGCCACACACACTTGGCCCTTCAGACCCCTCG	4546
Db	2401	TGGAGGGAGGGACATPACCGGAGGCCGCCGCCACACACACTTGGCCCTTCAGACCCCTCG	2460
QY	4547	ACCAAGCTTTCTCTTTCTGCCCCCAACCCACGCTTGCTTCGTAGTTAGGAACGTGAGGCGG	4606
Db	2461	ACCAAGCTTTCTCTTTCTGCCCCCAACCCACGCTTGCTTCGTAGTTAGGAACGTGAGGCGG	2519
QY	4607	CGAGTGACAGGTAAACGGGGCCCAAGCCCTCG	4635
Db	2520	CGAGTGACAGGTAAACGGGGCCCAAGCCCTCG	2548
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AX402958		2243 bp	DNA linear PAT 07-JUN-2002
LOCUS			
DEFINITION	AX402958	Sequence 10 from Patent WO0204490.	
ACCESSION	AX402958		
VERSION	AX402958.1	GI:21387941	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Tang,Y.T., Azimzai,Y., Das,D., Thornton,M., Lu,D.A., Tribouley,C.W., Yue,H., Gandhi,A.R., Walla,N.K., Khan,F.A., Lu,Y., Yao,M.G., Hatalia,A.J., Elliott,V.S., Patterson,C., Lal,P., Ramkumar,J., Nguyen,D.B. and Bagn,M.R.		
TITLE	Lipid metabolism molecules		
JOURNAL	Patent: WO 0204490-A 10 17-JUN-2002;		
FEATURES	Incyte Genomics, Inc. (US)		
source	Location/Qualifiers		
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	Query Match 46.6%; Score 2161.4; DB 6; Length 2243;		
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 2162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	112	GGCCTTGAGGCTGAGGGGCTGAGTGCCTCATTTCCAGCCGCTCGGGGAAACCGGGCTGGGA	171
Db	1	GGCCTTGAGGCTGAGGGGCTGAGTGCCTCATTTCCAGCCGCTCGGGGAAACCGGGCTGGGA	60
QY	172	GACCCCATGCTGGGGGGTGAAGCTTGAGCCAGGGCAGATGCCGTGAGAGGCTCCGAGAGA	231
Db	61	GACCCCATGCTGGGGGGTGAAGCTTGAGCCAGGGCAGATGCCGTGAGAGGCTCCGAGAGA	120
QY	232	GGGCTGGGACCAACAGAGCTTGAGTGTGATGAGCGCTGTGSCCCAGGCTACACCCGAC	291
Db	121	GGGCTGGGACCAACAGAGCTTGAGTGTGATGAGCGCTGTGSCCCAGGCTACACCCGAC	180
QY	292	AGGGACACCGGGGGCCCTGGAGGACAGAGACCTCAGAGAGCTCTCTGCTCTCG	351
Db	181	AGGGACACCGGGGGCCCTGGAGGACAGAGACCTCAGAGAGCTCTCTGCTCTCG	240
QY	352	TGGAGGGGCGCCCAAGCTGTGATCCAGCCAGTCCAGCTTTAGTTGTGCGCCCGAC	411
Db	241	TGGAGGGGCGCCCAAGCTGTGATCCAGCCAGTCCAGCTTTAGTTGTGCGCCCGAC	300
QY	412	CGACAGTCTGTAGTCCCTCATGATGGGCTCCCGCAGCCGAGCCGCTTCTGTGGCCAG	471
Db	301	CGACAGTCTGTAGTCCCTCATGATGGGCTCCCGCAGCCGAGCCGCTTCTGTGGCCAG	360

AUTHORS	Ohara, O.
TITLE	Direct Submission
JOURNAL	Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,

BASE COUNT	1063 a	2450 c	2196 g	1237 t
ORIGIN				

Query Match	33.2%;	Score 1540.4;	DB 9;	Length 6946;
Best Local Similarity	99.9%;	Pred. No. 5.9e-236;		
Matches 1552; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1

QY	3082	AGCAAGCAAGGCGCTTGAGGCTTAAAGGCGCTCTTCTCCAGAGGCCCAAGGCGCGCTGCG	3141
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QY	3142	TGACAGATCATGCTGTGAGGCGGCGCCCGGCGCTTCGGTTAGCCAGCGATCTCTGC	3201
Db	3588	TGACAGATCATGCTGTGAGGCGGCGCCCGGCGCGCTTCGGTTAGCCAGCGATCTCTGC	3647
QY	3202	GGCGCAGGCGCAGCGCCCGGACCAAGAGCCAGAGCGCGGGCGCGAGGGGCTTCCCGGAGC	3261
Db	3648	GGCGCAGGCGCAGCGCCCGGACCAAGAGCCAGAGCGCGGGCGCGAGGGGCTTCCCGGAGC	3707
QY	3262	TGATCTTGAGTACACGCGGACACAGGCTCCAGGGGGTGGCAGACGATGTGTCGCCCCCG	3321
Db	3708	TGATCTTGAGTACACGCGGACACAGGCTCCAGGGGGTGGCAGACGATGTGTCGCCCCCG	3767
QY	3322	GGCGCGGACCTGCGCTCCGCGAAGCCGCCAGAGGGGGCGCGGACAGGGGACGCCCGGAG	3381
Db	3768	GGCGCGGACCTGCGCTCCGCGAAGCCGCCAGAGGGGGCGCGGACAGGGGACGCCCGGAG	3827
QY	3382	GTAAGCGCGCAGCTGCGGTGGCAGAGAAGCGCTGTGCGATGCGGCGCCCGCGTGTCC	3441
Db	3828	GTAAGCGCGCAGCTGCGGTGGCAGAGAAGCGCTGTGCGATGCGGCGCCCGCGTGTCC	3887
QY	3442	TGAGAGCGCCCGGGGCGTGCAGGATAGGCGGCCACATGCAATGAAGTGTGTGGATGCTCT	3501
Db	3888	TGAGAGCGCCCGGGGCGTGCAGGATAGGCGGCCACATGCAATGAAGTGTGTGGATGCTCT	3947
QY	3502	GCGCGCGGTGAACATCCGAGGGGCGCTGCAAGGAGCGGCGCACCCAGCGCGGCGCTTGCA	3561
Db	3948	GCGCGCGGTGAACATCCGAGGGGCGCTGCAAGGAGCGGCGCACCCAGCGCGGCGCTTGCA	4007
QY	3562	GCAAGCAGAGAGCCATTGCGACACAGCCCGGGGCGCGGCGTACATCATGAGGGGCGCCCT	3621
Db	4008	GCAAGCAGAGAGCCATTGCGACAGAGCCCGGGGCGCGGCGTACATCATGAGGGGCGCCCT	4067

QY	3622	GGGTGGGCTGGAGACCTTCAACGCTATCCCGGGGAGAGAGAGAGGCCCCCAAGGGTCTCG	3681
Db	4068	GCTGTGGCTGGAGACCTTCAACGCTATCCCGGGGAGAGAGAGAGGCCCCCAAGGGTCTCG	4127
QY	3682	GGGCTTGGAGGACAGGGGTCACAGCGGGTACGGGCTCCATGTCTCTGGACTTCACAGCCAG	3741
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QY	3742	ACAGCCGGGGCATCCCGGAAAGTCCCCCGCTGGGCTGAGGGGTGCCGACGGCAACCG	3801
Db	4188	ACAGCCGGGGCATCCCGGAAAGTCCCCCGCTGGGCTGAGGGGTGCCGACGGCAACCG	4247
QY	3802	GGGCTTGGAGGAGATGAGTGGCTTTGTGCTCAAAAGCTGAGAGATACAGAGTA	3861
Db	4248	GGGCTTGGAGGAGATGAGTGGCTTTGTGCTCAAAAGCTGAGAGATACAGAGTA	4307
QY	3862	AATCCCAATGTTCTCCGCGGGTAAGCCCTCTTGTCCTGGTGTCTCCCGACGCC	3921
Db	4308	AATCCCAATGTTCTCCGCGGGTAAGCCCTCTTGTCCTGGTGTCTCCCGACGCC	4367
QY	3922	CTGGATGAGCTGGGGCTGGGTACCTGCGMGCGCTTCGCGTGAACGGTGTGACTCGG	3981
Db	4368	CTGGATGAGCTGGGGCTGGGTACCTGCGMGCGCTTCGCGTGAACGGTGTGACTCGG	4427
QY	3982	TGCTGTGTCTGTGCTCTGTATCCGTGGCACTGTCTCTGGGCACTGTGCTCCCTGGC	4041
Db	4428	TGCTGTGTCTGTGCTCTGTATCCGTGGCACTGTCTCTGGGCACTGTGCTCCCTGGC	4487
QY	4042	TTCCTGTGGCCCATATAGCCCCAGCCCTCTGTCTAGCTTGAGGCGCTTGGGACTTGGGTG	4101
Db	4488	TTCCTGTGGCCCATATAGCCCCAGCCCTCTGTCTAGGCTTGAGGCGCTTGGGACTTGGGTG	4547
QY	4102	GAGCTGTATTGAGGCGCCGACAGGCTGGGAGAAACAGCTGCTTGTGTAAGGGTCTGGG	4161
Db	4548	GAGCTGTATTGAGGCGCCGACAGGCTGGGAGAAACAGCTGCTTGTGTAAGGGTCTGGG	4607
QY	4162	CCGGGACTGTGGCTTGAACATGTGTGGGCCCTTCGGCTGGGCGCTTCCCAACTGACTTC	4221
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QY	4222	CTGGGCGGCTGGCGACTGCACTGGGCCCTGTATGCTTTCTTGGAACTGGGGGCACTGTAAC	4281
Db	4668	CTGGGCGGCTGGCGACTGCACTGGGCCCTGTATGCTTTCTTGGAACTGGGGGCACTGTAAC	4727
QY	4282	CATCCATTCCCAACCTCCCTCTAAGGGACAGGCTCCAGGGGTCCCTACTGGGAAAGTCTGATG	4341
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QY	4342	TGGGCAAGTAGTGAAGCTGCTGGGCGTCTCTTGCGCCCCCTTGGAGACCTGAGCCTGCTG	4401
Db	4788	TGGGCAAGTAGTGAAGCTGCTGGGCGTCTCTTGCGCCCCCTTGGAGACCTGAGCCTGCTG	4847
QY	4402	AGTGTGCTGTGAAGTAGATTCCTTGGGCCCCAGGGCTTCGCTGTGGCTTGGGCTGAAGCAAC	4461
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QY	4462	CCACTTGAAGGGGTGTCTCTTATGCTTGAAGGAGGAGACATACACGAGCGCCGCCACAC	4521
Db	4908	CCACTTGAAGGGGTGTCTCTTATGCTTGAAGGAGGAGACATACACGAGCGCCGCCACAC	4967
QY	4522	CACCTTGGCCCTTCAGACCCCTCTGACCAAGCTTTCTTTTCTGCCCCCACTCAAGCTTGC	4581
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QY	4582	CTCCGATGTTAAGAACTGAGACGGCGAGGTACAGGTAAAGGGGCGACGCCCG	4635
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RESULT 6			
AL139246			
LOCUS	AL139246	154736 bp	DNA linear PRI 16-NOV-2001

DEFINITION Human DNA sequence from clone RP3-395M20 on chromosome 1p36.11-36.33, complete sequence.

ACCESSION AL139246

VERSION AL139246.20 GI:16973797

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Moore, M.

AUTHORS Direct Submission

TITLE Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

JOURNAL On Nov 17, 2001 this sequence version replaced gi:15912352.

COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chrl

RP3-395M20 is from the library RP3-3 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-395M20. The true left end of clone RP4-755G5 is at 90075 in this sequence. The true right end of clone RP4-755G5 is at 90078 in this sequence. The true right end of clone RP11-361M21 is at 135438 in this sequence.

FEATURES

Location/Qualifiers

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/note="Tandem repeat. Forced join. Gap size estimated to be approximately 800bps by restriction digest data."

misc_feature

125344..125387

/note="Sequence from overlapping clone RP4-755G5 (AL589746). Assembly confirmed by restriction digest."

BASE COUNT 29047 a 47325 c 48771 g 29593 t

ORIGIN

Query Match 33.2%; Score 1540.4; DB 9; Length 154736;

Best Local Similarity 99.9%; Pred. No. 3.2e-236;

Matches 1552; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3082 AGGTCAAGCAGGCTGGGCTAAAGGCTCTTCCTCGAGGAGCCCAAGCCGGCTGCG 3141

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QY 4162 CCGGAGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 4221

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QY 4222 CTGGGCGGCTGCGACCTGATGAGCCCTGATGCTTCTGCGAGCTGGGAGCTGAGGCTCATGTAC 4281

Db	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Reference	Authors	Title	Journal	Comment
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Qy	4342	TGGGAGGATGAGCAGCGCTGGGGGCTCTCCTGGGCCCCCTGGGAAGGCTGGAAGGCTGCTG	4401											
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Db	56620	AGTGTGGGTGAGATGATATTCCTGGGGCCCCAGGAGCTTCGTGCTTTGGGCTGAGACACC	56679											
Qy	4462	CCACTAGAAGGGGTGTCTCTCTTAGCTTGAGGGAGGGAATACACGAGCCGCCCTCAAC	4521											
Db	56680	CCACTAGAAGGGGTGTCTCTCTTAGCTTGAGGGAGGGAATACACGAGCCGCCCTCAAC	56739											
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LOCUS	AK096620													
DEFINITION	AK096620	3283 bp	mRNA	linear	PRI 15-JUL-2002									
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ACCESSION	AK096620													
VERSION	AK096620.1	GI:21756155												
KEYWORDS						oligo capping; f15 (full insert sequence).								
SOURCE						Homo sapiens fetal brain cDNA to mRNA, clone_11b:OCBBF2 clone:OCBBF2012936.								
ORGANISM						Homo sapiens								
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
REFERENCE						1								
AUTHORS						Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hito,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuna,M., Murakawa,K., Kanohori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Maehara,Y., Negai,K. and Isogai,T.								
TITLE						NEDO human cDNA sequencing project								
JOURNAL						Unpublished								
REFERENCE						2 (bases 1 to 3283)								
AUTHORS						Isogai,T. and Yamamoto,J.								
TITLE						Direct Submission								
JOURNAL						Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan								
COMMENT						(E-mail:genom@csbri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB) ; cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.								
FEATURES						Location/Qualifiers</								

[illegible]

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Qy	2043	GTCCTCACTGTCCTCCATCTGAAAGCTGGAAGCTGGAAGCAAGGCTGAAGAGACGTG	2102
Db	1920	GTCGGGCACT-----ACTGAAGCCAGCGCATGAAGGCTTAAATGCAACCTGAAGCA	1972
Qy	2103	GAGT-CTGGGAGAGATCCCGGGCCAGCAGACGCAATGGCCGCTGTGTGGAAAGCTT	2161
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Db	2033	TGGAATAATTAATAAATACTAATAATCAAGGTCTTAATCTTACAGTATGATGATG	2092
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Qy	2273	GAGGAGATGAGGCTCCCGGCGCTCTCTGACCTGTGAGAGTACACCAATCCGTGCG	2332
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Qy	2333	CAACCAAGATGAGAGGCGGCTCTCAAGCTGAGAGTGTCTGCTTCAAGCAGAC	2392
Db	2213	CGGTGAGCATTTG---TGAATGAGGAAACACAGGAAATGTATATCTTCAAGTAAAC	2269
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Db	2270	AAGAGCAGATGAGGCTGTGCGGAAATCAAGAGCTGATGATTTATTAATCAAAAGCA	2329
Qy	2453	GCTCTCCGATCTACCCCTCCCTCAAGCTGTGAGCTCCAGAACTACAAACCGGAGCC	2512
Db	2330	ACCCAGAGATTTACCTCTGCTGCTACAGCATGATTTCAAGTAACTTCAACCTCTCC	2389
Qy	2513	CTTCTGAAAGCGCGGCTGCAATGTTGCTCTGAACTTCAAGTCAAGAGGCGGATGCT	2572
Db	2390	CTACTGAAAGCGAGGCTGCGAGCTAGTGGCACTGATTTCAATCTGAAAGAGCGATGAT	2449
Qy	2573	GAGCTGAAACGAGCCAAAGTTCAAGCCCAAGGTGCTGCGCTACGATCTCAAGCTGG	2632
Db	2450	GCAGTAAACCGAGCAAAATTCAGGCAAAATGGCAATTTGGCTATGTCTTCAAAACCCA	2509
Qy	2633	GTGATGTGCCAGGCGGTGTTCAACCCCAACTCGAGAGACCCCTGCGCGGAGCTCAA	2692
Db	2510	GCAATGTGCAAGATCTTCAACCCCTTCTGTGAGACCTCTTCTGCGCAACCCCA	2569
Qy	2693	GAGAGCTGTGTCTCCGAGTCACTAGTGGCAGAGCTTCCCAAGCGGCGCATTCAT	2752
Db	2570	AAAGAGCTCATCTGAAAGTATCACTGAGCAGCACTCCCAACCTTCAACATTCAT	2629
Qy	2753	GCTGGGAGCCGTGGGAGATCATGACCCCTTGTGAGAGTGAAGATCTTGGGCTCC	2812
Db	2630	GTTTGAATGAGAGCGAGATCATGACCTTTTGTGAGAGTGAATTTTGAATTTGCC	2689
Qy	2813	TGTGACTGACAGAGGAGCAGACCCGCTGTGTGAGCAGCAACGGTTCAACCCCACTG	2872
Db	2690	AGTATTTGTTGTAAGATCAACCCGTTGTGATGAGCAATGATTTAACTCTGTG	2749
Qy	2873	GAGAGAGCCCTGTTTTCATGTGCAATGCGGAGATGCGCTGTGCTTCTCTGT	2932
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Db	2810	GTGGATCAGATCCATTTGGAAGAGACTTTGTTGACAAAGAACTGTGACTTCAAGCAG	2869
Qy	2993	CATATGCGAGGCTTACAGACAGTGTACTTGAAGGAGTGAAGAGCTTCTTCTGT	3052
Db	2870	CTTATGCTGTGCTTACCGGAGTGTCTATTGGAAGGCTGACAGAAAGCATCTATTTGT	2929
Qy	3053	GCATGTGCTGTGATGATCAAGCGGTGAAGTCAAGCAGCTCTGGGCTTAAAGGCTT	3112
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Qy	3173	CCGGCCCTCCGTTAGCAGAGGATCTGTGGCGGCAAGGCGCCCGGCAAGAGCCA	3232
Db	3044	GAAAGCATCAATGAGATGAATTTCCGCGACGACAGCTGAGGCGCCCAAGAGCAG	3103
Qy	3233	GAAAGCGGCGGAGGCGCTTCCGAGCTGTG	3265
Db	3104	GAAAGAGCAAAATGGGCTTCCAGAAATGT	3136
RESULT 8			
BC019679			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
<p>NTM-MGC Project URL: http://mgc.nci.nih.gov</p> <p>Contact: MGC help desk</p> <p>Email: cgabs-r@mail.nih.gov</p> <p>Tissue Procurement: David N. Louis, M.D.</p> <p>CDNA Library Preparation: Life Technologies, Inc.</p> <p>CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)</p> <p>DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center</p>			

HSSNNSHYVRKSTIGRIIRRTASAPAKGRKSKMPHOEWEIKDSVSEATRDQD
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BASE COUNT 1659 a 1214 c 1203 g 1475 t

Query Match 16.8%; Score 780; DB 6; Length 551;
 Best Local Similarity 64.4%; Pred. No. 1e-114;
 Matches 1255; Conservative 0; Mismatches 670; Indels 23; Gaps 5;

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 QY 1209 CTGACGAGCTTCCGACGAGGAGGAGAGATGGCGGTGTGACCTCCAGAGCTGCCAG 1268
 DB 61 CTGGCTAGTTTGTGAAGGTGAGCAAAAGATATATGTGCAACGGCTATTTCTTT 120
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 DB 121 GACATCATTAAGAGTTTGAAGTTTGAAGAAATAAGGTGAATAATGTTCTTGGCATA 180
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 DB 181 GAAGGCTTCCAGAACTTACAGCTGCTGCTGTGACATATTTAACCATTTGACACAT 240
 QY 1389 CATGTGACACGAGGACATGACGAGCGGTGAGGACATCTTCACTCACTCTGCCACAC 1448
 DB 241 GAAGGTACACAGACATGATCAGCCCTGTGACACTACATCTTCTCTCCAT 300
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 QY 1509 CTGACAGGCTGTGCTGCTGCTGTGAGGTGATCTGTGGATGTGGCCGACGGGAGCCC 1568
 DB 361 CTGCAAGAGGGCTGTGCTGTGTGAGGATGTGATGTGGATGTGGCCAGATGAGAGCCA 420
 QY 1569 ATTGTACACATGGCTACACTGTGACCTTCAAGATCTCTTCAAGACGCTCATTTGAAAC 1628
 DB 421 GTATGATCATATGTGTACACTCTCACTTCAAAATTTCTTCAAGATGTGTGAGACCC 480
 QY 1629 ATCACAAAATATGCTTTCATCAAGAAATGATACCAAGATCTGTCAATGCAAAACAC 1688
 DB 481 ATCACAAGGATCTCTTGTGAAGAAATGATGCTTCTATATGTCTATGCAAGATCAC 540
 QY 1689 TGCAGGTGATCCAGAGAGAAATGTGCCAGTATCTGATGACATCTTGTGGGACAAAG 1748
 DB 541 TGCAGTATCCAGAGAGAAAGATGTCTCACTTCAAGAAATTTTGGAGACAA 600
 QY 1749 CTGACCTGTCACTCACTGAGCAGTGAAGATGCACACACTCCCTCTCCAGAGATGCTC 1808
 DB 601 CTGACCTGTCACTCTTGTATACAGGGAGTGAAGACACTTCCAAAGCCCTCAAAATTTG 660
 QY 1809 AAGGCGAAGATCTCTGTGAAGGGGAGAAAGCTCCAGCAACATCAAGCAGAGATGGAG 1868
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RESULT 10
 AB028992 AB028992 5551 bp mRNA linear PRI 04-AUG-1999
 LOCUS
 DEFINITION Homo sapiens mRNA for KIAA1069 protein, partial cds.

Accession	Version	Keywords	Source	Organism	Reference Authors	Title	Journal
Db	1251	AGCAGTCAGGTTTTCAGCAAAAATCAGACAGCTTCATGATTTATATCAAAAGCACT	1310				
Qy	2456	CTCCCGCATCTACCCCTCTCTCTTACCGTGTGACTCCAGCAACTCAACCCGAGCCCTT	2515				
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Qy	2516	CTGGAAAGCGCGGCTGCCAAATGATTGGCCCTTAACTACACAGTCACAGAGGGCGGAGATCTGCA	2575				
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DEFINITION	AK022610	1977 bp	mRNA	linear	PRI 01-AUG-2007		
VERSION	AK022610						
KEYWORDS	AK022610.1	GI:10434099					
SOURCE	AK022610	oligo capping; fls (full insert sequence).					
ORGANISM	AK022610	Homo sapiens					
REFERENCE	AK022610	Homo sapiens					
AUTHORS	AK022610	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	AK022610	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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	AK022610	Isegai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,					
	AK022610	Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K.,					
	AK022610	Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y.,					
	AK022610	Saito, K., Yamamoto, J., Wakematsu, A., Nakamura, Y., Negahari, K.,					
	AK022610	Maeno, Y., and Kanehori, K.					
	AK022610	NEBO human cDNA sequencing project					
	AK022610	Unpublished					
	AK022610	2 (bases 1 to 1977)					
	AK022610	Isegai, T. and Otsuki, T.					
	AK022610	Direct Submission					
	AK022610	Submitted (23-AUG-2000) Takao Isegai, Helix Research Institute,					

COMMENT	FEATURES
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@shri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Heliix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	Location/Qualifiers 1..1977 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NT2RM4000657" /cell_line="NT2" /cell_type="teratocarcinoma" /clone_lib="NT2RM4" /note="Cloning vector: pME18SFL3-mRNA from uninduced NT2 neuronal precursor cells." 474..1874 /note="Unnamed protein product" /codon_start=1 /protein_id="BAB14129.1" /db_xref="GI:10434100" /translation="MTNFGHKTKTSRSKSYSTDEEDPTQSTGEKGGQLYLRGRRTKMLCRELSDLVVYTVSAADIVDGTGVNLSFSETRAHVOVKSEQEMIVNOKQLTIVPSAIRIDSNSNPLPYNNAGGOLVAINYSGEMMOLNARKPFKANNCCVYLKPOOMCKGFNPSGDPPLPANKPKOILIVYSQQLPKRPDPSFGREGIITDPFAYEILIGIPVDCDDQRTVRVDNDFNPFVMEETLFTVHMEILVPLFVHDHPIDRDPVGRTVFSFLVGRHYVLEGLTEASIVHTITINEYKNNQLGKLFPKNRHSSETRNSHYVKRKSIGRIILRTIASAPAKGRKSKMGFOEMVILKDSVSEATDODGVILRTSLQARVPMVPVDRLNLGALSLPSVSEATKDIEGKNSLSDSFCRPTBQAKEMCKVPFPRLCEVCMMEISET"
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Db 1 CTATCGAAGAACTACTGCGACGTATCCAGCAGAAAGAAAGATTGCTCGACTGCGAAAGAA 60	
1735 TCTCTGGGAGCAACCTGGAACCTGTCATCAGTGAAGCAGTGAAGATGCGACACACCTCCCT 1794	
Db 61 TATTGGAGAGAACTGACCTGCTCATCTTTGATACAGGGAGTGAAGACAGCTTCCAA 120	
1795 CTCACAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAGAAAGCTCCAGGCCAATCAT 1854	
Db 121 GCCCTCAAAAGTTTGAAGGCCAAATTTCTAGTGAAGGGTAAAGATTGCCTTTACACTTG 180	
1855 GCGAGGATGCGAGAGAGGGAGGTGTCGTATAGAGCAAGTCTGTATGATGATTGACGATG 1914	
Db 181 GGGATGATGACAGAGAGGGGAAAGTTTCCATAGACACAGTGCAGATGAATTAAGAAAG 240	
1915 ACTGCAAGCTC---CTAATGGGGATGCAATCCACCAATGAAAGCGTATGAAGAAACACG 1971	
Db 241 AGTGCAAATTCAGCTCATTTATATGTAATGGACCACTAGCATCAGGTGGAATCTTTCA 300	
1972 CTAAAGAGAACTGGATTTCCCTCATCAAGAAAGTCGAAGATTCGGGACTGTGAGACCCCA 2031	
Db 301 TAAAGAAAAAATCGAGATCACTGTTAAAGAAATTCGAAATTTGGAATTAAGAAAGATCTG 360	
2032 ACAACTTCTCCGTCTCACACGTGTCCTCCATCTTGAAAGCTCGAGCGCAAGCAAGGCTG 2091	
Db 361 ATAATTTCACAGTGCAGGCACT-----ACTGAAGGCCACCACTGAAGGCTTAATATGCA 413	
2092 AAGAGCGATGAGATCTCG- GAGAGATGCGCGGGCCAGAGACGAAATGCGCGCTCGTC 2150	
Db 414 CACTGGAAGCAGAGTCCAGTGTAAAGGAAAGTGAAGAAAGAAATCACTAGGAAGATCCCTC 473	
2151 GTGGGAAGCTTCTCCAGGCGCAAGAAAGGGCAGCAGAGCTAAGAAAGCGGCGCAGCGTG 2210	

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D	534	GATGATGAGGAAGACACACAGCGAGAGTATCGGCAMAGAGGGTGGCCAGCTGTACAGATTG	593
Q	2262	ACC GG GAG AAG AAG AACC ATG AAG CTG TCC CG GGC CCT CTG CA CTT GGT GAA GAT AACC	2321
D	594	GGTGCGCGAAGAAAAACATGAAAGCTCTGCGGAAAGACTCTGATTTTGGTGTGTACACA	653
Q	2322	AAGTCGTGGCAACCCACGACATAGAGATGAGCGCGCTCGAGTGGCAGGTTGCTGC	2381
D	654	AAC TCGGTGGCGCGCTCAGGACATTTG--TGATGAGCGGAACCAAGAAATGTGTTATCA	710
Q	2382	TTTACGAGACCAAGGCCCAACGATTTCTGACACAGAGCGCGGAGATCACTACGCTTC	2441
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D	771	AATCAAAAGCACTCAGAGAGATTACCCCTGCTCGCTACGCAATTGATTCAGATTACTTC	830
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D	831	AACCTCTCCCTCTACTGGAACGAGCGTGCACCTATGTGGCACTGAATTAATCAATCTGAA	890
Q	2562	GAGCGAGATGCTGCAGCTGGAACCGAGCCAAAGTTACAGCGCCAAACGGTGGCTGCGATACGA	2621
D	891	GAGCAATGATGCACTTAAACCGAGCCAAATTCAGGCAAAATGGCAATGTGTGGTATGTC	950
Q	2622	CTCAAGCCTGGGTGATGTGCGCAGAGGGCGTGTCAACCCCACTGGAGAGACCCCTGCCC	2681
D	951	CTCAAAACCCAGCAAAATGTCAAAAGGATCTTTCAACCTTTCTCTGTGACCTCTTCTCT	1011
Q	2682	GCGAGCTCAAGAAAGCAGCGTGTGCTCCGATCATCAAGTGGCCAGAGGTTCCCAAGCGC	2741
D	1011	GCAACCCCAAAAAGCAGCTCATCTTAAGATTAATCAAGTGAAGCAACTCCCAACCTT	1071
Q	2742	GCGACATCATGCTGGGGGAGACCGTGGGAGATCATCGACCCCTTTGTGAGGTGAGATC	2801
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Q	2802	ATTGGGCTCCCTGTGACATGCAAGCAGAGGAGACACCCGCTGTGACGACACCGGCTTC	2861
D	1131	ATTGATATGCCAGTAGATTTGTTGAAGATCAAAACCGGTGTGATATGACATGATTTT	1191
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D	1191	AAACCTGTGTGGGAAAGAAACATGACATTTACAGTACACATGCCAGAAATAGCTTTGGTT	1251
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DEFINITION	AX411650					
ACCESSION	AX411650					
VERSION	AX411650.1	GI:21444192				
KEYWORDS						
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ORGANISM	human.					
REFERENCE	1	Zhu, Z.				
AUTHORS		Regulation of human phosphatidylinositol-specific phospholipase				
TITLE		c-like enzyme				
JOURNAL		Patent: WO 0226996-A 4 04-APR-2002;				
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RESULT 13
LOCUS AK023083 3263 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens CDNA FLJ13021 fis, clone NT2RP3000742, weakly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (BC 3.1.4.11).

ACCESSION AK023083
VERSION AK023083.1 GI:10434839
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens tetracarcinoma cell line:NT2. CDNA to mRNA, clone 11b:NT2RP3 clone:NT2RP3000742.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayaashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishi,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negahari,K., Masuko,Y. and Kanehori,K.
TITLE NED0 human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3263)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genom@shri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NED0 human cDNA sequencing project supported by Ministry of International Trade and Industry for Japan: cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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BASE COUNT 829 a 820 c 888 g 726 t

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 VERSION AF498759.1 GI:20269956
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 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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 1 Smith, T.P.L.
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 P.O. Box 166, Clay Center, NE 68933, USA
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2161.4	46.6	2243	24 ABA94696	Human lipid metabo
4	1111.2	24.0	2433	24 ABL60537	Human lipid metabo
5	780	16.8	5551	23 AAS7856	DNA encoding novel
6	780	16.8	5551	23 AAD31081	Human PI-PLC-like
7	545.2	11.8	1977	22 AAH17609	Human cDNA sequenc
8	442.8	9.6	534	24 ABK71572	Human dltph polyinu
9	328	7.1	646	24 AAD31082	Human PI-PLC-like

10	323.4	7.0	3263	22	AAH16211	Human CDNA sequenc
11	308.6	6.7	2289	22	AAD17564	Novel human phosph
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13	308.6	6.7	2629	24	ABK10063	Human phospholipas
14	308.6	6.7	2709	22	AAD17567	Novel human phosph
15	307.6	6.6	1840	22	AAD19219	Human lipid metabo
16	306.6	6.6	2520	24	ABL60544	Human phospholipas
17	301.8	6.5	3425	22	AAH43471	Nucleotide sequenc
18	300.2	6.4	3544	22	AAH42603	Human phospholipas
19	297	6.4	2211	24	AAD34464	Gene #3294 used to
20	289.8	6.3	2627	24	ABN6796	DNA encoding novel
21	281.2	6.1	2158	23	ABK43682	Human polynucleoti
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23	276.8	6.0	3068	24	ABK94917	Human novel polynu
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26	276.2	6.0	2540	24	AAD23722	Human lipid metabo
27	238.8	5.2	3594	24	ABK94695	DNA encoding inosi
28	202.4	4.4	5233	17	AAH16825	Human CDNA clone
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34	194.2	4.2	4565	24	ABK68245	Kidney cancer rela
35	194.2	4.2	4565	24	ABK68492	Human breast cance
36	194.2	4.2	4565	24	ABK68865	Human breast cance
37	176.6	3.8	432	22	AAH15182	Phospholipase C-ga
38	176.6	3.8	3870	17	AAH12292	Phospholipase C-ga
39	176.4	3.8	3893	17	AAH12293	Human cDNA clone
40	174	3.8	863	23	AAH07553	Human cDNA sequenc
41	173	3.7	2416	22	AAH16555	Drosophila melanog
42	167.4	3.6	5370	23	ABL07877	Human cDNA differe
43	167.4	3.6	5370	23	ABL07877	Human cDNA differe
44	161	3.5	4519	24	ABK64021	Human cDNA differe
45	160	3.5	4242	24	ABK64021	Human cDNA differe

ALIGNMENTS

RESULT 1	ABA96005	standard; CDNA; 4237 BP.
ID	ABA96005;	
XX	04-MAR-2002	(first entry)
DT	04-MAR-2002	(first entry)
XX	Human lipid metabolism enzyme-5 (LME-5) CDNA.	
DE	Human; LME-5; lipid metabolic; neuroprotective;	
XX	immunopressiveive; anti-inflammatory; cardiovascular; gene therapy;	
KW	enzyme therapy; cancer; neurological disorder; autoimmune disorder;	
KW	inflammatory disorder; cardiovascular disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	99..3818
FT		/tag= a
FT		/product= "LME-5"
XX		
PN	WO200185956-A2.	
XX		
PD	15-NOV-2001.	
XX		
PF	11-MAY-2001; 2001MO-US15210.	
XX		
XX	11-MAY-2000; 2000US-203511P.	
PR	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	

XX (INCYTE GENOMICS INC.
 PA Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
 PI Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;
 PI Ding L, Thornton M;
 XX
 DR MPl: 2002-089794/12.
 DR P-PSDB; ABB08205.
 XX
 PT New lipid metabolism enzymes useful for diagnosing, treating and
 PT preventing cancer, neurological disorders, autoimmune/inflammatory
 PT disorders, and cardiovascular disorders
 XX
 PS Claim 5; Page 121-122; 122pp; English.
 XX
 CC The sequence encodes a novel human lipid metabolism enzyme (LME-5) of
 CC the invention. The invention relates to novel human LME's, and the
 CC polynucleotides which identify and encode them. The enzymes of the
 CC invention have cytosolic, neuroprotective, immunosuppressive,
 CC anti-inflammatory, and cardiovascular activity. The polypeptides and
 CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
 CC metabolism enzymes are useful in the diagnosis, treatment and prevention
 CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
 CC cardiovascular disorders, and in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
 CC for compounds that modulate the activity of LME. Polynucleotides encoding
 CC LME may be used for somatic or germline gene therapy, to detect and
 CC quantify gene expression in biopsied tissues in which expression of LME
 CC may be correlated with disease, to generate a transcript image of a
 CC tissue or cell type, to generate hybridization probes useful in mapping
 CC the naturally occurring genomic sequence, and for screening libraries of
 CC compounds in drug screening techniques. The polypeptide sequences may be
 CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
 CC primers derived from polynucleotide sequences encoding LME may be used to
 CC detect single nucleotide polymorphisms.
 CC
 CC Sequence 4237 BP; 816 A; 1327 C; 1370 G; 724 T; 0 other;
 XX
 SQ
 Query Match 79.5%; Score 3684.6; DB 24; Length 4237;
 Best Local Similarity 94.6%; Pred. No. 0;
 Matches 3526; Conservative 0; Mismatches 4; Indels 219; Gaps 2;

Db	507	AGACCCAGGAGACCGGCCCTTGTGCTCAACCTGGGGGGGCTGTCTTGTCCGGGTCA	566
Qy	937	-----AGNGCTGAAGACAGAGTTTGAACGAGGCC	965
Db	567	CACACTGGGGAGATGGCCCGGCGCAGAGGTGGAGTGGCTGAAGGACAGAGTTTGAACGAGGCC	626
Qy	966	GACAAAGAACGGGGATGGCAGCTTGAAGATTGGCCAGAGTCTTGCAGCTTGCAACAAGTCC	1025
Db	627	GACAAAGAACGGGGATGGCAGCTTGAAGATTGGCCAGAGTCTTGCAGCTTGCAACAAGTCC	686
Qy	1026	AACGTGAACCTGCCCCCGGCGCAGAGGTGAAGCAATTTTCAG-----	1066
Db	687	AACGTGAACCTGCCCCCGGCGCAGAGGTGAAGCAATTTTCAG-----	746
Qy	1067	-----	1066
Db	747	CTGGAGCAAGGGAAGCTGGCTGTCTCAGAGAGGGCCCTGGTCCAGGTCCCAATGGGG	806
Qy	1067	-----GGAACGGACACGGATGACCAACAGGAGAGCTGGGTTTT	1106
Db	807	ACCAGAGCCTTGGATTGACAGGAAGCGGACACGGATGACCAACAGGAGAGCTGGGTTTT	866
Qy	1107	GAAAGTTTGTGCTTCTCAAGATGATGTCACCGCGGGGACCTTACCTGCTCATG	1166
Db	867	GAAAGTTTGTGCTTCTCAAGATGATGTCACCGCGGGGACCTTACCTGCTCATG	926
Qy	1167	CTGACCTTACAGCAACCAAGAGACCACTGGATGCGGCCAGCTTGAGCGCTTCTGACAG	1226
Db	927	CTGACCTTACAGCAACCAAGAGACCACTGGATGCGGCCAGCTTGAGCGCTTCTGACAG	986
Qy	1227	GTGAGAGAAAGATGGGGGTGTCACCTTGAAGAGTCTCCAGACATCATCGACAGTTT	1286
Db	987	GTGAGAGAAAGATGGGGGTGTCACCTTGAAGAGTCTCCAGACATCATCGACAGTTT	1046
Qy	1287	GAGCCATGCCAGAAAACAAGATGAAGGGGCTCTGGGCAATGATGGCTTCAACCACTAC	1346
Db	1047	GAGCCATGCCAGAAAACAAGATGAAGGGGCTCTGGGCAATGATGGCTTCAACCACTAC	1106
Qy	1347	ACCAGAGCCCTGTGTGTCATCTTCAACCTTGAACCAACCATGATGACAGAGCATG	1406
Db	1107	ACCAGAGCCCTGTGTGTCATCTTCAACCTTGAACCAACCATGATGACAGAGCATG	1166
Qy	1407	ACGAGCGCGTGAAGCACTTCACTCATCCTGCTCCCAACAACCTTACCTGCGGTGAC	1466
Db	1167	ACGAGCGCGTGAAGCACTTCACTCATCCTGCTCCCAACAACCTTACCTGCGGTGAC	1226
Qy	1467	CAGCTATGTCACAGTCAAGGATGACATGATGCTTGGGTCTGAGAGCTGGTCCGC	1526
Db	1227	CAGCTATGTCACAGTCAAGGATGACATGATGCTTGGGTCTGAGAGCTGGTCCGC	1286
Qy	1527	TGGGTGAAGGTGACATGCTGGATGAGGCGGCGGAGAGCCCATGTTGACATGGCTAC	1586
Db	1287	TGGGTGAAGGTGACATGCTGGATGAGGCGGCGGAGAGCCCATGTTGACATGGCTAC	1346
Qy	1587	ACTCTGATCTCAAGATCTCTTCAAAAGAGTCAATGAACCATCAACCAATATGCTTC	1646
Db	1347	ACTCTGATCTCAAGATCTCTTCAAAAGAGTCAATGAACCATCAACCAATATGCTTC	1406
Qy	1647	ATCAAGATGATGATCCAGTATCTGTCTCATGAAAACCACTGACATGATTCAGCAG	1706
Db	1407	ATCAAGATGATGATCCAGTATCTGTCTCATGAAAACCACTGACATGATTCAGCAG	1466
Qy	1707	AAGAAATGGCCAGATGATGATCTGATCTGTTGGGGCAACATGAGCACTGATCAACAG	1766
Db	1467	AAGAAATGGCCAGATGATGATCTGATCTGTTGGGGCAACATGAGCACTGATCAACAG	1526
Qy	1767	AGCAGTGAAGATGACCAACACTTCCCTCTTCCACAGATGCTCAAGGAGAGATCTCTG	1826
Db	1527	AGCAGTGAAGATGACCAACACTTCCCTCTTCCACAGATGCTCAAGGAGAGATCTCTG	1586
Qy	1827	AAGGGAAGAGTCTCCAGCACAATCAGCGAGATGCGAGGAAGCGAGGTGTCTGAT	1886

[illegible]

DR	P-PSDB: AAN77498.	
XX		
PT	New lipid metabolism enzymes, useful for diagnosing, treating or	
PT	preventing immune system disorders (e.g. Crohn's disease), neurological	
PT	disorders (e.g. Parkinson's disease), or cell proliferative disorders	
PT	(e.g. cancers) -	
XX		
XX		
PS	Claim 56; Page 120-122; 122pp; English.	
CC		
CC	The present invention relates to the isolation of human lipid	
CC	metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the	
CC	polynucleotide sequences encoding them. The LMM polypeptides,	
CC	polynucleotides, agonists and antagonists are useful for diagnosing,	
CC	treating or preventing disorders associated with aberrant expression	
CC	of LMM, particularly immune system disorders (e.g. acquired	
CC	immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,	
CC	asthma or Crohn's disease), neurological disorders (e.g. epilepsy,	
CC	Huntington's disease, dementia or Parkinson's disease), developmental	
CC	disorders (e.g. Down's syndrome) or cell proliferative disorders	
CC	(e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,	
CC	myeloma or sarcoma). The present sequence encodes for human LMM-6.	
XX		
XX		
SEQ	Sequence 6551 BP; 1230 A; 2108 C; 2172 G; 1041 T; 0 other;	
	Query Match 61.2%; Score 2838.4; DB 24; Length 6551;	
	Best Local Similarity 87.7%; Pred. No. 0;	
	Matches 3342; Conservative 0; Mismatches 11; Indels 457; Gaps	
OY	546 GTGGAGCGGTGATGGGTGCCATGCAAGAGGGAGTGCAGATGTGAAGCTGCTGCGCGC	605
DB	1468 GTGGAGCGGTGATGGGTGCCATGCAAGAGGGAGTGCAGATGTGAAGCTGCTGCGCGC	1527
OY	606 TCCAAAGGCGTGGTCCGCTTCTACTACTGTGACGACGACCGCTCTGTGATCGCTGAGAG	665
DB	1528 TCCAAAGGCGTGGTCCGCTTCTACTACTGTGACGACGACCGCTCTGTGATCGCTGAGAG	1587
OY	666 CCTTACGCAAGAACGAGAGAGGCCAAGATTCGATCGACTCCATCCAGAGGTGAGT	725
DB	1588 CCTTACGCAAGAACGAGAGAGGCCAAGATTCGATCGACTCCATCCAGAGGTGAGT	1647
OY	726 GAGCGGCGAGTGGAGAGTCTTCAGAGGCTACCCCTGACCGGACCTTGACCCCACTGCTGC	785
DB	1648 GAGCGGCGAGTGGAGAGTCTTCAGAGGCTACCCCTGACCGGACCTTGACCCCACTGCTGC	1707
OY	786 TTCAGACTCTACCAAGGAGCCACCGCGAGTCCGTGACCTGTCTCCACGACGACGAG	845
DB	1708 TTCAGACTCTACCAAGGAGCCACCGCGAGTCCGTGACCTGTCTCCACGACGACGAG	1767
OY	846 GTGGCGGCACTGGGTGTACTGTGCTGTGGCTACTCTCATATGGCCGATATAGGACGAGAC	905
DB	1768 GTGGCGGCACTGGGTGTACTGTGCTGTGGCTACTCTCATATGGCCGATATAGGACGAGAC	1827
OY	906 AGCGTGGTCCGCCCCAGCGCAGCAGGAGAC-----	936
DB	1828 AGCGTGGTCCGCCCCAGCGCAGCAGGAGAC-----	1887
OY	937 -----	936
DB	1888 AGACCCAGGGGACCGGCGCCCTTGGCTGTCACTCGGGGGGGCTGTCTCTTGC GGGTCA	1947
OY	937 -----AGTGGCTGAAGCAGAGCTTGAAGAGGCC	965
DB	1948 CACACTGGGGAAATGGCCCGCCAGAGGTTGATGGCTGAAGACAGATTTGAAGAGGCC	2007
OY	966 GACAAGAAACGGGGATGGCAGCTTGAGCATTTGGCCAGGTCCTGCAGCTGTGCAACAAGCTC	1025
DB	2008 GACAAGAAACGGGGATGGCAGCTTGAGCATTTGGCCAGGTCCTGCAGCTGTGCAACAAGTTC	2067
OY	1026 AACGTGAACCTGCCCCCGGCGAGAGGTTGAAGCATGTTTCAG-----	1066
DB	2068 AACGTGAACCTGCCCCCGGCGAGAGGTTGAAGCATGTTTCAGGGGTGAGCTGATGATCCTGG	2127
OY	1067 -----	1066

Db 2128 CTGAGCAAGGAGAGCTGGCTCTCAAGACAGGGCCCTGGTGGAGGTCGAATGGGG 2187
Qy 1067 -----GGAAGCGACACGGATGACCAACCAAGGACGCTGGGTTTT 1106
Db 2188 ACCCAAGGCTTCATTTGACAGAAAGCGGACACGGATGACCAACCAAGGACGCTGGGTTTT 2247
Qy 1107 GAAGAGTTCTGTGCTTTTCAAGATGATGTCACCGGCGGGGACCTTACCTGCTCATG 1166
Db 2248 GAAGAGTTCTGTGCTTTTCAAGATGATGTCACCGGCGGGGACCTTACCTGCTCATG 2307
Qy 1167 CTGACCTACAGCAACCAAGAGACCACTGATGCGGACGCTTGCAG 1226
Db 2308 CTGACCTACAGCAACCAAGAGACCACTGATGCGGACGCTTGCAG 2367
Qy 1227 GTGAGAGAAAGATGGCGGGTGTGACCTTGAAGAGCTGCCAGACATCATCGACATTT 1286
Db 2368 GTGAGAGAAAGATGGCGGGTGTGACCTTGAAGAGCTGCCAGACATCATCGACATTT 2427
Qy 1287 GAGCCATGCCCAAAAAACAAGATTAAGGGGCTGCGGACATGATGGCTTCACTCACTAC 1346
Db 2428 GAGCCATGCCCAAAAAACAAGATTAAGGGGCTGCGGACATGATGGCTTCACTCACTAC 2487
Qy 1347 ACCAGAGCCCTGCTGTGTGACATCTTCAACCTGAGACCAACCATGTGACACAGACATG 1406
Db 2488 ACCAGAGCCCTGCTGTGTGACATCTTCAACCTGAGACCAACCATGTGACACAGACATG 2547
Qy 1407 ACCGAGCCGCTGAGCCACTATCTTATCACTCGTCCCAACCACTTCTCTGTGGGTGAC 1466
Db 2548 ACCGAGCCGCTGAGCCACTATCTTATCACTCGTCCCAACCACTTCTCTGTGGGTGAC 2607
Qy 1467 CAGCTCATGTCCCAAGTACAGGGGTGGAATGATGCTGGGCTGAGGCTGAGCTGGCTGGC 1526
Db 2608 CAGCTCATGTCCCAAGTACAGGGGTGGAATGATGCTGGGCTGAGGCTGAGCTGGCTGGC 2667
Qy 1527 TGCGTGAAGGTGACCTGCTGGATGGGCGGACGGGAGGCCATTTGACCAATGGCTAC 1586
Db 2668 TGCGTGAAGGTGACCTGCTGGATGGGCGGACGGGAGGCCATTTGACCAATGGCTAC 2727
Qy 1587 ACTCTGACTTCAGAGATCTCTTCAAGAGAGTCAATTGAAAACATCAACAAATATGCTTC 1646
Db 2728 ACTCTGACTTCAGAGATCTCTTCAAGAGAGTCAATTGAAAACATCAACAAATATGCTTC 2787
Qy 1647 ATCAAGATGATGATCCAGATGATCTGTGCATGAAAAACACTGAGTGCATCCAGAC 1706
Db 2788 ATCAAGATGATGATCCAGATGATCTGTGCATGAAAAACACTGAGTGCATCCAGAC 2847
Qy 1707 AAGAAAATGSCCAGATCTGATGACATCTTGGGACCAAGCTGGAACCTGTATCAAGTG 1766
Db 2848 AAGAAAATGSCCAGATCTGATGACATCTTGGGACCAAGCTGGAACCTGTATCAAGTG 2907
Qy 1767 AGCAGTGAATGCGACCACTCCCTCTTCAAGATGCTCAAGGGCAGATTCCTGTG 1826
Db 2908 AGCAGTGAATGCGACCACTCCCTCTTCAAGATGCTCAAGGGCAGATTCCTGTG 2967
Qy 1827 AAGGGGAAGAGCTCCAGCAACATCAGCGAGATGCGAGGAAGGCGAGGTCTTGAT 1886
Db 2968 AAGGGGAAGAGCTCCAGCAACATCAGCGAGATGCGAGGAAGGCGAGGTCTTGAT 3027
Qy 1887 GAGGACATGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1946
Db 3028 GAGGACATGCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3087
Qy 1947 AATCGAAAGCTGTGAAAAACATCTGTAAGAGAAATCGGATTCCTCATCAAGAGATCG 2006
Db 3088 AATCGAAAGCTGTGAAAAACATCTGTAAGAGAAATCGGATTCCTCATCAAGAGATCG 3147
Qy 2007 AAGATTCGGGACCTGAGAGACCCCAACAACTTCTCGTCTCAACTCTGCCCATCTTGA 2066
Db 3148 AAGATTCGGGACCTGAGAGACCCCAACAACTTCTCGTCTCAACTCTGCCCATCTTGA 3207
Qy 2067 AAGCTCGACGCA----- 2080

Db 3208 AAGCTCGACGCAAGTGAAGAGCCAAAAAGTGAACCCCTGATGCGGACAGGCCCCCCC 3267
Qy 2081 ----- 2080
Db 3268 GACAGCAGCCTGTGGGCGACGCCAGGGCCCCCGAACCAGAGAGATGTCAGGACAGGCCA 3327
Qy 2081 ----- 2080
Db 3328 GGTCCAGCTGGGAGAGACGGGACAGATCGAGCTGTTTGTGTGTGTGTGTGTGTGTGTGT 3387
Qy 2081 ----- 2080
Db 3388 CGAGTCTGT 3447
Qy 2081 -----GAGCAAGGCTGAAGAGACCTGAGATCTGGGAGAGATGCGGGGCGAC 2129
Db 3448 GGGTGTGGAGAGAGCAAGCTGAAGAGAGACCTGAGATCTGGGAGAGATGCGGGGCGAC 3507
Qy 2130 AGACGCAATGGCCGCTGT 2189
Db 3508 AGACGCAATGGCCGCTGT 3567
Qy 2190 CTGAAGAGGGGCGGACGGTGAAGAGAGAGATGAGAGGTCAAGACTCCCGGAGGCGCAG 2249
Db 3568 CTGAAGAGGGGCGGACGGTGAAGAGAGAGATGAGAGGTCAAGACTCCCGGAGGCGCAG 3627
Qy 2250 AGCCAGGGGCGACCCGCGAGAGAGACATGAAGCTGTCCGGGCTCTTCTGACCTG 2309
Db 3628 AGCCAGGGGCGACCCGCGAGAGAGACATGAAGCTGTCCGGGCTCTTCTGACCTG 3687
Qy 2310 GTGAAGTACCAAGTCCGTGGCCACCCACGATAGAGATGAGAGCGGCTTCCAGCTGG 2369
Db 3688 GTGAAGTACCAAGTCCGTGGCCACCCACGATAGAGATGAGAGCGGCTTCCAGCTGG 3747
Qy 2370 CAGGTGTGCTCTTGAAGAGAGACCAAGGCCACAGATTTCTGACAGAAAGCGGCGCAG 2429
Db 3748 CAGGTGTGCTCTTGAAGAGAGACCAAGGCCACAGATTTCTGACAGAAAGCGGCGCAG 3807
Qy 2430 TACCTAAGCTTCAACAGACAGAGCTTCCGCACTTACCTCTCTCTTCACTGTGTGAC 2489
Db 3808 TACCTAAGCTTCAACAGACAGAGCTTCCGCACTTACCTCTCTCTTCACTGTGTGAC 3867
Qy 2490 TTCAGCACTACACCCGAGCCCTTCTGTGAACCGCGGCTGCAATGGTGGCCCTGAAC 2549
Db 3868 TTCAGCACTACACCCGAGCCCTTCTGTGAACCGCGGCTGCAATGGTGGCCCTGAAC 3927
Qy 2550 TACCAATGAGAGGGGCGATGCTGACGCTGAACGAGCCAAATTCAGGCGCAACGCTGAC 2609
Db 3928 TACCAATGAGAGGGGCGATGCTGACGCTGAACGAGCCAAATTCAGGCGCAACGCTGAC 3987
Qy 2610 TGCAGCTAGTACTCAAGCTGGTGCATGTGCCAGGGGCTTCAACCCCACTGAG 2669
Db 3988 TGCAGCTAGTACTCAAGCTGGTGCATGTGCCAGGGGCTTCAACCCCACTGAG 4047
Qy 2670 GACCCCTGCGGGGAGCTCAAGAGAGAGCTGTGCTCCGATCACTAGTGGCCAGAC 2729
Db 4048 GACCCCTGCGGGGAGCTCAAGAGAGAGCTGTGCTCCGATCACTAGTGGCCAGAC 4107
Qy 2730 CTTCGCAAGCGCGGACCTCAATGCTGGGGAGCCGCGGAGATCACTGACCCCTTGTG 2789
Db 4108 CTTCGCAAGCGCGGACCTCAATGCTGGGGAGCCGCGGAGATCACTGACCCCTTGTG 4167
Qy 2790 GAGGTGAAGATCAATGGGCTCCCTGTGACTGACGAGAGAGAGACCCGCGTGTGAC 2849
Db 4168 GAGGTGAAGATCAATGGGCTCCCTGTGACTGACGAGAGAGAGACCCGCGTGTGAC 4227
Qy 2850 GACAAAGGCTTCAACCCCACTGGAGAGAGACCTGTGTTTATAGTGTGACATGCGGAG 2909
Db 4228 GACAAAGGCTTCAACCCCACTGGAGAGAGACCTGTGTTTATAGTGTGACATGCGGAG 4287
Qy 2910 ATGCGCTGTGCTTCTCTGCTGTGGACCAAGATCCATCGGGGCTGACTTATTTGC 2969
Db 4288 ATGCGCTGTGCTTCTCTGCTGTGGACCAAGATCCATCGGGGCTGACTTATTTGC 4347


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Db 61 GACCCATGCTGGGGGTGAGCTTGAGAGCCAGGGGAGTGGGGAGAGGCTCCGGAGAGA 120
Qy 232 GGGCTGGGACACACAGAGCTGGGTGTGTATGCTGCTGCGCCAGGCTACACCCGAC 291
Db 121 GGGCTGGGACACACAGAGCTGGGTGTGTATGCTGCTGCGCCAGGCTACACCCGAC 180
Qy 292 AAGGACACCGGGGGGCTGGGAGCAGAGAGACTGAGAGCAGCTCTCTGCTCTG 351
Db 181 AAGGACACCGGGGGGCTGGGAGCAGAGAGACTGAGAGCAGCTCTCTGCTCTG 240
Qy 352 TGGACGGCCGGCCAGCTGTGTATCCAGCCAGCTCCAGCTTTCAGTTGCTGCCAC 411
Db 241 TGGACGGCCGGCCAGCTGTGTATCCAGCCAGCTCCAGCTTTCAGTTGCTGCCAC 300
Qy 412 CGACAGTCTCAAGTCTCCATGATGCTCCCGGACAGCCGGCCCTTCCTGGCCAG 471
Db 301 CGACAGTCTCAAGTCTCCATGATGCTCCCGGACAGCCGGCCCTTCCTGGCCAG 360
Qy 472 CTCTTCGGCCGTGAGGACCCAGGGCCGGATCCGGAGCAGGTGGCTTTCAGGCGCA 531
Db 361 CTCTTCGGCCGTGAGGACCCAGGGCCGGATCCGGAGCAGGTGGCTTTCAGGCGCA 420
Qy 532 ACATTCGCTGCTGTGTGAGACCGGTGCAATGGGTGCATGCAAGAGGGATGCAATG 591
Db 421 ACATTCGCTGCTGTGTGAGACCGGTGCAATGGGTGCATGCAAGAGGGATGCAATG 480
Qy 592 AGCTGCTGTGCGCTCCAGAGGCTGTGCTGCTTCTACCTGAGACAGCCGCTCT 651
Db 481 AGCTGCTGTGCGCTCCAGAGGCTGTGCTGCTTCTACCTGAGACAGCCGCTCT 540
Qy 652 GCATCCGCTGAGAGGCTCTCAAGCAAGAGAGGCAAGATCTCCATGACCTCCATCC 711
Db 541 GCATCCGCTGAGAGGCTCTCAAGCAAGAGAGGCAAGATCTCCATGACCTCCATCC 600
Qy 712 AGAGGTGAGTGAAGGGGCGGCGAGTCCGAGGCTTTCAGCCCTACCTGACGCGAGCTTC 771
Db 601 AGAGGTGAGTGAAGGGGCGGCGAGTCCGAGGCTTTCAGCCCTACCTGACGCGAGCTTC 660
Qy 772 ACCCCAACTGTGCTTACGATCTACACAGGAGCCAGCCGAGTGGCTGGAAGCTGGCT 831
Db 661 ACCCCAACTGTGCTTACGATCTACACAGGAGCCAGCCGAGTGGCTGGAAGCTGGCT 720
Qy 832 CCACACGAGAGGAGTGGCGCGCACTGGGTCACTGGCTTGGCTGCTGCTGAGCGCGCA 891
Db 721 CCACACGAGAGGAGTGGCGCGCACTGGGTCACTGGCTTGGCTGCTGAGCGCGCA 780
Qy 892 TCAGCGACGAGAGCAGCTGTGCTGCGCGCAGCGGACCAAGGAGCTGCTGAGAGAGA 951
Db 781 TCAGCGACGAGAGCAGCTGTGCTGCGCGCAGCGGACCAAGGAGCTGCTGAGAGAGA 840
Qy 952 CGTTTGAAGAGGCGGAGCAAGAGACGGGAGTGGCAGCTGAGATTTGGAGGCTCTGAGC 1011
Db 841 CGTTTGAAGAGGCGGAGCAAGAGACGGGAGTGGCAGCTGAGATTTGGAGGCTCTGAGC 900
Qy 1012 TGCTGCAAGAGCTCAACGTGAACCTGCCCGGACAGAGGTGAGACAGATTTTCAGGAG 1071
Db 901 TGCTGCAAGAGCTCAACGTGAACCTGCCCGGACAGAGGTGAGACAGATTTTCAGGAG 960
Qy 1072 CGGACACGAGATGACCAAGAGAGAGCTGGGTTTGAAGATTCTGTGCTTTCAGAGA 1131
Db 961 CGGACACGAGATGACCAAGAGAGAGCTGGGTTTGAAGATTCTGTGCTTTCAGAGA 1020
Qy 1132 TGAATTCACCGCGCGGAGACCTTACCTGATGCTGATGCTGATGCTGATGCTGATGCT 1191
Db 1021 TGAATTCACCGCGCGGAGACCTTACCTGATGCTGATGCTGATGCTGATGCTGATGCT 1080
Qy 1192 ACCTGATGCTGCGCGAGCTGACGCTTCTGACGTTGAGACAGAGAGTGGCGGCTGGA 1251
Db 1081 ACCTGATGCTGCGCGAGCTGACGCTTCTGACGTTGAGACAGAGAGTGGCGGCTGGA 1140
Qy 1252 CCTGGAAGCTGCGAGAGATCATGAGCAGTTTGAAGCTTCCCAAGAGATA 1311

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Db 1141 CCTCGAGAGCTGCAGAGATCATGAGCAGTTTGAAGCCATGCCCCAGAAAAGAGATA 1200
Qy 1312 AGGGCTGCTGGAGCATTTGATGGCTTTCACCAACTACACAGAGGCTGTGTGATCATCT 1371
Db 1201 AGGGCTGCTGGAGCATTTGATGGCTTTCACCAACTACACAGAGGCTGTGTGATCATCT 1260
Qy 1372 TCACCTGAGCAGCAGCATGTGACCAAGAGATGACGAGCGGCTGAGCCATCTTCA 1431
Db 1261 TCACCTGAGCAGCAGCATGTGACCAAGAGATGACGAGCGGCTGAGCCATCTTCA 1320
Qy 1432 TCACCTGCTCCCAAGACCTTACCTGAGGCTGACCAAGTATCCAGTCCAGGGTGG 1491
Db 1321 TCACCTGCTCCCAAGACCTTACCTGAGGCTGACCAAGTATCCAGTCCAGGGTGG 1380
Qy 1492 ACATGATGCTTGGGTCTGAGAGCTGCTGCGCTGCTGCTGAGAGTGAAGTCTGGAGT 1551
Db 1381 ACATGATGCTTGGGTCTGAGAGCTGCTGCGCTGCTGCTGAGAGTGAAGTCTGGAGT 1440
Qy 1552 GGGCCGAGCGGGAGCTCATTTGTGACCATGCTTACCTTGTGATCTTCCAAAGTCTCTTCA 1611
Db 1441 GGGCCGAGCGGGAGCTCATTTGTGACCATGCTTACCTTGTGATCTTCCAAAGTCTCTTCA 1500
Qy 1612 AAGAGTATGAAACATGCAAAATATGCTTATCAAGAAATGAGTACCAAGTATCC 1671
Db 1501 AAGAGTATGAAACATGCAAAATATGCTTATCAAGAAATGAGTACCAAGTATCC 1560
Qy 1672 TGTTCATGAAACCATGAGTGTATCATGACAGAGAGAAATGGCCGATATGATCTG 1731
Db 1561 TGTTCATGAAACCATGAGTGTATCATGACAGAGAGAAATGGCCGATATGATCTG 1620
Qy 1732 ACATCTTGGGAGCAAGCTGACCTGTATCATGAGAGAGAGTGGAGATGCCACACTCC 1791
Db 1621 ACATCTTGGGAGCAAGCTGACCTGTATCATGAGAGAGAGTGGAGATGCCACACTCC 1680
Qy 1792 CCTCTCACAGATGCTCAAGGGCAGATCTCTGTGAAGAGAGAGTCCAGCCACA 1851
Db 1681 CCTCTCACAGATGCTCAAGGGCAGATCTCTGTGAAGAGAGAGTCCAGCCACA 1740
Qy 1852 TCAGCGAGAGTCCGAGAGAGAGAGGAGTGTGTGATGAGAGCAGTCTGATGATGAG 1911
Db 1741 TCAGCGAGAGTCCGAGAGAGAGAGGAGTGTGTGATGAGAGCAGTCTGATGATGAG 1800
Qy 1912 ATGACTGCAAGCTCTCAATGGGAGTGCATCCAGATTCGAAAGGTGTAGAAAACATG 1971
Db 1801 ATGACTGCAAGCTCTCAATGGGAGTGCATCCAGATTCGAAAGGTGTAGAAAACATG 1860
Qy 1972 CTAAGAGAAAATGATTCCTCATCAAAAGTGCAGAAATTCGAGATGTGAGAGCCCA 2031
Db 1861 CTAAGAGAAAATGATTCCTCATCAAAAGTGCAGAAATTCGAGATGTGAGAGCCCA 1920
Qy 2032 ACAACTTCTCGGTCTTCACACTGTCTCCCATCTGAAAAGCTGGAAGCGCAAGAGCTG 2091
Db 1921 ACAACTTCTCGGTCTTCACACTGTCTCCCATCTGAAAAGCTGGAAGCGCAAGAGCTG 1980
Qy 2092 AAGAGAGCTGAGTCTGGGAGAGATGCGGGGGCAGAGAGCAATGAGCGGCTGCTG 2151
Db 1981 AAGAGAGCTGAGTCTGGGAGAGATGCGGGGGCAGAGAGCAATGAGCGGCTGCTG 2040
Qy 2152 TGGAGAGCTTCTCAGGCGCAGAAAGAGGAGAGCTGAGAGAGGCGGCGAGCTGG 2211
Db 2041 TGGAGAGCTTCTCAGGCGCAGAAAGAGGAGAGCTGAGAGAGGCGGCGAGCTGG 2100
Qy 2212 AAGAGAGAGATGAGGATGAGACTCCCGGAGGCGCAGAGCGGAGGCGAGCTGGCAGA 2271
Db 2101 AAGAGAGAGATGAGGATGAGACTCCCGGAGGCGCAGAGCGGAGGCGAGCTGGCAGA 2160
Qy 2272 AGA 2274
Db 2161 AGA 2163

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RESULT 4
ABJ60537

ID	ABL60537 standard; cDNA; 3433 BP.
XX	ABL60537;
AC	
XX	27-AUG-2002 (first entry)
XX	
DE	Human lipid metabolism enzyme (LME)-1 cDNA (clone id: 7472210CBL).
XX	
KW	Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective; gene;
KW	neurotropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;
KW	antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;
KW	gene therapy; protein therapy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	309..3353
FT	/product= a
FT	/note= "lipid metabolism enzyme"
FT	/note= "LME-1"
XX	
PN	W0200229036-A2.
XX	
PD	11-APR-2002.
XX	
PF	05-OCT-2001; 2001WO-US33302.
XX	
PR	06-OCT-2000; 2000US-238388P.
PR	13-OCT-2000; 2000US-240616P.
PR	02-NOV-2000; 2000US-245719P.
PR	08-NOV-2000; 2000US-247503P.
PR	17-NOV-2000; 2000US-249503P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;
PI	Wajia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;
PI	Lal PG, Tribouley CM;
XX	
DR	WPI; 2002-315862/35.
XX	
DR	P-PEDB; ABB08001.
XX	
PT	Lipid Metabolism Enzymes and nucleic acids; useful for preventing,
PT	diagnosing and treating e.g. cancer, Alzheimer's disease and
PT	Cretzfeld-Jakob disease -
XX	
PS	Claim 5; Page 121-122; 127pp; English.
XX	
CC	The invention relates to human lipid metabolism enzymes (LMEs) and
CC	encoding polynucleotides. The LMEs can be expressed by standard
CC	recombinant technology. The LME polypeptides, polynucleotides and
CC	modulators may be used in the prevention, diagnosis and treatment of
CC	diseases associated with inappropriate LME expression such as cancer
CC	(e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
CC	Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
CC	(e.g. Cretzfeld-Jakob disease and Acquired Immune deficiency syndrome
CC	(AIDS) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
CC	pectoris and mitral valve prolapse). The present sequence represents the
CC	human LME-1 encoding cDNA.
XX	
SQ	Sequence 3433 BP; 1042 A; 741 C; 842 G; 808 T; 0 other;
XX	
Query Match	24.0%; Score 1111.2; DB 24; Length 3433;
Best local similarity	65.5%; Pred. No. 4.4e-200;
Matches 1711; Conservative	0; Mismatches 878; Indels 23; Gaps
45	GGACCCAGGCGCGATCCGAGAGCAGGTGGCTTTCTTGACGCCAATCTTGCCCGT 544
D6	326 GGAAGAAAGAACTGCTGTCAGTACCGCAGCATTTTCTGCGGACAAACAGTGTTC 385
45	GCTGAGCGCGTCATCGGTCATGCAAGAGGGGATCGATGCTGAGACTGCGTGGCGG 604
45	366 TGTTAAAGATGCAATGAGTGTGATCAGTCCCGGACACAGATGATCAAGCTGAAACGTGG 445

QY	605	CTCCAAAGGAGCCTGGAGTCGGCTTTCTA	CTCACTCACTGAGACGAGACACCGCTCTCGATCCGGCTGAG	664	
Db	446	AACCAAAAGGCGCTGTCCGCCCTCTTTTAC	CTGGATGAGACCCGGACACGCGCTCCGATGGCG	505	
QY	665	GCCCTCAGCGCAAGAACGAAAGGCCAAGAT	CTCCATCGACTCCATCCAGAGGGTAGTA	724	
Db	506	AACCTCTAGGAAGAGTAGAAGGCAAAAATA	CTTTATTTGATTTCACTTTACAAAGTAGCTGA	565	
QY	725	GGGGGCGGACAGTGGAGGCTTTCCAGCGCT	CACTCCGAGAGTGGACCCCACTGCTG	784	
Db	566	GGGCCGAGCTGTAAATTTTTCACAGACAG	AGCTGAGGGGAATTTGACCCACGCTGCTG	625	
QY	785	CTTGAGCATCTTACCAACGCGACGCAACG	CGAGTGGCTGAGACTTGGTCTCCACAGACGCA	844	
Db	626	CTTGACATCTTACCATGAGCAACCAACG	ATGAGTCCCTGGACCTCATCCTCCACCCGA	685	
QY	845	GGTGGCGGACCTTGGGTCTACTGGCTTGC	GTCTCACTCATAGGCCGATCAGCGAGAGA	904	
Db	666	GGAAGCCCGACCTGGATCAAGGCGCTCA	AGTACTCGATGGCGGATCAGTAGAAGA	745	
QY	905	CAGCGCTGGCTGC	CGCGCAGGCGACACAGGGGACCA	GTGGCTGAAAGCAGACGTTTGAGAGGC	964
Db	746	CTCCCTTGCCAAAAGGACAGAGAC	CCATGACCAATGGGTGAAGCACA	CTTTGAGGAAGC	805
QY	965	GCAQAGAACGGGATGGCAGCCTGAGCAT	TGGCGAGGCTCTGCAAGCTGCTGCACAGCT	1024	
Db	806	TGATTAAGATATGTGACCGGCTTGGCT	GAATTTTGAAAGATACATCAGCTGATCA	TAAACT	865
QY	1025	CAAGTGAACCTGCCCCCGGAGAGGGTGA	AGAGATGTTCAAGGAAACCGACACGAGTA	108	
Db	866	GAAATGTTAATCTGCCCGAAGAAAGTC	AGACAAATGTTTCAGGAAGCCGACACAGATA	925	
QY	1085	CCACCAAGGACCGTGGGTTTGAAGAT	TCTGTGCTTCTCAACAATGATGTCCACCG	1144	
Db	926	GAACTACAGGAACTTTGACATTTGAA	AGGTTCTGTGTTTTTTCAAAATGATGTCTTGAG	985	
QY	1145	CCGGGACCTTCACTGCTCATGCTGAC	CTTACAGCAACCAAGACACACTTGGATGCCG	1204	
Db	986	ACGAGACCTTTATTTTGTACTTTTGA	GTCAAGTGAAGAAAGATCACCTTAACTGTGGA	1045	
QY	1205	CAGGCTCAGCGCTTCTGTGACGTGAG	GAGAAAGATGGCGGGTGTGACCTCGAGAGCTG	1264	
Db	1046	AGAACTGGCTCAGTTTTTGAAGGTGA	GCAAAAGATGAAATATGTGACACAGCACTATTG	1105	
QY	1285	CCAGGACATATGAGAGCATTTGAG	AGCCATGCCAGAAAAAAGAGTAAAGGGCGCTGCGG	1324	
Db	1106	TCTTGACATCATAAAGAAAGTTTGA	AGTTTCAAGAGAAATAAGTGAAAAATGTCTTGG	1165	
QY	1325	CATTGATGGCTTACCAACCATCAAC	CCAGGAGCCGTGGTGTGACATCTTCAACCCGTGACA	1384	
Db	1166	CATGAAAGGCTTACAGAACTTCA	TGCTGATGCTGCTGTGACATATTTAACCACTTGCA	1225	
QY	1385	CCACCATGTGCACAGAGCATGACG	AGCCGCTGAGCACTACTTCATCACCTGCTGCCA	1444	
Db	1226	CCATGAAGTGTACCAAGACATGAT	CAGCCCTCTGCAACTCTCATTTGCTTCTCTCA	1285	
QY	1445	CAACACTACTCTGTGGGTGACCA	AGCTCATATGCCAGTGCACATGTATGCTTG	1504	
Db	1286	CAATACATCTTACTGAGAACCA	CGCTCTCTTCTCAAGTCAAAAGTGATATGTATGACG	1345	
QY	1505	GGTCTTGCAAGGCTGGCGGCTGC	CTGTGAGGTGACCTGTGGATGGGCGCGACGGGGA	1564	
Db	1346	GGGTGTGCAGAAAGGGCTGTGTG	CTGTGTGGAATTTGACGTGGCCAGATGAGAA	1405	
QY	1565	GCCCATTTGTGCACCATGCTCA	CACTTGACTTCCAAAGATCCTCTTCAAAAGCGTCATTTGA	1624	
Db	1406	GCCAGTAGTACATCAATGAGTTAC	TCTCACTTCAAAAATTCCTCTTCAAGAGATGTTGTGGA	1465	
QY	1625	AACCATCAACAAATATGCTTAT	CATCAAGAAATAGAACCAAGATACCTGTCACTGAAAA	1684	
Db	1466	GACATCATACAGCATGCTTGTGTGA	AGATAGATTTCTCTGTATATTTGTCTTATCTGAGAA	1525	

QY 1685 CCACGTCAGTGCATCCAGCAGAGAAATGGCCAGTATCTGACTGACATCTCTGGGGA 1744
 Db 1526 TCACGTCAGTATCCAGCAGCAAGAAAGATTGCTGATACCTGAAAGAAATTTGGGGA 1585
 QY 1745 CAAAGTCGACCTGTGATCAGTGAAGGAGTGAAGATGCCACACACTCTCCCTCCACAGAT 1804
 Db 1586 CAAACTGACCTGTGATCAGTGAAGGAGTGAAGATGCCACACACTCTCCCTCCACAGAT 1645
 QY 1805 GCTCAAGGCGAAGATCTCTGTGAAGGGAAGAAAGCTCCAGCCAAATCAGAGAGATGC 1864
 Db 1646 TTTGAAAGGCAAAATTTCTAGTGAAGGGAAGAAAGCTCCAGCCAAATCAGAGATGC 1705
 QY 1865 GGAGGAGGCGAGTGTCTGATGAGACAGTGTGATGATGATGATGATGATGATGATGATG 1924
 Db 1706 AAGAGAGGGAAGTTTCCGATGAGACAGTGTGATGATGATGATGATGATGATGATGATG 1765
 QY 1925 C---CTCAATGGGAGTGCATCCAAATGCAAAAGCGTGTGAAGAAACACTGTGAAGGAA 1981
 Db 1766 CAAAGTCATTTATGATGATGAGACCACTGAGCATCAGTGTGATGATGATGATGATGATG 1825
 QY 1982 ACTGATTTCCCTCATCAAGAGATGCAAGATTTGGGACCTGTGAGAGACCCCAACACTTCTC 2041
 Db 1826 ACTGGAGTCACTGTGTAAAGAAATCTCAAAATTCGAGATTAAGAAAGATCTGATGATGATG 1885
 QY 2042 CGTCTCCACATGCTCCCAATCTGAAAGCTCGGACCGAAGAGAGAGAGAGAGAGAGAGAG 2101
 Db 1886 AGTGGGGGACT-----ACTGAAAGGCGACGATGATGATGATGATGATGATGATGATG 1938
 QY 2102 GGAGT-CTGGGAGAGATGCGGGGCGAGCAGACGCAATGCGGCTGTGTGTGGGAGCT 2160
 Db 1939 AGAGTCAGATGTAAGGAAAGTGAAGAAATCACATGAGACGATCCCTCATGACCAACT 1998
 QY 2161 TCTCCAGGCGCAAGAAAGGAGCAGACAGTGAAGAGCGGCGAGTGTGAGAGAGAGAGAG 2220
 Db 1999 TTGGAAGAACTAAGAAAACTACAAAATCAAGCTGTAAATTTTACATGATGATGAGAG 2058
 QY 2221 ATG-----AGGTCAGAGACTCCCGGAGGCGCAGAGCCGAGGAGGAGAGAGAGAGAGAG 2271
 Db 2059 AAGACACACAGCAGAGTACTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2118
 QY 2272 AGAAGACATGAAGCTGTCCCGGAGGCTCTCTGACCTGTGAAAGTACCAAGTCCGTGG 2331
 Db 2119 GGAAGAACATGAAGCTGTCCCGAAGAGCTCTGTGATTTGGTTGTGTACACAAACTCTGTGG 2178
 QY 2332 CCAACCCACGATAGAGATGAGAGCGGCGCTCCAGCTGGAGAGAGAGAGAGAGAGAGAG 2391
 Db 2179 CCGCTCAGGACATTTG---TGAATGACGAAACACAGAAATGTGTATCATTTAGTGAAG 2235
 QY 2392 CCAAGGCCACAGATTTCTGACAGAGAGAGCGGCGAGTACTTACGCTTCACAGAGAG 2451
 Db 2236 CAAAGACATCAGAGTGTTCAGGAAABAAATCAGAGAGTTCATGATTTATATCAAAAGC 2295
 QY 2452 AGCTTCCCGCATCTACCT 2511
 Db 2296 AACTCAGAGGATTTTACCT 2355
 QY 2512 CTTTCTGAAAGCGCGGTGCGCAATGTGTGCGTGAATCAAGTCAAGAGAGAGAGAGAGAG 2571
 Db 2356 CTTACTGAAAGCGCGGTGCGCAATGTGTGCGTGAATCAAGTCAAGAGAGAGAGAGAG 2415
 QY 2572 TGCAAGTGAACCGAGCCAAAGTTTCAAGCCGAGTGTGCGGCTGACTCAAGCTG 2631
 Db 2416 TGCAAGTGAACCGAGCCAAAGTTTCAAGCCGAGTGTGCGGCTGACTCAAGCTG 2475
 QY 2632 GGTGATGTGCGAGGCGGTGTTCAACCCCACTGCGAGAGAGAGAGAGAGAGAGAGAGAG 2691
 Db 2476 AGCAAAATGTGAAAGTACTTTCACCTTTCTGTGAGACCTTCTCTGCGCAACCCCA 2535
 QY 2692 AGAAGCAGCTGTGCTGCGATCATCAGTGTGCGAGAGCTTCCCAAGCGCGAGTCTCA 2751
 Db 2536 AAAAGCAGCTCATCTTGAAGTTATCAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAG 2595
 QY 2752 TGCTGGGGAACCGTGGGAGATCATCAACCCCTTTGTGAGGTGAGATCATTTGGGCTCC 2811

Db 2596 TGTTTGAGATTCAGGCGGAGATCATTTGACCTTTTGTGAAAGTTGAATTTATGATTC 2655
 QY 2812 CTGTCAGCTCCAGCAGAGGAGCAGACCGCGGTGTGAGACACAAAGGTTCAACCCCACT 2871
 Db 2656 CAGTAGATTTGTTTGAAGATCAAAACCGTGTGTGATGATGATGATGATGATGATGATG 2715
 QY 2872 GGGAGAGACCTGTGTTTTCATGTGTGACATGCGGAGATGCGGTGTCCTCTCTG 2931
 Db 2716 GGGAGAAACACTGACATTTACAGTACATGCGAGAAATAGCTTTGTTGGTTCCTTG 2775
 QY 2932 TCTGGGACCAAGATCCATGCGGCGTGTCACTTTCAGGAGAGAGAGAGAGAGAGAGAG 2991
 Db 2776 TGTGGATCAAGATCCCATGAGAGAGACTTTGTGACAAAGAACTGTGACCTTACGA 2835
 QY 2992 GCATGATGCGAGCTTACAGACAGCTGATCAGAAAGGATGAGAGAGAGAGAGAGAGAGAG 3051
 Db 2836 GCTTAGTGCTGCTGCTACCGCATGTCTATTGGAAGAGACTGACAGAAAGATCATATTG 2895
 QY 3052 TGCAATGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3083
 Db 2896 TACAATPACATCATGAATCTATGAAAG 2927

RESULT 5

AAS77856
 ID AAS77856 standard; cDNA; 5551 BP.

AC AAS77856;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #13660.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HSE-) HXSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB; ABG13669.

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PS Claim 1; SEQ ID No 13660; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (II) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. Aa64197-Aa64564 represent novel human
diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPRO
at ftp.wipro.int/pub/published_pct_sequences.

Sequence 5551 BP, 1659 A, 1214 C, 1203 G, 1475 T, 0 other;

Query Match 16.8%; Score 780; DB 23; Length 5551;
Best Local Similarity 64.4%; Pred. No. 1.2e-137;
Matches 1255; Conservative 0; Mismatches 670; Indels 23; Gaps 5;

1149 GACCTTACCTGCTCATGCTGACCTTACAGCAACCAAGAGACACCTGATCCGCCAGC 1208
1 GACCTTATTTGTTACTTTTGAAGCTACAGTGAAGAAAGATCCTTAAGTGAAGA 60
1209 CTGACGCGCTTCTCGAGGTGAGAGCAAGATGGCGGTGTGACCTCGAGAGCTGCCAG 1268
61 CTGGCTCACTTTTGAAGGTGAGCAAAAGATTAATTAATGACAAACGACTATTGTCTT 120
1269 GACATCATGACGACGATTTGAGCCATGCCCCAGAAACAAAGATTAAGGGCTGCTGGCAT 1328
121 GACATCATTAAGAAAGTTTGAAGTTTCAAGAAAGAAATTAAGTAAAGTTTCTTGACATA 180
1329 GATGCTTACCAACTTACACAGAGCCCTGCTGATGATCTTCAACCTGAGACCCAGC 1388
181 GAAGGCTTACAGAACTTACATGCTGATGCTGCTGATGATTTTAAACCATGACCAT 240
1389 CATGTCACACAGAGATGACAGAGCCGCTGAGCCACTTCTTATCACTCTGCCCAAC 1448
241 GAAGGTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
1449 ACCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
301 ACATACCTGACCTGAGAGACCAAGCTCTTCTCTGATCTTCAAGAGTGAATTAATGAC 360
1509 CTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568
361 CTGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
1569 ATGTCGACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628
421 GATGATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1629 ATCAACAATATGCTTCTGATCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1688
481 ATCAACAAGATGCTTCTGATCAAGATGATGATGATGATGATGATGATGATGATGATGAT 540
1689 TGCAGTGTATCCAGCAGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1748
541 TGCAGTATCCAGCAGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
1749 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
601 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
1809 AAGGCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1868
661 AAGGCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
1869 GAAGGCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1925
721 GAAGGCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
1926 CTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1985
781 CTGAT 840

1986 GATTCCTCATCAAGAGTGAAGATTCGGGACTGTGAGAGACCCCAACAACCTTCTCCGC 2045
841 GATTCCTCATCAAGAGTGAAGATTCGGGACTGTGAGAGAGAGATCTGATGTTTCAAGAG 900
2046 TCCACTGCTGCCATCTGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGA 2105
901 CGGCACT-----ACTGAAGCCAGCATGAAGCTTAAATGACACCTGAGAGAG 953
2106 T-CTGGGAGAGATGCGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2164
954 TCCAGATGTAAG 1013
2165 CAGGCGCAAG 2223
1014 AAAACATTAAG 1073
2224 -----AGGTCAGAGACTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2275
1074 CACAGACAGAGATGATGAG 1133
2276 GACCATGAGCTGCTCCGGGCTCTCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2335
1134 AACCATGAGCTGCTCCGGGAG 1193
2336 CCAAGATGAGATGAG 2395
1194 TCAGAGACTTGG--TGATGAG 1250
2396 GAGCCACAGATTTCTGACAG 2455
1251 AGCAGATCAGGTTGTTCAAG 1310
2456 CTCCGCTATCTACCT 2515
1311 CAGAGAGATTTACCT 1370
2516 CTGAG 2575
1371 CTGAG 1430
2576 GCTGAG 2635
1431 GTTAAACAG 1490
2636 CATGTCAG 2695
1491 AATGTCAG 1550
2696 GCAGCTGATGCTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2755
1551 GACCTCATCTGAAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1610
2756 GGGGAGCCGTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2815
1611 TGGAGATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1670
2816 GGAATGAG 2875
1671 AGATGCTGTAAGATCAAAACCGTGTGTAGATGATGATGATGATGATGATGATGATGATGAT 1730
2876 GGAAGCCGTGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2935
1731 AGAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1790
2936 GGAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2995
1791 GATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1850
2996 GATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3055
1851 AGTGCCTGCTACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1910
3056 TGTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3083


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QY 2106 T-CTGGGAGGATCCGGGGCCAGCAGACGCAATGCGCCCTGTCGTGGAGACTTCTC 2164
DB 1954 TCCAGATGTAAAGAAAGTGAAGAAATTCACATGAGACATCCCTCATCAACACTTTGG 1013
QY 2165 CAGGCCCAAGAAAGAGGCGAGCAAGTGAAGAAAGCGCCAGCGTGGAGAGAGATG- 2223
DB 1014 AAAACATTAAGAAAACTACAAATCAGGTCCTAAATCTTACAGTACATGATGAGAGAA 1073
QY 2224 -----AGGTCAGAGACTCCCCGGGAGCCAGAGCCGAGGGGGGAGCCCCGCAAGAA 2275
DB 1074 CACACAGAGAGTACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1133
QY 2276 GACCATGAAGCTGTCCGGGCGCTCTCTGACCTGTGAAGTACCAAGTCCGTGGCCAC 2335
DB 1134 AACCATGAAGCTGTCCGGGAACTCTGATTTGGTTGGTGTACAAACTCCGTGGCCGC 1193
QY 2336 CCACGACATAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 2395
DB 1194 TCAGAGCATTTG--TGGATGACGAAACACAGAGAAATGTTATCATTCAGTGAAGAAAG 1250
QY 2396 GGGCCACAGATTTGTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2455
DB 1251 AGCAGATCAGTTGTTTCAGCAAAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
QY 2456 CTCCCGCATCTACCCCTCTCTCTACCTGTGATCTTCAGCAACTCAACACCGCAGCCCTT 2515
DB 1311 CACGAGATTTACCCCTCTCTCTACCGCATGATTCAGTAACTTCAACCTCTCCCTCA 1370
QY 2516 CTGAAACCGCGGCTCCCAATGTGTGCTGAACTACAGTACAGAGAGAGAGAGAGAG 2575
DB 1371 CTGGAAGCCAGGCTCCAGCTAGTGGCACTGAATTTATCAATGAGAGACAAATGATGA 1430
QY 2576 GCTGAACCGAGCCAAAGTTGAGCGCCAGCGTGGCTCGGCTACGTAACAGCTGGAGTG 2635
DB 1431 GTTAAACCGAGCCAAATTCAGGCAATGTGGCTATGTCTCAAAACCCAGCA 1490
QY 2636 CATGTCAGAGGCGGTGTTCAACCCCACTCGAGAGAGACCCCTGCGCGGAGCTCAAGAA 2695
DB 1491 AATGTGCAAAAGTACTTTCAACCCCTTTCTGTGAGACCTCTTCTCTGCAACCCCAAAA 1550
QY 2696 GCAGCTGTGTCTCGGATCATGAGTGGCCAGCAGCTTCCCAAGCCGCGAGCTCATGCT 2755
DB 1551 GCAGCTCATCTGAAAGTTATCAAGTGAAGCAACTCCCAAACTCCAGACTCATGTT 1610
QY 2756 GGGGAGCCGTGGAGAGATCATGACCCCTTTGTGAGGTGAGATCATTTGGCTCCCTGT 2815
DB 1611 TGGAGATCGAGGCGAGATCATTTGACCCCTTTGTGAGGTGAGATCATTTGGATTCAGAT 1670
QY 2816 GAGCTGACAGCGAGAGAGACCCGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2875
DB 1671 AGATTTGTTAAAGATCAAAACCCGTGTGTGATGACAAATGAGATTTAAACCTGTGTGGA 1730
QY 2876 GAGAGCCCTGTTTTCATGTGTGACATGCGGAGATCGCGTGTCTCGCTTCTGCTG 2935
DB 1731 AGAAACCTACATTTTACAGTACATGCAAGAAATAGCTTTGGTTGGTTCCCTTGTGTG 1790
QY 2936 GAGACCATGATCCCATGCGGGGTGACTTATTTGGCCAGAGAGAGAGAGAGAGAGAG 2995
DB 1791 GGATCAGATCCCATTTGAGAGAGCTTTGTTGAGCAAAAGAACTGTGACCTTTCAGAGCTT 1850
QY 2996 GATGCCAGGCTACAGACAGCTGTACTAGAAAGGATGAGAGAGAGAGAGAGAGAGAG 3055
DB 1851 AGTGCCTGGCTACCGGAGATGTCTATTGGAAGAGCTACAGAAAGCATCATATTTTGTA 1910
QY 3056 TGTGTGCTGTAGTGAATCATGCGGTGAAG 3083
DB 1911 CATTAACCATCAATGAATCTATGAAAG 1938

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RESULT 7
AAH17609
ID AAH17609 standard; cDNA; 1977 BP.
XX

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AC AAH17609;
XX
XX 26-JUN-2001 (first entry)
DE Human cDNA sequence SEQ ID NO:17123.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuka T;
XX WPI; 2001-318749/34.
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX PS Claim 8; SEQ ID 17123; 2537bp + CD ROM; English.
XX
XX CC The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
XX AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX SQ Sequence 1977 BP; 634 A; 429 C; 457 G; 457 T; 0 other;
XX
XX Query Match 11.8%; Score 545.2; DB 22; Length 1977;
XX Best Local Similarity 61.5%; Pred. No. 1.8e-93;
XX Matches 987; Conservative 0; Mismatches 588; Indels 29; Gaps 6;
XX
XX QY 1675 CCATCGAAACCACTGACGTCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1734
XX DB 1 CTATCGAATCACTGACGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
XX
XX QY 1735 TCTTGGGAGCAAGCTGAGCTGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1794
XX DB 61 TATTCGAGAGCAAACTGAGACTGTCTGTGTATACAGGGAGGTGACAGAGCTTCCAA 120

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QY 1795 CTCACAGATGCTCAAGGCGAAGATCCTGTAAGGGAAGAGCTCCGACCAATCA 1854
 DB 121 GCCCTCAAAAGTTGAAAGGCAAAATCTAGTGAAGGTAAAGAGTTGCTTATCACTTG 180
 QY 1855 GCGAGATGCGAGGAAGGCGAGGTGTGATGAGACAGTGTGATGATTAAGATG 1914
 DB 181 GGGATGATGAGGAAGGGAAGTTCCGATGAGGACAGTGCAGATGAATTTGAAGAG 240
 QY 1915 ACTGCAAGCTC---CTCATGGGATGATCCCAATGAAACCTGTAAAGAAACAGT 1971
 DB 241 AGTGAATTCAGCTTCATTAATATGATGAGGACCACTAGACATCGGTGAATCTTTCA 300
 QY 1972 CTAAAGGAATTCAGATTCCTCATCAAGAGTCAAGATTCGGAGCTGTGAGACCCCA 2031
 DB 301 TAAGAAAAAATCTGAGTCTCTTTAAAGAAATCTCAATTTGAGATTAAGAAATCTG 360
 QY 2032 ACAATCTTCTCGTCTCAACCTGTCCCATCTGGAAGAGTCCGACCAAGAGAGCTG 2091
 DB 361 ATAGTTTCAAGTGGGGGACT-----ACTGAAGGCCACGATGAAGGCTTAAATGCA 413
 QY 2092 AAGAGACGTGAGTCTGG--GAGAGATGCCGGGCGACAGACGCAATGGCCGCTGTC 2150
 DB 414 CACCTGAAGAGATCTCAAGTGTAAAGAAAGTGAAGAAATCAATGATGATGATCTTC 473
 QY 2151 GTGGGAAGCTTCTCCAGGCGCAAGAAAGGCGACAGCTGAAGAGGCGGCGACGCTG 2210
 DB 474 ATGACCACTTTGGAAAAAATTAAGAAATCAAAATCAAGCTTAATCTTAACATCTAC 533
 QY 2211 GAGAGGAGATGAGGTGACGACTCCCC-----GGAGGCCAAGCCGAGGGGCG 2261
 DB 534 GATGATGAGGAACACACAGCAGAGTACTGGCAGAGGGGTGGCCAGCTGTACATATG 593
 QY 2262 ACCCGGAGAAAGAACCAATGAAGCTGTCCGGGCCCTCTCAACCGGTGAATACCC 2321
 DB 594 GGTGCGGAGAAAGAAACCAATGAAGCTGTCCGAGAAATCTCTATTTGTTGTTGAC 653
 QY 2322 AAGTCCGTGCGCAACCCAGCATAGAGATGAGAGCGGCGCTCCAGCTGAGTGTGCTC 2381
 DB 654 AACTCCGTGCGCGTCAAGCATTTG---TGGATGACGGAACCAAGAAATGTGTTATCA 710
 QY 2382 TTGAGCGAGACCAAGGCGCCAGATTTCTGACAGAAAGCCGCGCAGTACTTACGCTTC 2441
 DB 711 TTGAGTAAACAAAGACACATCAGTGTGTTCAACAAATCAAGACGTTCAATGATTTAT 770
 QY 2442 AACGAGAGAGCTCTCCGCAATCTACCCCTCCCTACCGTGTGAGTCTCAGACAACTAC 2501
 DB 771 AATCAAAAGCAATCTCAGAGATTTACCCCTCTGCTTACCGCATTTCAATCAATCTTC 830
 QY 2502 AACCCGAGCCCTTCTGGAAGCGCGGCTGCAATGTTGCTCCCTGAATCACTACATGAG 2561
 DB 831 AACCCTCTCCCTTACTGGAAGCGAGGCTGCGCATGTAAGTATTCATATCTGAA 890
 QY 2562 GGGCGATGCTGCACTGAACCGAGCCAAGTTCAAGCCCAAGTGTGCTGCGCTACGTA 2621
 DB 891 GGAAGATGATGAGTAAACCGAGCCAAATTCAGGCAATGTGCTATGTC 950
 QY 2622 CTGAAGCTGGGTGATGTCGCGAGGGGTGTTAAACCCCAATCGAGAGACCCCTGAGCC 2681
 DB 951 CTGAAGCCCAAGAAATGTGAAGTACTTTCAACCCCTTCTGTGAGACCTCTTCTCT 1010
 QY 2682 GGGAGCTCAAGAAAGCAGTGTGCTCCGATCATCATGAGGCGACAGCTTCCAAAGCCG 2741
 DB 1011 GCGAAGCCCAAGAAAGCAGTGTCTGAAAGTTATCATGTGGAAGCAATCTCCCAAACT 1070
 QY 2742 GCGCATCTCATGCTGGGGGACCGTGGGAGATCATCAACCCCTTGTGTGAGGTGAGATC 2801
 DB 1071 CCAAGATCTCATGTTGAGATCGAGGAGATCATTTGACCCCTTGTGTGAAGTTGAAAT 1130
 QY 2802 ATTGGGCTCCCTGTGAGACTGACAGAGGAGACAGCCGCGTGTGAGACGAAACGAGGTT 2861
 DB 1131 ATTGGATTTCCAGTATGATTTGTTGTAAGATCAAAACCGGTGTGTGATGACAAATGAT 1190
 QY 2862 AACCCACCTGTGAGAGACCTGTGTTTCAATGTGCAATGCCGAGATCGCGCTGCTG 2921

DB 1191 AACCTGTGTGGAAGAAACCTGACATTTACATGATGACATGCGCAAAATAGCTTGTG 1250
 QY 2922 GCGTTCCTGCTGTGGAGCAACATCCCATCGGGGTGACTTTCATTTGSCAGAGAGCTG 2981
 DB 1251 CGGTCTCTGTGTGATTCAGATCCATTTGACGAGACATTTGTTGACAAAGAACTGTG 1310
 QY 2982 GCGTTCAGCAGCATGATGCCAGCTACAGACAGTGTACTAGAAAGGATGGAAGAGGCC 3041
 DB 1311 ACCTTCAGACACTTAGTGTGCTGCTACCGGATGTCTATTGGAAGGACTGACAGAGCA 1370
 QY 3042 TCCATCTTGTGCAATGTGCTGTGATGATCAAGCGGTAAAGTCAAGCAGCTTGTGGC 3101
 DB 1371 TCCATATTGTACACATTAACATTAATTAATTAATTAATTAATTAATTAATTAAT 1430
 QY 3102 CTAAAGGCGCTCTTCTCCGAGGCGCAAGCGCGCTGCTGACAGTCACTGTGCTGGG 3161
 DB 1431 CTGAAGGAGACTGTTCATTAATTAATTCCTAGGACAGTCTTCAAGAAACATTTCCAT 1490
 QY 3162 CGGCCCCCGGCGCCCTCCGTTAGCCAGGATCTGCGGCGCAGCGCCGCGCCG 3221
 DB 1491 GTAC-----GGAAGCATTCATTGAGATGAATTTCTGCGACGACAGCTAGCGCCCA 1544
 QY 3222 ACCAAGACCCAGAACCGGCGCGGCGGCTTCCCGAGCTGTG 3265
 DB 1545 GCCAAGGCGAGGAAAAAGAGCAAAATGGGCTTCCAGAAATAGT 1588
 RESULT 8
 ABK71572
 ID ABK71572 standard; cDNA; 534 BP.
 XX
 AC ABK71572;
 XX
 PT 30-JUL-2002 (first entry)
 XX
 DE Human dithp polynucleotide #38.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
 KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 KW inflammatory disorder; viral infection; bacterial infection; seizure;
 KW fungal infection; parasitic infections; developmental disorder; breast;
 KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
 KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
 KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
 KW skin; testis; thymus.
 XX
 OS Homo sapiens.
 XX
 PN WO20020754-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US27127.
 XX
 PR 05-SEP-2000; 2000US-229747P.
 PR 05-SEP-2000; 2000US-229748P.
 PR 05-SEP-2000; 2000US-229749P.
 PR 05-SEP-2000; 2000US-229750P.
 PR 05-SEP-2000; 2000US-229751P.
 PR 05-SEP-2000; 2000US-230583P.
 PR 05-SEP-2000; 2000US-230585P.
 PR 05-SEP-2000; 2000US-230514P.
 PR 05-SEP-2000; 2000US-230515P.
 PR 05-SEP-2000; 2000US-230517P.
 PR 05-SEP-2000; 2000US-230518P.
 PR 05-SEP-2000; 2000US-230519P.
 PR 05-SEP-2000; 2000US-230597P.
 PR 05-SEP-2000; 2000US-230598P.
 PR 05-SEP-2000; 2000US-230599P.
 PR 05-SEP-2000; 2000US-230610P.
 PR 05-SEP-2000; 2000US-230655P.

Query Match	Best Local Similarity	Score	DB	Length
Matches 477; Conservative 0; Mismatches 57; Indels 0; Gaps 0;	9.6%;	442.8;	DB 24;	534;
Sequence 534 BP, 125 A; 154 C; 140 G; 115 T; 0 other;				
Query 1107	GAAGGTTCTGCTTCTTACAAAGATGATGTCACCCCGCGGACCTTACTGCTCATG	1166		
1	GAGGAATTCCTGGCCTTCTTACAAAGATGATGTCACCTCGCGGACCTTACTGCTCATG	60		
Query 1167	CTGACCTACAGAACCAACAAGAGACCACTCGAATGCGCGAGCTCGAGGCTTCCGAG	1226		
Db	CTGACCTACAGAACCACTTAAAGACCACTTGAATGCTTCCGACCTGACGCTTTTGTGAG	120		
61	CTGACCTACAGAACCACTTAAAGACCACTTGAATGCTTCCGACCTGACGCTTTTGTGAG	120		
Query 1227	GTGAGCAGAAAGATGCGGGGTGTGACCTCTGAGAGCTGCGAGACATCATCGAGCAGTTT	1286		
Db	GTGAGCAGAAAGATGCGGGGTGTGACCTCTGAGAGCTGCGAGACATCATCGAGCAGTTT	180		
121	GTGAGCAGAAAGATGCGGGGTGTGACCTCTGAGAGCTGCGAGACATCATCGAGCAGTTT	180		
Query 1287	GAGGCATGCCAGAAACCAAGAGTAAAGGGGCGTGGGATGATGAGGCTTCAACCAATAC	1346		
Db	GAGGCATGCCAGAAATTAAGACCAAGGGGTGTGGGATGATGAGGCTTCAACCAATAC	240		
181	GAGGCATGCCAGAAATTAAGACCAAGGGGTGTGGGATGATGAGGCTTCAACCAATAC	240		
Query 1347	ACGAGAGCCCTGTGCTGTGACATCTTTCAACCTTGAGACCAACCATGTGACACGAGACATG	1406		
Db	ACGAGAGCCCTGTGCTGTGACATCTTTCAACCTTGAGACCAACCATGTGACACGAGACATG	300		
241	ACGAGAGCCCTGTGCTGTGACATCTTTCAACCTTGAGACCAACCATGTGACACGAGACATG	300		
Query 1407	ACGAGAGCCCTGTGAGCCTACTTATTCACCTGTGCTCCACAAACCTACTCTGTGGTGAAC	1466		
Db	ACGAGAGCCCTGTGAGCCTACTTATTCACCTGTGCTCCACAAACCTACTCTGTGGTGAAC	360		
301	ACGAGAGCCCTGTGAGCCTACTTATTCACCTGTGCTCCACAAACCTACTCTGTGGTGAAC	360		
Query 1467	CAGCTCATGTCCCACTACAGGGGTGACATGTATGTGGTCTCTCAGGCTGAGTGGCGGC	1526		
Db	CAGCTCATGTCCCACTACAGGGGTGACATGTATGTGGTCTCTCAGGCTGAGTGGCGGC	420		
361	CAGCTCATGTCCCACTACAGGGGTGACATGTATGTGGTCTCTCAGGCTGAGTGGCGGC	420		
Query 1527	TGCGTGAAGGTGACCTGCTGGATGGCCGACGCGGAGGCCATTTGTGCACCATGGCTAC	1586		

Dd 421 TGTGTAAGTGGACTGGATGGCCTCGATGGGAAACCATTTGTCACCAATGGCCTAC 480

Oy 1587 ACTCGACTTCCAAGATCCTCTTCAAAGAAGCGTCATTGAAAACATCAACAATAAT 1640
|||||
|||

Db 481 ACTGCAGCTCCAAGATCCTTTTCAAAGATGTCATGGAAACCATCAACAAATAT 534
|||||
|||

RESULT 9
AAD31082/c
ID AAD31082 standard; cDNA; 646 BP.
XX
AC AAD31082;
XX
DT 26-JUL-2002 (first entry)
XX
DE Human PI-PLC-like enzyme expressed sequence tag #1.
XX
KW Human; phosphatidylinositol-specific phospholipase C-like enzyme;
KW PI-PLC-like enzyme; chromosome 3; asthma; cancer; central nervous system,
KW CNS disorder; Parkinson's disease; dementia; COPD; protein therapy;
KM chronic obstructive pulmonary disease; gene therapy; vaccine;
KN expressed sequence tag; EST; ss.

Os Homo sapiens.
Ox
PN W0200226996-AZ.
PX
PD 04-APR-2002.
PF 24-SEP-2001; 2001WO-BP11012.
PR 27-SEP-2000; 2000US-235552P.
PS
PA (FARB) BAYER AG.
XX
PI Zhu Z;
DR WP1; 2002-372128/40.
XX
XX
PT Isolated polynucleotides encoding human phosphatidylinositol-specific
PT phospholipase C-like enzymes, useful for preventing, diagnosing and
PT treating e.g. asthma, cancer, a CNS disorder or chronic obstructive
PT pulmonary disease -
XX
XX
PS Disclosure; Fig 4; 125bp; English.
XX

The invention relates to polynucleotide encoding human phosphatidylinositol-specific phospholipase C-like enzyme (PI-PLC-like enzyme). Human PI-PLC-like enzyme gene is located on chromosome 3. The PI-PLC-like enzyme polypeptide and polynucleotide may be used in the prevention, diagnosis and treatment of diseases associated with enzyme dysfunction, e.g. asthma, cancer, central nervous system (CNS) disorder (e.g. Parkinson's disease, dementia) and chronic obstructive pulmonary disease (COPD). The polynucleotide and polypeptide may be used to treat disorders associated with decreased PI-PLC-like enzyme expression by rectifying mutations or deletions in a patient's genome that affect the activity of PI-PLC-like enzymes, by expressing inactive proteins or to supplement the patients own production of PI-PLC-like enzymes. The polynucleotide and its complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples. The PI-PLC-like enzymes may also be used as antigens in the production of antibodies and in assays to identify modulators of PI-PLC-like enzyme expression and activity. The anti-PI-PLC-like enzyme antibodies and antagonists may be used to down-regulate expression and activity of CC the enzyme and as diagnostic agents for detecting the presence of PI-PLC-like enzyme in samples. The present sequence is human phosphatidylinositol-specific phospholipase C-like enzyme encoding expressed sequence tag (EST).

XQ Sequence 646 BP; 168 A; 161 C; 136 G; 181 T; 0 other;

Query Match 7.1%; Score 328; DB 24; Length 646;
Best Local Similarity 71.2%; Pred. No. 1.3e-52;
Matches 433; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 1318 TCGTGGGCAATTGATGGCTTACCACTACACAGAGCCCTGCTGATCATCTTCAACC 1377
DB 636 TTTCTTGGATAGAAAGCTTACGAACTTCATGCTGCTGCTGATCATATTTAAAC 577

QY 1378 CTGAGACCACTGATGACCAAGACATGACCGCGGTGAGCCATCTTCAACCT 1437
DB 576 CATTTGACCATGAAAGTATCAAGACATGATGAGCCCTCTGCAACTTATCTTCTT 517

QY 1438 CGTCCCAACCACTGATGCTGCTGATGACGATGCTGCTGCTGCTGCTGCTGCT 1497
DB 516 CCTCTCACTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 457

QY 1498 ATGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
DB 456 ATGACAGGGGTGCTGCAAGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397

QY 1558 ACGGGAGCCCATTTGTCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
DB 396 ATGAGAGCCAGTATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337

QY 1618 TCATTGAAACCATCAACAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677
DB 336 TTTGTGAGACATCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277

QY 1678 TCGAAAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737
DB 276 TCGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 217

QY 1738 TTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1797
DB 216 TCGAGACCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 157

QY 1798 CACAGATGCTCAAGGGCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857
DB 156 CTGAAAGTTGAAAGGCAAAATTTCTAGTGAAGGTAAGAGTTGCTTATCACCTT 97

QY 1858 AGGATGCGAGGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1917
DB 96 ATGATGACAGGAGGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 37

QY 1918 GCAAGCTC 1925
DB 36 GCAAAATTC 29

RESULT 10
AAH16211
ID AAH16211 standard; cDNA; 3263 BP.

XX AAH16211;
AC
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:15019.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
PS
PS
XX
XX Claim 8; SEQ ID 15019; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 3263 BP; 829 A; 820 C; 888 G; 726 T; 0 other;

Query Match 7.0%; Score 323.4; DB 22; Length 3263;
Best Local Similarity 50.7%; Pred. No. 1.3e-51;
Matches 1013; Conservative 0; Mismatches 916; Indels 70; Gaps 7;

QY 1085 CCACCAAGGAGCGCTGGTGTGAGAGTCTGCTTCTTACAGATGATGCCACCG 1144
DB 590 CCAAGTCTGGAACCTTGAAGAGGAGGAGGATTTGATCAAGTTATAGGATGACCTAAACG 649

QY 1145 CCGGAGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
DB 650 TCGTGAAGTGAAGAACTGTTGAAAGTTTTCAGCTGATGGGCGAAGCTGACTTGCT 709

QY 1205 CAGCTGCAAGCGCTTCTGCAAGTGGAGCAGAAATGCGGGGTGACCTCGAGAGCTG 1264
DB 710 GGAATTTTGAATTTCTTCCAGAGAGCAGAAAGAGAGAGCTGCACTTCTGACCTTGC 769

QY 1265 CCAGGACATCATGAGCAGATTGAGCCATGCCCAGAAAAACAAGATMAAGGGCTGCTGGG 1324
DB 770 TCTGGAACCTATGACCCGTATGAACCTTTCAGACAGTGGCAAACTGGCGCATGTCTGAG 829

QY 1325 CATTTAGTCTTACCAACTATACCAAGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 1384
DB 830 TATGATGCTTCTTCAGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889

QY 1385 CCACCATGTCACCAAGGACATGAGCGAGCGCTGAGCCACTTCTATCACTGCTGCCA 1444
DB 890 CCTCCCATCTATTCAGAGATATGATCTAACCTCTGAACCACTACTTCTGCTTCTCA 949

QY 1445 CAACACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1504
DB 950 TAAACACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009

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QY 1505 GGTCTGCAAGGCTGGCTGCGCTGCTGGAGGTGACTGCTGGATGGGCGCCGACGGGGA 1564
DB 1010 GGGCCCTGAACGGGGGGTGGCTGGCTGGAGGTGATGTATGGGATGAGCTTAAACGGGGA 1069
QY 1565 GGGCATTTGTGACACATGAGTACACATCTGACTTCCAGATCTCTTCAAAAGACGTGATGA 1624
DB 1070 ACCTGTGCTTACACAGGACACACCTGACCTCCGGCATCTCTTCAAAAGATGCTGGAC 1129
QY 1625 AACCATCAACAAATATGCTTCTCATCAAGAAATGATACCAATGATCTCTGATCAAGAAA 1684
DB 1130 CACAGTAGACACAGTATGCTCTTCCAGATCAGACTACCCAGTATCTCTCTGAGAC 1189
QY 1685 CCATGAGTGTATCATCAGACAGAAATAATGGCCAGTATCTGACTGATCATCTTGGGGA 1744
DB 1190 CCATGAGTGTGAGACAGACAGACACATGGCCGCTCATCTGACTGATCATCTTGGGGA 1249
QY 1745 CAAGCTGAGCTGTATCATGATGACAGTGAAGATGACCAACACTCTCTCTCAAGAT 1804
DB 1250 GCGAGCTGTGAGACCACTTGGATGGGGTGTGCCCATCTGAGCTGCTCTGAGGGA 1309
QY 1805 GCTCAAGGCGAATATCTGTGAAAGGGAAGAAAGCTTCCAGCCACATCATGAGAGATGC 1864
DB 1310 GCTTCGAGAGAAATCTGTGTGAAGGGAAGAAATTAACATTTGAGGAACCTGGAATA 1369
QY 1865 GGAGAAAGCGAGGTGTGTGATGAGACAGTGTGATGATGATGATGATGATGATGATGATG 1924
DB 1370 TGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1429
QY 1925 CCTCAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1982
DB 1430 TGAGAGTGTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1489
QY 1983 -----CTGATTCCTCATCAAGAGTGAAG----- 2009
DB 1490 CAAGCCATCTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1549
QY 2010 -----ATTGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
DB 1550 CCGAGAGCTTACACATATTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1609
QY 2063 TGGAAAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2122
DB 1610 AACCAAGGCGAAGCGCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1669
QY 2123 GGCCAGCAGACCAATGAGCGCGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2182
DB 1670 GGAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1729
QY 2183 C-AGCAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2241
DB 1730 CAAGGTAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1789
QY 2242 GAGGCGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2301
DB 1790 GAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1849
QY 2302 CTGACCTG-----TGAAGTACACCAAGTCCGTGAGAGAGAGAGAGAGAGAGAGAG 2351
DB 1850 AGAGAGGACACATGAACTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1909
QY 2352 GAGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2410
DB 1910 TAGGAGAGGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1969
QY 2411 -----GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2466
DB 1970 TATACCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2029
QY 2467 ACCCTCTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2526
DB 2030 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2089
QY 2527 GCTGCAATATGTTGCTCTGAACTACAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 2586

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DB 2090 GGTCCAGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2149
QY 2587 CCAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2646
DB 2150 GGCATTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2209
QY 2647 GCGTGTCAACCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2706
DB 2210 TCCAGAGTCTTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2269
QY 2707 TCCGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2766
DB 2270 TCCAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2325
QY 2767 GGGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2826
DB 2326 -----ATTGAGATCCAGCTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2380
QY 2827 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2886
DB 2381 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2440
QY 2887 TTTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2946
DB 2441 GTTTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2500
QY 2947 CCA---TCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3003
DB 2501 GGAATATCCGAAATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATG 2560
QY 3004 GCTACAGACAGCTGATCT 3022
DB 2561 GTTACGCGACATTCACCT 2579

RESULT 11
AADI7564
ID AADI7564 standard; cDNA; 2289 BP.
AC AADI7564;
DT 10-DEC-2001 (first entry)
XX
DE Novel human phospholipase cDNA #8.
XX
KW Human; novel human protein; NRP; phospholipase protein; phospholipid;
KW phospholipase C delta-4; cell activation; signal transduction; cancer;
KW drug screening; biological disorder; mental disorder; medical disorder;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2289
FT /tag=a
FT /product="Human phospholipase #7"
XX
PN WO200168871-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US07994.
XX
PR 13-MAR-2000; 2000US-0188885.
XX
PR 15-MAR-2000; 2000US-0189693.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B, Donoho G, Hilpun E, Turner CA, Abuin A;
PI Friedrich G, Zambrówicz B, Sands AT;
XX
XX WPI; 2001-582456/65.

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DR P-PSDB; AAEL10440.

PT New polynucleotides encoding human phospholipase protein involved in
PT cell activation and signal transduction, useful for drug screening,
PT diagnosis and in gene therapy of biological disorders -
XX
PS Claim 8; Page 40-41; 45pp; English.

The present sequence is a cDNA encoding novel human protein (NHP), phospholipase protein. Phospholipases hydrolyse phospholipids and play a key role in the cell activation and signal transduction. NHPs share structural similarity with animal phospholipases, including phospholipase C delta-4. NHP oligonucleotides are useful in conjunction with polymerase chain reaction (PCR) to screen libraries, isolate clones, and prepare cloning and sequencing templates, and alternatively as hybridisation probes for screening libraries and assessing gene expression patterns. They are used in the identification, selection and validation of novel molecular targets for drug discovery, where identification and characterisation of human genomic clones is helpful for identifying polymorphisms, determining the genomic structure of a given locus/allele and designing diagnostic tests. The microarray comprising NHP cDNA is useful for screening collections of genetic material from patients having a particular medical condition, which is used to identify mutations associated with a particular disease and also as diagnostic or prognostic assay. NHP nucleotide sequences are useful for drug screening. Nucleotide construct encoding NHP products are used in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products *in vivo*. The NHP sequences are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. They can be used to therapeutically augment the efficacy of chemotherapeutic agents used in the treatment of breast or prostate cancer.

SQ Sequence 2289 BP; 568 A; 588 C; 623 G; 510 T; 0 other;

Query Match	6.7%;	Score 308.6;	DB 22;	Length 2289;
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Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2.

QY	744	TTTCAAGGCTACCTCGACGGGAGCTTGACCCCAATGCTGGCTTTGAGCATTTACACGAGC	803
Db	229	TTTGCTGCTAGCTCGGACAGAGAGACTCCCCCTTGAGACGAGGCTTACCACTGTCTTCCAT	288
QY	804	AAGCAACCGCGAGTGGCTGAGACTTGTCTCCACAGCAGCGAGGTGGCGGCACTGGGCTC	863
Db	289	GGGCGCGCTCCAACTTGGACTGATGGCCAAAGTGTGAGGAGGCGCAGATTATGATG	348
QY	864	ACTGCTCTGCGCTACTCTCATAGGCCGGGATATAGCGACGAGACAGCTGGCTGTGGCGGACG	923
Db	349	CGAGGGCTTCAGACTGTGTGGATCTTTGTACACAGCATGGACCATAGGAGCGCCT----	404
QY	924	CGCACACAGGACCGAGTGGCTTAACAGACGTTTTCAGGAGGCCGACAAAGAACGGGATGGC	983
Db	405	-----GGACCAATGGCTGAGGGAATTGGTTTCAACGTGGAGACAAAATCAGATGGT	456
QY	984	AGCTTGAGACTTTGGCGAGAGTCTCTGACTGTGTCACAGCTCAACTGAACTGCTCCCGG	1043
Db	457	AAGATGACTTTTCCAAAGATTCACACGGGTATTGGACTTAATGATGTGAAAATGACCA	516
QY	1044	CAGAGGGTGAAGCAGATTTTCAGGGAAGCGGACACGGATATCCACCAAGGACGCTGGGT	1103
Db	517	GAAATGCTTTCAGTCTTTTTCAGGACAGACACG---TCCCAAGTGTGAACCTCGGAA	573
QY	1104	TTTGAAGAGTTCTGTGCTTTCTTCAAGATGATGTCAACCCCGGGAAGCTTTACTGCTC	1163
Db	574	GGAGAAAGATTGTCACAGTTCTATTAGGCAATTGACTAAAGTCTGAGGTCAGAGAACTG	633
QY	1164	ATGCTGACCTTAAGAACACCAAGAGCACACTGGATGCGCCGACGCGTCAGCGCTCTCG	1223
Db	634	TTTGAAGATTTTTCAGCTGATGGGCGAAGTACTCTGCTGGAAATTTTGGATTTCTTC	693

QY	1224	CAGGTGAGCACAAGATATGCGGGTGTGACCTCGAAGAGCTGCAGAGACATCATCGAGAG	1283
Db	694	CAGAGAGACAGAAAGAGAGAGACTGCACCTCTGAGCTTGTCTGGAACTCATTTGACGCG	753
QY	1284	TTTGAACCATGCCAGAAAAAAGAGATGAAGGGGCTGTGGGACTTATGAGCTTACCACAC	1343
Db	754	TATGAACCTTTACAGACAGTGGCAAACTGGCGGACATGTGCTGATGTGATGAGCTTCCACG	813
QY	1344	TACACAGAGAGCCCTGTGTGTGACATCTTCAACCTCGAGAGACCAACATGTGGACAGAGAC	1403
Db	814	TACCTTGTCTTAAGAGATGGAGACATCTTCAACCAACACCTGCTCCCACTCATACAGAT	873
QY	1404	ATGACGAGCGCGTGAGCCACTACTTCACTCACTCGTCCCAACAACCTAATCTGTGGT	1463
Db	874	ATGATCTCAACCCCTGAACCACTACTTCACTCTGCTCTTCTATTAACACTTACAGTGGGG	933
QY	1464	GACCAAGTCATGTCCCAAGTCACGGGTGACATGTATGCTTGGTCTCGACGGCTGTGC	1523
Db	934	GACCAAGCTTTGGCGGCGAGAGCAGCTCTCAGGGAATATATACGGGCGCTTGAAGCGGGGTGC	993
QY	1524	CGCTGGGTGAGGGTGGACCTGCGGGGATGGGCGCAGCGGGAGGCCATTGTGCACATGAGC	1583
Db	994	CGCTGGGTGAGGGTGGATGTATGGATGACCTTACGGGGAACCTGTCTTTACACGGA	1053
QY	1584	TACACTCTGACTTCCAAAGTCTCTTCCAAAGACGTCAATTGAACCATCAACAATATGCG	1643
Db	1054	CACACCTGTACCTCCCGCATCTGTTCAAAAGATGTCGTGGCCACAGTACACAGTATGCG	1113
QY	1644	TTTCATCAGAATAGTATCCCAATGATCTCTGTCCATCGAAAAACAATGTGCATCTCAG	1703
Db	1114	TTCCAGACATCAAGACTACCCCACTCATCTTGTCTCTGGAGACCCAATGCACTGGGAGCAG	1173
QY	1704	CAGAAGAAATGGCCAGATGTGACTGACATCTTGGGGAACAAGCTGACCTGTATCA	1763
Db	1174	CAGCAAGCATGAGCCCGTATCTGACTAGATCTGTGGGGAAGAGAGCTGTGAGACACAC	1233
QY	1764	GTGAGCAGTGAAGATCCACCACTCTCCCTCTCCACAGATGCTCAAGGGCAAGATCTTC	1823
Db	1234	TTGGATGGGGTGTGCTGCCACTCAGCTGCGCTGCCTGAGGAGCTTCCGAGGAAGATCTTG	1293
QY	1824	GTTGAAGGGGAAGAAAGTCTCCAGCCACAATCAGCAGAGATGCGAGGAAGGCGAGTGTCT	1883
Db	1294	GTTGAAGGGGAAGAAAGTTAACCTTGAAGAGACCTGGAAATATGAGGAAGGAGAACAGAA	1353
QY	1884	GATGAGGACAGTGTCTGATGAGATTTAGCATGACATGCAAGCTCTCATGTGGGATGTGATCC	1943
Db	1354	CTTGATTTGGAAGATCAGAAATTTGGCGCTGAGATGCCAGTTTGAAGCTGAGCCTGAGCCC	1413
QY	1944	ACCAATGAAAGCGTGAAGAAAACCTGCTAAGAGGAAACTGAGATTCTCTCAT	1996
Db	1414	CAGAGCAGAACTTCAGAATATAGACAAAAAAGAAATATCAAGCCCATCTT	1466
RESULT 12			
AAD23721			
ID	AAD23721 standard; DNA; 2289 BP.		
AC	AAD23721;		
XX	07-MAR-2002 (first entry)		
DE	Human phospholipase C delta 5 (PLCD5) DNA #1.		
XX	Human; phospholipid C delta 5; PLCD5 protein; deep vein thrombosis;		
KM	angina pectoris; percutane transluminal coronary angiography; PTCA;		
KM	thrombo embolic insult; disseminated intravascular coagulation;		
KM	arteriosclerosis; epilepsy; depression; neurodegenerative disease;		
KM	stroke; rheumatoid arthritis; immune disorder; chromosome localisation;		
XX	vaccine; gene therapy; ds.		
OS	Homo sapiens.		
XX			

Key Location/Qualifiers
 CDS 1..2289
 FT 1.2289
 FT /+tag= a
 FT /product= "Human PLCD5 protein"
 PN MO200183771-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 27-APR-2001; 2001MO-EP04784.
 XX
 PR 29-APR-2000; 2000EP-0109318.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Brandt S, Duecker K, Gietz J;
 DR MPI; 2002-034515/04.
 DR P-PSDB; AAB14268.
 XX
 PT New phospholipase C delta 5 polypeptides, useful for treating deep vein
 PT thrombosis, instable angina pectoris, percutane transluminal coronary
 PT angiography, disseminated intravascular coagulation and epilepsy -
 XX
 PS Claim 4; Page 34-37; 51pp; English.
 XX
 CC The patent discloses phospholipid C delta 5 (PLCD5) proteins and their
 CC corresponding polynucleotides. PLCD5 sequences are useful for treating
 CC deep vein thrombosis, instable angina pectoris, percutane transluminal
 CC coronary angiography (PTCA), thrombo embolic insult, disseminated
 CC intravascular coagulation, arteriosclerosis, epilepsy, depression,
 CC neurodegenerative diseases, stroke, rheumatoid arthritis and immune
 CC disorders. PLCD5 sequences are also useful as vaccines for inducing
 CC immunological response in a mammal. PLCD5 DNAs are also useful for
 CC chromosome localization studies, as valuable tools in tissue expression
 CC studies and in gene therapy. The present sequence is a DNA encoding
 CC human PLCD5 protein.
 XX
 SQ Sequence 2289 BP; 568 A; 587 C; 623 G; 511 T; 0 other;

Query Match 6.7%; Score 308.6; DB 24; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 7.3e-49;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

QY 744 TTCCAGGCGTACCGCTGACGCGACGCTTCGACCCCACTGCTGCTTCAGCATCAACCGGC 803
 DB 229 TTCTGTGTAGCTGCGACGAGGCTCCCTGACGAGGCTTCACTGTCTTTCAT 288
 QY 804 AGCCACCGCAGTCTGTGACCTGTCTCCACGACGAGGTGCGGCACTTGGTC 863
 DB 289 GGCCTGCGCTCCAACTGGACCTGATGGCCCAAGTGTGAGGAGGCCAGATATGGATG 348
 QY 864 ACTGGCTGTGCTAATCTATGCGCGCATGAGGACGAGGACAGCTTGGCTGCCGCCAG 923
 DB 349 CGAGGCTCTCAGCTGTGGATCTTGTCAACGATGACCATGAGAGGCGCT--- 404
 QY 924 CGCACCAGGACCGAGTGTGTAAGCAGACGTTGACGAGCGCCCAAGAACCGGGATGGC 983
 DB 405 -----GACCAATGGCTGAGCGATGTGTTCAACGTGAGACAAATAACGATGGT 456
 QY 984 AGCTTGAGCATTTGGGAGGTCTCTGAGCTGTGACAACTCAACGTGAACCTGCCCGG 1043
 DB 457 AAGATGAGTTTCCAGAAAGTTTACGCGTTATTGCACTTATGATGTGAAATGAGCAA 516
 QY 1044 CAGAGGTGAAGAGATTTTCAGGGAAGGAGACGAGATGACCAACCAAGGACGCTGGGT 1103
 DB 517 GAATATGCTTCACTGCTTTTTCAGGACAGACAG---TCCCATGCTGAAACCTTGAA 573
 QY 1104 TTGAAGAGTTCTGCTCTTCTACAGATGATGTCCACCGCGCGGAGACTTACCTGCTC 1163
 DB 574 GAGAAAGATTTCTACAGTTCTTATGAGCATTTAAACGTGCTGAGGTGAGGAAGCTC 633
 QY 1164 ATGCTGACCTTACGAAACCAAGACCACTTGATGCGGACGCTGACGCGCTTCTGT 1223

DB 634 TTGAAAGTTTTCACGCTGATGGGACAGAGTGACTGTCTGAAATTTTGGATTTCTC 693
 QY 1224 CAGGTGAGCAGAAAGATGCGGGGTGTGACCTTCAGAGCTGCCAGACATCATGAGCAG 1283
 DB 694 CAGAGGAGCAGAAAGAGAGAGACTGCACCTCTGACCTTGTCTGGAACATATGAGCCG 753
 QY 1284 TTTGAGCCATGCCCAAAAACAAGATGAAGGGGCTGTGGGCAATTTGATGGCTTCAAC 1343
 DB 754 TATGAACCTTCAGACAGTGGCAAACTGGCGATGTGCTGATGATGATGGCTTCTCAGC 813
 QY 1344 TACACAGAGCCCTGCTGGTGTGATCATCTTCAACCTGTAGACCAACATGTGACCAAG 1403
 DB 814 TACCTTCTCTTAAGATGAGACATCTTCAACCCAGCTGCTCCCTCATCTATCAGGAT 873
 QY 1404 ATGACGACCGCTGAGGCACTTATCATCACTGTGCCACAACACCTTACTGTGGGT 1463
 DB 874 ATGACTCAACCCCTGAACCACTTACTTATGCTCTTCTATTAACCTTACTTATGAGGG 933
 QY 1464 GACCAAGCTCATGTCCCACTGACGAGGTGACATGTATGCTTGGTCTTGCAGGCTGCTGC 1523
 DB 934 GACCAAGCTTGTGGCCAGAGCAGGTGAGGATATTAACGGGCTTGAACCGGGGTGC 993
 QY 1524 CGCTGCGTGGAGTGTGACTGCTGGGATGGGCCGACGAGGACCATTTGTGACCAATGCG 1583
 DB 994 CGCTGCGTGGAGTGTGATGTATGGATGACCTTACGCGGAACTGTGCTTTACACGGA 1053
 QY 1584 TACACTGTGACTTCCAAAGATCTCTTCAAAAGCTCATTTGAACCATCAACAAATATGCC 1643
 DB 1054 CACACCTGACCTCCCGCATCTCTTCAAAAGTGTGCTGGCCACAGTATGACAGATATGCC 1113
 QY 1644 TTCAATCAAGATGATGCCAGTATCTGATGATCTTGTCCCTGGAGACCACTGACAGTGGAG 1703
 DB 1114 TTCAAGATCAAGCTTCAACGATCTTGTGCTGAGACCACTGACAGTGGAGCAG 1173
 QY 1704 CAGAAAGAAATGCGCCAGTATCTGACTGACATCTTGGGAGCAAGCTGACCTGTATCA 1763
 DB 1174 CAGCAGACCAATGGCCCGTCACTGATCTGAGATCTTGGGAGAGCAGCTGACACACACC 1233
 QY 1764 GTGACAGTGAAGTGCACACCACTCCCTCTTCACAGATGCTCAAGGGCAAGTCTTC 1823
 DB 1234 TTGATATGGGTGCTGCCACTGACTGCTCCCTGAGAGGCTTGGAGGAAGATCTTG 1293
 QY 1824 GTGAAGGGAAGAAAGTCCAGCCAGCAATCAGAGGATGCGAGGAAGCGGATGTCT 1883
 DB 1294 GTGAAGGGAAGAAAGTTTAACTTGAAGAAACCTGGAATATATAGAGAGAGAGAA 1353
 QY 1944 ACCAATGAAAGCTGTAGAAAACACTGCTTAAGAGAAATGGAATTCCTCAT 1996
 DB 1414 CAGAGGAGAACTTCAAGATTAAGAACAAAAGAAATCAAGCCCATCTT 1466

RESULT 13
 ABRK10063
 ID ABRK10063 standard, cDNA, 2629 BP.
 XX
 AC ABRK10063;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DB Human phospholipase C 16816 cDNA.
 XX
 KW Human, phospholipase C, PLC, phospholipase C 16816; brain disorder; gene;
 KW cellular proliferative disorder; differential disorder; prion disease;
 KW glial disorder; cerebrovascular disease; acute meningitis; cirrhosis; ss;
 KW demyelinating disease; degenerative disease; heart disorder; rickets;
 KW ischaemic heart disease; myocardial disease; neoplastic heart disease;
 KW vascular disease; inflammatory disease; bone metabolism disorder;
 KW chronic renal disease; haematopoietic disorder; autoimmune disease;

XX arthritic; systemic lupus erythematosus; Sjogren's syndrome; psoriasis;
XX Crohn's disease; uveitis; atopic allergy; balloon angioplasty;
XX coronary artery bypass graft surgery.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 257..2545
FT /tag= a
FT /product= "Human phospholipase C 16816"
FT /transl_except= (pos:760..762, aa:Arg)
FT /transl_except= (pos:1981..1983, aa:Gly)
FT /note= "This region is specifically claimed"
XX WO200206302-A2.
XX 24-JAN-2002.
XX 17-JUL-2001; 2001WO-US22760.
XX 17-JUL-2000; 2000US-218675P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Meyers R, Rudolph-Owen L, Tsai FY;
XX WPI, 2002-188535/24.
XX P-PSDB; AAU76816.
XX New human phospholipase C protein for diagnosing and treating disorders
XX e.g. Alzheimer's disease, heart failure, cancer, psoriasis, Sjogren's
XX disease, and to identify modulators for therapeutic use -
XX Claim 1; Fig 1; 129pp; English.
XX The invention relates to human phospholipase C (PLC) polypeptides 16816
XX and 16839. The polypeptides can be used in the treatment and diagnosis of
XX various disorders including cellular proliferative and/or differentiative
XX disorders (e.g. carcinoma and leukemia), brain disorders including glial
XX disorders (e.g. cerebral edema), cerebrovascular diseases (e.g.
XX ischemia and hypertensive encephalopathy), infections (e.g. acute
XX meningitis and prion diseases), demyelinating diseases (e.g. multiple
XX sclerosis), degenerative diseases (e.g. Alzheimer's disease), heart
XX disorders including heart failure, ischemic heart disease (e.g.
XX myocardial infarction), myocardial disease (e.g. myocarditis), neoplastic
XX heart disease (e.g. angina pectoris), vascular diseases (e.g.
XX atherosclerosis), inflammatory disease (e.g. Kawasaki syndrome), bone
XX metabolism disorders (e.g. osteoporosis), cirrhosis, rickets, chronic
XX renal disease, haematopoietic disorders, autoimmune diseases (e.g.
XX diabetes mellitus), arthritis, systemic lupus erythematosus, Sjogren's
XX syndrome, psoriasis, Crohn's disease, uveitis, atopic allergy, and
XX angioplasty and related techniques) and vascular replacement (e.g.
XX coronary artery bypass graft surgery). This sequence represents cDNA
XX encoding the human phospholipase C 16816.
SQ Sequence 2629 BP; 648 A; 677 C; 735 G; 569 T; 0 other;
Query Match 6.7%; Score 308.6; DB 24; Length 2629;
Best Local Similarity 54.2%; Pred. No. 7.5e-49;
Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;
QY 744 TTCCAGCGCTACCTGAGGAGGAGCTTGAAGCCCAAGTCTGCTGAGATCTACAGGCG 803
DB 485 TTGCTGCTGAGCTGAGGAGAGAGCTTCCCTGAGAGAGGCTTCACATTGTCTTCAT 544
QY 804 AGCCACCGCGAGTCTGCTGCTGCTCAACAGCAGAGGAGGCGGAGCACTTGAGTC 863
DB 545 GGGCGGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 604
QY 864 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
DB 605 CGAGGCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 924 CGCACGAGGACGAGTGGCTGAGAGCAGACGCTTGAAGGCGGACGAGAAAGGCGGATGCG 983
DB 661 -----GAGCAATGCTGAGGAGATGCTTCAAGCTGAGAGCAAAATATCAGATGCT 712
QY 984 AGCTGAGCATTTGGCGAGGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
DB 713 AAGATGAGTTTCCAAAGAGTTCAGCGGCTTATTCACCTAATGATGAGAAATGACAA 772
QY 1044 CAGAGGTGAAGCAGATGCTCAGGAGAGGAGCAGCAGGATGACCAAGGAGAGCTGGGT 1103
DB 773 GAATATGCTTCAAGCTTCTTTTCAAGGACAGACAGC---TCCAGTGTGAAACCTGGAA 829
QY 1104 TTTGAGAGTTCTGCTGCTTCTTCAAGATGATGCTCAACCCCGGAGCTCTACCTGCT 1163
DB 830 GAGAGAAATTCGATACGCTTCTATTAAGGACATGCTAAACGTGCTGAGGTGACAGAACTG 889
QY 1164 ATGCTGACCTTACAGCAACCAAGAGCAGCAGCTGATGCGGAGCTGAGGCTTCTG 1223
DB 890 TTTGAAAGTTTTCAGCTGATGAGGAGAGAGCTGCTGCTGAGATTTTGGATTTCTC 949
QY 1224 CAGGTGAGCAGAAAGATGAGCGGCTGAGACCTCGAGAGCTGCCAGACATATGAGCAG 1283
DB 950 CAGAGGAGCAGAAAG 1009
QY 1284 TTTGAGCCATGCGCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
DB 1010 TATGAACTTTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1069
QY 1344 TACACAG 1403
DB 1070 TACCTCTCTTAAAG 1129
QY 1404 ATGAGCAG 1463
DB 1130 ATGATCTCAACCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
QY 1464 GACGAGCTGATGCTGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
DB 1190 GACGAGCTTTCGAG 1249
QY 1524 GCTGCTGAG 1583
DB 1250 GCTGCTGAG 1309
QY 1584 TACACTGATCTTCAAGATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
DB 1310 CACACCTGATCTTCCGAGATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
QY 1644 TTTATCAGAGATGAGTACCTGATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
DB 1370 TTCCAGACATCAG 1429
QY 1704 CAG 1763
DB 1430 CAGCAG 1489
QY 1764 GTGAGCAGTGAAGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1823
DB 1490 TTGAGATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
QY 1824 GTGAG 1883
DB 1550 GTGAG 1609
QY 1884 GATGAG 1943
DB 1610 CTTGAGTGAAG 1669
QY 1944 ACCAATGAG 1996
DB 1670 CAG 1722

QY 1824 GTGAAGGGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1883
DB 1551 GTGAAGGGAGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1610
QY 1884 GATGAGAGAGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1943
DB 1611 CCGAGAGAGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1670
QY 1944 ACCAATCGAAGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1996
DB 1671 CAGAGAGAGAGAGAGCTCCACCGCAATCAGCGAGATGCGAGAGAGGAGGTCT 1723

RESULT 15
AAD19219
ID AAD19219 standard; DNA; 1840 BP.
XX
XX AAD19219;
AC
XX
XX 18-DEC-2001 (first entry)
XX
XX Human CG121 (or C592) lipase DNA #1.
DE
XX Human; apolipoprotein; lipase; lipoprotein receptor; ALu; angina;
XX cardiovascular disease; lipid metabolism; myocardial infarction;
XX cerebral ischaemia; arterial thrombosis; thrombolytic; antilipemic;
XX coronary artery thrombosis; cerebral artery thrombosis; stroke;
XX intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
XX neuroprotectant; cerebroprotective; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 140..1840
FT /tag= a
FT /product= "Human CG121 (or C592) lipase protein"
FT /note= "CDS does not include stop codon"
XX /partial
XX
XX PN MO200179446-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 16-APR-2001; 2001WO-US12529.
XX
XX PR 14-APR-2000; 2000US-197137P.
XX 20-JUN-2000; 2000US-0598042.
XX 03-AUG-2000; 2000US-0631451.
XX 22-SEP-2000; 2000US-0667298.
XX 17-NOV-2000; 2000US-0714936.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Ballinger DG, Joeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
XX Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
XX Wang D;
XX
XX DR WPI; 2001-611724/70.
XX
XX DR P-PSDB; AAE11925.
XX
XX PT Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
XX receptor polypeptides, useful for preventing diagnosing and treating
XX lipid metabolism disorders, thrombosis and cardiovascular diseases -
XX
XX PS Claim 1; Page 155-158; 266pp; English.
XX
XX The invention relates to polynucleotides encoding proteins CG122, CG179,
XX CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
XX involved in lipid metabolism and cardiovascular disease such as human
XX apolipoproteins, lipases and lipoprotein receptor proteins. These DNA
XX and protein sequences are useful for treating or preventing disorders
XX associated with apolipoproteins, lipases and lipoprotein receptor (ALu)
XX expression and for treating lipid metabolism, cardiovascular diseases

CC and thrombosis. Antibodies against these proteins are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of these sequences. ALu polypeptides are also
CC useful for identifying agents (agonists and antagonists) that bind to
CC them and cells expressing ALu proteins are useful for identifying a
CC therapeutic agent for use in treatment of a pathology related to
CC aberrant expression or physiological interactions of this polypeptide.
CC Vectors comprising these DNA and protein sequences are also useful for
CC producing ALu proteins. The nucleic acids and polypeptides of the
CC invention are also useful for the treatment of occlusive cardiovascular
CC diseases, myocardial infarction, cerebral ischaemia, angina, arterial
CC thrombosis, coronary artery thrombosis and cerebral artery thrombosis
CC or intracardiac thrombosis and stroke. The nucleotides of the invention
CC are used in gene therapy. The present sequence is human CG121 (or C592)
CC lipase DNA.
XX
XX SQ Sequence 1840 BP; 455 A; 483 C; 508 G; 394 T; 0 other;
XX
XX Query Match 6.6%; Score 307; DB 22; Length 1840;
XX Best Local Similarity 54.1%; Pred. No. 1.4e-48;
XX Matches 678; Conservative 0; Mismatches 560; Indels 15; Gaps 2;
XX
QY 744 TTCAGGCTTACCTGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 803
DB 368 TTGCTGCTTACCTGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 427
QY 804 AGCAGCGGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 863
DB 428 GGGCGGCTTACCTGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 487
QY 864 ACTGCGCTTACCTGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 923
DB 488 CGAGGCTTACCTGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCCT 543
QY 924 CGCAGCGGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 983
DB 544 -----GAGCAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 595
QY 984 AGCTGAGCATTTGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 1043
DB 596 AAGATGAGTTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 655
QY 1044 CAGAGGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1103
DB 656 GAATATGCTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 712
QY 1104 TTTGAGAGTTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 1163
DB 713 GGAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 772
QY 1164 ATGCTGAGCTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 1223
DB 773 TTTGAGAGTTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 832
QY 1224 CAGTGAAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1283
DB 833 CAGAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 892
QY 1284 TTTGAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1343
DB 893 TATGAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 952
QY 1344 TACAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1403
DB 953 TACCTGCTTCAAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGC 1012
QY 1404 ATGAGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1463
DB 1013 ATGAGTCAAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1072
QY 1464 GACGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1523
DB 1073 GACGAGAGAGAGAGAGCTTGCAGCCCACTGCTTACAGCATTCACAGGCAGGC 1132

QY 1524 CGCTGCTGAGGTGAGACTGCTGGAGTGGGCCGAGCGGGAGCCCATTTGACCACTGSC 1583
Db 1133 CGCTGGGTGGAGGTGATGTGATGGAGCTAGCGGGAACTGTGTTTACACGSA 1192
QY 1584 TACACTCTGACTTCCAAGATCTCTTCAAGAGCGTCATTGAAACCATCAACAATATGCC 1643
Db 1193 CACACCTTGACCTCCGCACTCTGTTCAAGATGTGTGGCCACAGTAGACAGTATGCC 1252
QY 1644 TTTCATCAAGATAGTACCAGATGATCTGTCCATCGAAAAACCATGCAGTGTCATCCAG 1703
Db 1253 TTCCAGACATCAGACTACCCAGTCATCTGTCTCTGAGAGCCCATGCACTGGGAGCAG 1312
QY 1704 CAGAGAAAATGGCCAGTATCTGACTGACATCTTGGGGACAAGCTGGACCTGTCATCA 1763
Db 1313 CAGCAGACATGGGCTGCTCATCTGACTGAGATCTGGGGAGCAGCTGCTGAGCACCACTC 1372
QY 1764 GTGAGCAGTGAAGATGCAACCACTCCCTCTTCCACAGATGCTCAAGGGCAAGATCTC 1823
Db 1373 TTGGATGGGGTGTGCTGCTCACTCAGCTGCCCTGCTGAGAGGCTTGGAGAAAGATCTG 1432
QY 1824 GTGAAGGGGAAGAGCTCCAGCCACATCAGGAGATGCCGAGAGAGGCGAGTGTCT 1883
Db 1433 GTGAAGGGGAAGAGTTAACAATTGAGAGACCTGAAATATGAGAGAGGAGAGCAGAA 1492
QY 1884 GATGAGACAGTGTGATGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCC 1943
Db 1493 CTTGATTTGAGAGATCAGATTTGGCGCTGAGATCCAGTTTGAAGCTGAGCTGAGCCC 1552
QY 1944 ACCAATCGAAAAGCGTGTAGAAAACACTGCTAAGAGGAAACTGGATTCCCTCAT 1996
Db 1553 CAGGAGCAGAACCTTCAGATTAAGACAAAAAGAGAAATCCAAAGCCCATCTT 1605

Search completed: March 28, 2003, 16:33:51
Job time : 1148 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 12:21:40 ; Search time 6814 Seconds

(without alignments)
11016.449 Million cell updates/sec

Title: US-09-927-112-1

Sequence: 1 tccgacatcagactagctcgcg.....ggtacggggccaccgccccg 4635

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	14.0	889	14	BQ946757 AGENCOURT
2	610.4	13.2	930	14	BQ960462 AGENCOURT
3	588.8	12.7	759	12	BG472146 602513869
4	580.8	12.5	1016	12	BG394794 602457129
5	570.4	12.3	663	12	BG819793 602781835
6	550	11.9	561	10	BE255177 601115717

7	514.6	11.1	801	10	BE255354	BE255354 601115369
8	478	10.3	1002	14	BM903836	BM903836 AGENCOURT
9	472.6	10.2	577	14	BM932679	BM932679 UI-M-CGDP
10	465	10.0	733	14	BM950299	BM950299 UI-M-CHOP
11	462	10.0	696	10	BM430723	BM430723 BM430723
12	456.4	9.8	711	12	BG299246	BG299246 602395735
13	451.8	9.7	667	12	BB624082	BB624082 BB624082
14	416.4	9.0	436	12	BE908459	BE908459 601503091
15	394.8	8.5	714	14	BB652903	BB652903 BB652903
16	389.2	8.4	509	12	BF463298	BF463298 UI-M-CGDP
17	341.8	7.4	427	12	BE988680	BE988680 UI-M-CGDP
18	341.2	7.4	514	10	BB283947	BB283947 BB283947
19	328	7.1	646	10	AM853924	AM853924 RC3-CT025
20	321	6.9	645	14	BQ571436	BQ571436 UI-M-FCO
21	315.6	6.8	523	10	AM422385	AM422385 f161908.Y
22	294.2	6.3	395	10	BE244972	BE244972 TCBA3E16
23	288.2	6.2	2674	11	BC015249	BC015249 Mus muscu
24	280.8	6.1	678	10	AV361753	AV361753 AV361753
25	279.6	6.0	1222	13	BM465373	BM465373 AGENCOURT
26	275.8	6.0	684	13	BI756147	BI756147 60303048
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28	257.4	5.6	664	10	BB642639	BB642639 BB642639
29	237.6	5.1	713	10	AM422278	AM422278 f160608.Y
30	230	5.0	705	13	BI732646	BI732646 60335392
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32	201.6	4.3	814	12	BF604625	BF604625 270534 MA
33	201.4	4.3	539	10	BE303961	BE303961 602650250
34	198.6	4.3	817	9	AU124862	AU124862 AU124862
35	197.6	4.3	547	14	BQ420228	BQ420228 fa15e08
36	195.4	4.2	807	13	BG766678	BG766678 602739962
37	195.4	4.2	844	13	BI828021	BI828021 603073764
38	192.6	4.2	479	12	BF189752	BF189752 235445 MA
39	190.2	4.1	496	13	BM031429	BM031429 496828 MA
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41	184.2	4.0	1112	14	BQ072081	BQ072081 AGENCOURT
42	182.8	3.9	798	13	BM020264	BM020264 603648863
43	180.4	3.9	897	14	BQ647520	BQ647520 AGENCOURT
44	178.2	3.8	226	10	BB047756	BB047756 BB047756
45	178	3.8	226	10	BB047756	BB047756 BB047756

ALIGNMENTS

RESULT 1
LOCUS BQ946757 889 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT 8924326 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466785
ACCESSION BQ946757
VERSION BQ946757.1 GI:22362235
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 889)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Stransberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13991 row: k column: 10
High quality sequence stop: 676.
Location/Qualifiers
1..889
FEATURES
source

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6466785"
/clone_1ib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT      193 a      268 c      272 g      155 t      1 others
ORIGIN
Query Match      14.0%; Score 647; DB 14; Length 889;
Best Local Similarity 85.3%; Pred. No. 1.8e-117;
Matches 747; Conservative 0; Mismatches 121; Indels 8; Gaps 2;
QY 2512 CCTTCTGGAACGCGCGCTGCGCAATGTTGTCCTGAACTACAGTACAGAGGCGGATGC 2571
1 CCTTCTGGAACGCGCTGTTGCAATGTTGCTGCAACTACAGTACAGAGGCGGATGC 60
QY 2572 TGCAGCTGAACCGACCAAGTTGACGCGCAACGCGTGCCTGCTACGTAAGCTTG 2631
61 TACAGCTGAACAGGCGCAAGTTGACGCGCAACGCGTGCCTGCTACGTAAGCTTG 120
QY 2632 GGTGATGTCGACGCGGCTGTTCAACCCCACTCGGAGGACCCCGCGCGGACGCTCA 2691
121 AGTGCATGTCGACGCGGCTGTTCAACCCCACTCGGAGGATCCCGCGGCGGACGCTCA 180
QY 2692 AGAAGCAGCTGTCCTCGGATCATCATGTCGAGAGCTTCCCAAGCGCGGACGCTCA 2751
181 AGAAGCAGCTGTCCTCGGATCATCATGTCGAGAGCTTCCCAAGCGCGGACGCTCG 240
QY 2752 TGTCTGGGAGACCGTGGGAGATCATGACCCCTTTTGGAGTGGATCATTTGGCTCC 2811
241 TGTCTGGGAGACCGTGGGAGATCATGACCCCTTTGAGTGGAGTGGATCATTTGGCTCC 300
QY 2812 CTGTGAGCTCAGACGAGGACGACGCGCGTGGTGGACGACGAGGAGTTCAACCCACCT 2871
301 CGTGTGAGCTCAGACGAGGACGACGCGCGTGGTGGACGACGAGGAGTTCAACCCACCT 360
QY 2872 GGGAGAGACCTGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2931
361 GGGAGAGACCTGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 2932 TCTGGGACCAACGATCCATGCGGCGTGAATTTCAATGGCCAGAGAGCGCTTTCAGCA 2991
421 TCTGGGACCAACGATCCATGCGGCGTGAATTTCAATGGCCAGAGAGCGCTTTCAGCA 480
QY 2992 GCATGATGCGAGGCTACAGACGATGATGATGATGATGATGATGATGATGATGATGAT 3051
481 GCATGATGCGAGGCTACAGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 3052 TGCATGTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3111
541 TGCATGTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 3112 TCTTCTCGAGGCGCAAGGCGCGTCTGTCGACAGTATGTCGTCGTCGTCGTCGTCGTC 3171
601 TCTTCTCGAGGCGCAAGGCGCGTCTGTCGACAGTATGTCGTCGTCGTCGTCGTCGTCGTC 660
QY 3172 CCGGCGCTTCCTGTAAGCAGCGATCTTGGCGGACGCGGACGCGGACGCGGACGCGGAC 3231
661 CCGGCGCTTCCTGTAAGCAGCGATCTTGGCGGACGCGGACGCGGACGCGGACGCGGACGCG 720
QY 3232 AGAAGCGGCGCGGAGGCTTCCGAGGCTGTCCTGAGTACAGGAGCAAGGCTTCA 3291
721 AGAAGCGGCGCGGAGGCTTCCGAGGCTGTCCTGAGTACAGGAGCAAGGCTTCC 780
QY 3292 AGGAGGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3346
781 GAAAGGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840

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QY 3347 AGCC--AGGAGGCGCGCGGACGCGGACGCGCGCG 3379
Db 841 TTACTCAAGAGAGGTGAGGCGGACGAGCGCGCG 876
RESULT 2
LOCUS BQ960462
DEFINITION BQ960462 930 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8930277 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466491
5', mRNA sequence.
ACCESSION BQ960462
VERSION BQ960462.1 GI:22375940
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 930)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-x@mail.nih.gov
Tissue Procurement: The Cepho Laboratory
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
plate: ILNL3990 row: o column: 04
High quality sequence stop: 634.
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:6466491"
/clone_1ib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 222 a 267 c 292 g 148 t 1 others
ORIGIN
Query Match 13.2%; Score 610.4; DB 14; Length 930;
Best Local Similarity 86.0%; Pred. No. 3.1e-110;
Matches 700; Conservative 0; Mismatches 111; Indels 3; Gaps 2;
QY 2080 AGAGCAAGGCTGAAGAGAGCGTGGAGTCTGGGAGAGATGCGCGGCGGACGACGCAATG 2139
45 AGAGCAAGGCTGAAGAGAGCGTGGAGTCTGGGAGAGATGCGCGGCGGACGACGCAATG 104
Db 2140 GCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2199
105 GCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 164
QY 2200 CCGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2259
165 TGGCGAGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 224
Db 2260 CGACCGGCGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2319
225 CTGCGCGGCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 284
QY 2320 CCAAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2379
285 CCAAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 344

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QY 2380 CCTTCAGCAGACCAAGCCACCAAGATTCGTGAGAGAGAGCCGGCGAGTACCTACGCT 2439
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 Db 345 CTTTCAGTGAACCAAGGCCATCAATCTCTGAGAGAGAGGCCACCACTGCTCGCT 404
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 QY 2440 TCAACGACGACGACTCTCCCGCATCTACCCCTCTCTTACCGTGTGAGTCCAGCAACT 2499
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 Db 405 TCAACGACGACGACTCTCCCGCATATATACCCCTCTCTTACCGTGTGAGTCCAGCAACT 464
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 QY 2500 ACAACCCGACGCTTGTGAGAGCCGGCTGCCAAATGTTGCTGAACTACAGTACAG 2559
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 Db 465 ACAATCCACAACTTGTGAGAGCGTGTGCTGAGATGTTGCTGAACTACAGTACAG 524
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 QY 2560 AGGGCGGATGCTGACAGCTGAACCGACCAAGTTCAAGCGCCAAAGTGTGCGCTACG 2619
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 Db 525 AGGGCGGATGCTGACAGCTGAACCGACCAAGTTCAAGCGCCAAAGTGTGCGCTACG 584
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 QY 2620 TACTCAAGCTGGTGTATGTCCAGAGGCGTGTTCACACCCCACTCGAGAGAACCCCTGC 2679
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 Db 585 TGCTCAAAACCCAGTGTATGTGCGAGGAGTGTCTTCAACCCCACTCGAGAGAGTCCCTGC 644
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 QY 2680 CCGGCGAGCTCAAGAGCAGCTGGTGTCTCCGAGTCAATCAGTGGCAGAGCTTCCCAAG 2739
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 Db 645 CCGGCGAGCTCAAGAGCAGCTGGTGTCTCCGAGTCAATCAGTGGCAGAGCTTCCCAAG 704
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 QY 2740 CGCGGAGCTCAGTCTGCGGAGCCGTGGAGATCATCGACCCCTTGTGTGAGGTGAGA 2799
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 Db 705 CAGCGGAGCTGAGTCTGCGGAGCCGTGGAGATCATCGACCCCTTGTGTGAGGTGAGA 764
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 Db 765 TCATTGGGGGCTCCCGCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 824
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 QY 2859 --TTCAACCCCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 2890
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RESULT 3
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 DEFINITION 602513869F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645721 5',
 mRNA sequence.
 ACCESSION BG472146
 VERSION BG472146.1 GI:13404520
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 759)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: Inocyte Genomics, Inc.
 DNA Sequencing by: Inocyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LCM1419 row: 1 column: 18
 High quality sequence stop: 683.
 Location/Qualifiers

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 /db_xref="taxon:9606"
 /clone="IMAGE:4645721"
 /clone_id="NIH_MGC_16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dT priming. Directionally

BASE COUNT 148 a 248 c 256 g 107 t
 ORIGIN
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Query Match 12.7%; Score 588.8; DB 12; Length 759;
 Best Local Similarity 99.7%; Pred. No. 5.4e-106;
 Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 2855 CCGGTTCAACCCCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2914
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 Db 62 CCGGTTCAACCCCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
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 QY 2915 GCTGTGCTGCTTCTCTGTCTGTGAGCAACAGATCCATCGGGGTGATCATTTGCGCAGAG 2974
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 Db 122 GCTGTGCTGCTTCTCTGTCTGTGAGCAACAGATCCATCGGGGTGATCATTTGCGCAGAG 181
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 QY 2975 GACGCTGGCTTCAAGCAGATGATCCAGGCTTACAGACAGTGTACTTAAAGGATGGA 3034
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 Db 182 GACGCTGGCTTCAAGCAGATGATCCAGGCTTACAGACAGTGTACTTAAAGGATGGA 241
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 QY 3035 AGAGGCTTCATCTTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3094
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 QY 3095 TCTGGGCTTAAAGAGGCTTCTCTCGAGAGCCCAAGCCCGGCTGCTGAGACATCATGC 3154
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 Db 302 TCTGGGCTTAAAGAGGCTTCTCTCGAGAGCCCAAGCCCGGCTGCTGAGACATCATGC 361
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 QY 3155 TGTGTGGGCGGCCCCCGGAGCCCGGCTTCTCGTTAGCCAGAGATCTGTGCGGAGCCGAG 3214
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 Db 362 TGTGTGGGCGGCCCCCGGAGCCCGGCTTCTCGTTAGCCAGAGATCTGTGCGGAGCCGAG 421
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 QY 3215 CCGCCCGGACCAAGAGGCAAGAGCCGGGCGGAGGGGCTTCCCGAGCTGTGCTGGGTAC 3274
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 Db 422 CCGCCCGGACCAAGAGGCAAGAGCCGGGCGGAGGGGCTTCCCGAGCTGTGCTGGGTAC 481
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 QY 3275 ACAGGACACAGGCTCCAGAGGAGGTGAGCAGACGATGTGTCCCGGAGCCGAGCTTGC 3334
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 Db 482 ACAGGACACAGGCTCCAGAGGAGGTGAGCAGACGATGTGTCCCGGAGCCGAGCTTGC 541
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 QY 3335 TCCGGAAGCCCGAGCCAGAGAGGCGCGGAGCGGAGCGGAGCGGAGCGGAGGTAAG 3386
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RESULT 4
 LOCUS BG394794 1016 bp mRNA linear EST 12-MAR-2001
 DEFINITION 602457129F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579663 5',
 mRNA sequence.
 ACCESSION BG394794
 VERSION BG394794.1 GI:13288242
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1016)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM1297 row: 1 column: 08
 High quality sequence stop: 599.

FEATURES

source

Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_lib="NIH MGC 16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAACGAG (G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 324 a 302 c 247 g 143 t
 ORIGIN

Query Match 12.5%; Score 580.8; DB 12; Length 1016;
 Best Local Similarity 99.3%; Pred. No. 2.2e-104;
 Matches 604; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

FEATURES

source

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 loss"
 /lab_host="DH10B (T1 phage-resistant)"
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library."
 http://image.llnl.gov row: f column: 09
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 High quality sequence stop: 649.

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 QY 1340 CAATCTACACAGAGAGCCCTGCTGTGTGATCTTCAACCTTGAGACACCAATGTGACCA 1399
 DB 62 CAATCTACACAGAGAGCCCTGCTGTGTGATCTTCAACCTTGAGACACCAATGTGACCA 121
 QY 1400 GAGCATGACGACGACGCTGAGCCACTACTACTCATCCTGCTCCCAACAGCACTGCTGCT 1459
 DB 122 GAGCATGACGACGACGCTGAGCCACTACTACTCATCCTGCTCCCAACAGCACTGCTGCT 181
 QY 1460 GAGTGAACGAGCTGATGCCAGTCAAGGGTGAATGTGCTTGGGCTCTGAGGCTGG 1519
 DB 182 GAGTGAACGAGCTGATGCCAGTCAAGGGTGAATGTGCTTGGGCTCTGAGGCTGG 241
 QY 1520 CTGGCCCTGCTGAGAGTGAATGCTGCTGGAGTGGGCCGACGAGGAGCCATGTGACCA 1579
 DB 242 CTGGCCCTGCTGAGAGTGAATGCTGCTGGAGTGGGCCGACGAGGAGCCATGTGACCA 301
 QY 1580 TGGCTACACTGACTCTTCAAGATCTCTTCAAGAGCTCATTTGAAACCATCAACAAATA 1639
 DB 302 TGGCTACACTGACTCTTCAAGATCTCTTCAAGAGCTCATTTGAAACCATCAACAAATA 361
 QY 1640 TGGCTTCAATCAAGATGAGTACCCAGTGTCTGTGCTCATGAAAAACAATGAGTGCAT 1699
 DB 362 TGGCTTCAATCAAGATGAGTACCCAGTGTCTGTGCTCATGAAAAACAATGAGTGCAT 421
 QY 1700 CCAGCAGAGAAATATGGCCAGATATCTGACTGATCTCTTGGGGACAACTGGAAGTGC 1759
 DB 422 CCAGCAGAGAAATATGGCCAGATATCTGACTGATCTCTTGGGGACAACTGGAAGTGC 481
 QY 1760 ATCAGTGAACAGTGAAGATGACCACTCCCTCTCCACAGATGCTCAAGGGCAAGAT 1819
 DB 482 ATCAGTGAACAGTGAAGATGACCACTCCCTCTCCACAGATGCTCAAGGGCAAGAT 541
 QY 1820 CCTGTGAAGGAGAGAGCTCCAGCC- AACATCAGCAGGAGATGCGAGG- AAGCGAG 1877
 DB 542 CCTGTGAAGGAGAGAGAGCTCCAGCCAAACATCAGCAGGAGATGCGAGGAAAGCGAG 601
 QY 1878 GTGTCTGA 1885
 DB 602 GTGTCTGA 609

RESULT 5
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

663 bp mRNA linear EST 22-MAY-2001
 602781835F1 NCI CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4932488
 5', mRNA sequence.
 BG819793
 BG819793.1 GI:14167380
 EST.
 human.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

BASE COUNT 133 a 199 c 212 g 119 t
 ORIGIN

Query Match 12.3%; Score 570.4; DB 12; Length 663;
 Best Local Similarity 96.5%; Pred. No. 2.2e-102;
 Matches 637; Conservative 0; Mismatches 16; Indels 7; Gaps 5;

QY 2523 GCCGGCTGCCAAATGTTGCTGAACTACAGTCAAGAGGGGCGATGCTGCAGCTGAGAC 2582
 DB 4 GCCGGCTGCCAAATGTTGCTGAACTACAGTCAAGAGGGGCGATGCTGCAGCTGAGAC 63
 QY 2583 CGAGCCAAAGTTCA-GCGCCAAAGGCTGCGGCTCAAGTCAAGCCCTGGGTGATGTG 2641
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 QY 2642 CCAGGGGCTTTTCAACCCCACTCGAGAGACCCCTGCGGCGCACTCAAGAAAGAGCT 2701
 DB 124 CCAGGGGCTTTTCAACCCCACTCGAGAGACCCCTGCGGCGCACTCAAGAAAGAGCT 183
 QY 2702 GATGCTCCGATCATGATGAGGCGAGCA-GCTTCCAAAGCGCGGCACTCATGCTGGGGG 2760
 DB 184 GATGCTCCGATCATGATGAGGCGAGCACTGCTTCCAAAGCGCGGCACTCATGCTGGGGG 243
 QY 2761 ACCGTGGAGATCATGACCCCTTTGTGAGGTGAGATCATTTGGACTCCCTGTGACT 2820
 DB 244 ACCGTGGAGATCATGACCCCTTTGTGAGGTGAGATCATTTGGACTCCCTGTGACT 303
 QY 2821 GACGAGGAGAGAGACCCCGGTGTGAGAGAGCAACGCGTTCAACCCCACTGGAGAGAA 2880
 DB 304 GACGAGGAGAGAGACCCCGGTGTGAGAGAGCAACGCGTTCAACCCCACTGGAGAGAA 363

cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCAGCAGC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

BASE COUNT 153 a 251 c 239 g 89 t 1 others

Query Match 10.0%; Score 465; DB 14; Length 733;
Best Local Similarity 78.9%; Pired. No. 1.5e-81;
Matches 381; Conservative 0; Mismatches 146; Indels 9; Gaps 2;

3116 CCTCCGAGGAGCCAAAGCCCGGCTCGCTGACAGTCACTGCTGAGGCGGCGCCGCGCG 3175
1 CTTCCGAGGAGCAGCAGCAGGCTCGCTGACAGTCACTGCTGAGGCGGCGCCGCGCG 60
3176 GCGCTCCGTTAGCCAGGATCTCTGCGGCGCAGCGCCAGCCCGCAGCAGCAGAA 3235
61 GCGCTCCGTTAGCCAGGATCTCTGCGGCGCAGCGCCAGGCGCCCGCAGCAGAA 120
3236 GCGGCGCGGAGGCGCTTCCGAGGCTGCTCGGAGTACAGGAGCAGCAGGCTCCAGGG 3295
121 GCGCAGTCCGAGGCGCTTCCGAGGCTGCTCGGAGTACAGGAGCAGCAGGCTCCAGGG 180
3296 GGTGGCAGCAGATGTGTGTCGCGCGGCGCGGCGCGGAGCTCTCGGAGGCGCGCAGGA 3355
181 GCGCAGTGTAGTGTGTGTCGCGCGGCGCGGCGCGGAGCTCTCGGAGGCGCGCAGGA 240
3356 GCGGCGCGGAGGCGGCGCGCGGCGCGGCGCGGAGTACAGGAGCAGCAGGCTCCAGGG 3409
241 GAGGTACAGGAGCAGCAGGCGCGCGGCGCGGAGTACAGGAGCAGCAGGCTCCAGGG 300
3410 GAGCCTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTC 3469
301 GAGCCTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTC 360
3470 GCGCAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTC 3529
361 GCGCAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTCGAGTGTGTGTC 420
3530 GAGGAGGCGGCG 3589
421 AAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 480
3590 CCGGCGCGGAGGCG 3649
481 CAGGCGCGGAGGCG 540
3650 GAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3709
541 AAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 597
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598 CCGGCTCATGTCTCTCGGAGTCTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 657
3770 CCGGCTCATGTCTCTCGGAGTCTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3829
658 CCGGCTCATGTCTCTCGGAGTCTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 717
3830 GTTGTGCTCAAGAGCTG 3845
718 GTTGTGCTCAAGAGCTG 733

RESULT 11
BB430723
LOCUS BB430723 696 bp mRNA linear EST 31-AUG-2001
DEFINITION BB430723 RIKEN full-length enriched, adult male hippocampus Mus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

musculus cDNA clone C630034J05 3', mRNA sequence.
BB430723
BB430723.2 GI:15412030
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
'Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
'Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
'D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
'Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
'Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE JOURNAL COMMENT

On Jul 18, 2000 this sequence version replaced gi:9270450.
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh
'M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
'S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.

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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
'Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa
'K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,
'Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Funct. Genomics 2, pre. 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630034J05"
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/sex="male"
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/dev_stage="adult"
/lab_host="SOLR"
/note="Site 1: XhoI, Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in

FEATURES source

ID	TITLE	JOURNAL	COMMENT
Dp 489	TCNCTTCAACCCCAGACTCGGAGGATCCCCGTG-CGGGGCAGCTCAAAGAAGAGCTGGCCCT	547	
Oy 2708	COGGAATCATCAGTGCCGAGACGTTCCCAAGCCGCAGATCATGCTGGGGAGACCGTTGG	2767	
Dp 548	GAGGATCATCAGTGCCGAGACGTTCCCAAG-CAAAGGATCTGGTCTGGGCCAACCCTGG	606	
Oy 2768	GGAGATCATCAGACCCCTTTGTGAGGTGAGATCATTTGGGCT-CCCTGGAGATTGGC-AG	2824	
Dp 607	GGAGATCATCAGACACTPACTGGAGGCTGGAAGCTATTGGGCTCCCCCGTAGCTTGCCAGC	666	
Oy 2825	CAGGAGCACAGACCCGCGTGTGGAGCACAACGSGTTCAACCCCA	2868	
Dp 667	AACGAGACAGACCCGAGTGGTGAGCAGTAACGGAATTCAACCCA	710	
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LOCUS	B6624082		
DEFINITION	B6624082 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530433Cl3 5', mRNA sequence.	667 bp linear EST 26-OCT-2001	
ACCESSION	B6624082		
VERSION	B6624082.1 GI:16462692		
KEYWORDS	EST.		
SOURCE	house mouse. Mus musculus		
ORGANISM	Mus musculus Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Arkawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaigaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Komoto,H., Koude,M., Koya,S., Matsuyama,T., Miyazaki,A., Nemura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakita,D., Shibata,K., Shingawara,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki.Y.		
AUTHORS	RIKEN Mouse ESTS (Arkawa,T., et al. 2001)		
	Unpublished (2001) Contract: Yoshinide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/		
	Carninci,P., Shibata,Y., Hayasue,N., Sugahara,Y., Shibata,K., Itoh,M., Komoto,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)		
	wagl,K., Fujikawa,S., Inoue,K., Togawa,Y., Ikawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.		
	RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)		
	Komoto,H., Fukuishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y.		
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-285 (2001)		
	Kondo,S., Shingawara,A., Saito,T., Kaiyawa,H., Yamada,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.		
	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)		
	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.		
	e mouse tissues.		
FEATURES	Location/Qualifiers		

	source	1..667
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	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="7530433C13"	
	/clone_1ib="RIKEN full-length enriched, adult male eyeball"	
	/sex="male"	
	/tissue_type="eyeball"	
	/dev_stage="adult"	
	/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAAGAGATCCAAAGCTCTTTTTCCTTTTTTTCVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCTCGACTTAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PUC I. Cloning sites, 5' end: SalI; 3' end: BamHI"	
BASE COUNT	155 a	187 c 212 g 113 t
ORIGIN		
Query Match	9.7%; Score 451.8;	DB 10; Length 667;
Best Local Similarity	88.7%;	Pred. No. 5.8e-79;
Matches 489; Conservative	0;	Mismatches 62; Indels 0; Gaps 0;
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QY	1086 CACCAAGGGAC	1096

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QY 1823 CGTGAAGATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1868
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RESULT 2

US-08-138-133-1
; Sequence 1, Application US/08138133

; Patent No. 5519163
; GENERAL INFORMATION:
; APPLICANT: GIBBS, JACKSON B.
; APPLICANT: KOBLAN, KENNETH S.
; APPLICANT: MACLEOD, ANGUS M.
; APPLICANT: MERCHANT, KEVIN J.
; TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
; TITLE OF INVENTION: PHOSPHOLIPASE C
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID A. MUTHARD
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,133
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MUTHARD, DAVID A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3870 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-138-133-1

Query Match 3.8%; Score 176.4; DB 1; Length 3870;
Best Local Similarity 62.7%; Pred. No. 1.7e-27;
Matches 292; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

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QY 1463 TGACAGCTCATGTCACGATGAGGAGTGAACATGATGATGATGATGATGATGATG 1522
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QY 1823 CGTGAAGATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1868
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RESULT 3

US-08-138-641-3
; Sequence 3, Application US/08138641

; Patent No. 5474921
; GENERAL INFORMATION:
; APPLICANT: Koblano, Kenneth S.
; APPLICANT: Pomplano, David L.
; TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
; TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Muthard
; STREET: P.O. Box 2000, 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,641
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18937
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3893 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-138-641-3

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Query Match	3.8%;	Score 176.4;	DB 1;	Length 3893;
Best Local Similarity	62.7%;	Pred. No. 1.7e-27;		
Matches 292;	Conservative	0;	Mismatches 171;	Indels 3; Gaps 1

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Db	1263	GCAAGAGAACTGGCCCAAGCACTTCAGGAAGGTGTGGTGGACAGCTCTTCAACCAAGCC	1322
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? REGISTRATION NUMBER: 35,297
?
? REFERENCE/DOCKET NUMBER: 18938
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (908) 594-3303
?
? TELEFAX: (908) 594-4720
?
? INFORMATION FOR SEQ ID NO: 3:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 3993 base pairs
?
? TYPE: nucleic acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: CDNA
?
US-08-138-133-3

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Query Match	3.8%;	Score 176.4;	DB 1,	Length 3893;
Best Local Similarity	62.7%;	Pred. No. 1.7e-27;		
Matches 292;	Conservative 0;	Mismatches 171;	Indels 3;	Gaps 1.

Oy	1403	CATGACCGACGCGGTGAGCCACTTCTCATCTGTCGCCAACAACCTTACTGTGGG	1462
Db	963	CATGAACAACCACTGTCCTACTATTGGATCTCTTCGCTAATTAAGTATCTGACTGG	1022
Oy	1463	TGACCACTCATGTCCCACTGACGGGTGGACATGTAATGCTTGGGTCCTGACAGCTGG	1522
Db	1023	GGACCAAGTTCTCCAGCGAAGTCCCTCCGTAAGCTCAAGCTCCTGAGGATGGGCTG	1083
Oy	1523	CGCGTGGTGAAGGTGACGTGCTGGGATGGAGGCCGAGGAGGCCATTTGTGCACATGG	1583
Db	1083	TGCGTGCATGGAATTGGACTGCTGGGATGGGCCAGATGGGAATGCCAGTATTACATGG	1143
Oy	1583	CTACACTGTGACTTCCAAAGATCCTCTTCAAAGCGTCAATTGAACCATCAACAATATGC	1643
Db	1143	GCAACACCTCAACCAACAAGTATGAATTTCCAGATGCTCGACACACATCAAGAGACAGCG	1203
Oy	1643	CTTCATCAAGAATGAGATGCCAATGATTCCTGTCCATTCGAAACCACTGAGATGATCCA	1703
Db	1203	GTTGTGAGCTCACAAGTACCTCTCTCATCTGTCCATCGAGACCACTGAGGATTTGCCCA	1263
Oy	1703	GCAGAAAGAAAATGGCCCACTGATCTGACTGACATCCTCTGGGGACAAGCTGACCTTGATC	1763
Db	1263	GCAGAGAACTGGCCCAAGCATTTCAAGAAAGTGCTCGGTGACAAGCTCTTCAACAAGCC	1323
Oy	1763	AGTAGAGATGAGATGCCACCAACACTCCCTCTCCACAGATGCTCAAGGCAAGATCTCT	1823
Db	1323	CGTGAACATTGGCGCTG---ATGGGCTCCCTCTTCCCAACCAAGCTCAAGAGAGATCTCT	1379
Oy	1823	CGTGAAGGGAAGAGCTCCCAACAACATCAGCGGAGATGGGGAG	1868
Db	1380	GATTGAAGATGAAGAGCTGGCTGAGGGCAAGTGCCTTATGAGAGAGTG	1425

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RESULT 5
US-09-738-884-3
; Sequence 3, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASES
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C0000849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 13953
; TYPE: DNA
; ORGANISM: Human
US-09-738-884-3

Query Match      1.7%;   Score 77.2;   DB 4;   Length 13953;
Best Local Similarity 74.6%;   Pred. No. 6,6e-07;

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QY 740 GGTCTTCCAGCGCTTACCTGAGCGCAGCTTCCAGCCCACTGTGCTTGCATCTACCA 799
 Db 712 CGCTTACACCGCTTCCAGAGCAGCCATCGTGGGCTTCCAGAAATCGCCCTCGAGCT 771
 QY 800 CGGACAGCAGCGGAGTCTGAGCTTGTCTTCCAGCAGGAGTGGCGGCACTG 859
 Db 772 SSGCGGCGAGGRTCCGRTCTCACTGCTCTGCGCTTCCGCGTGGCCAGCAGTCT 831
 QY 860 GGTCTAGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 919
 Db 832 CATCAACGCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 891
 QY 920 CCAAGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 979
 Db 892 CMTGACCTTGAACCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 951
 QY 980 TGGCAGCTTGAACCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1029
 Db 952 CAGGGGCTTGGCAGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1001

RESULT 8

US-09-249-585A-4/c
 ; Sequence 4, Application US/09249585A
 ; Patent No. 6417002
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotlick, Robert
 ; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
 ; FILE REFERENCE: 0867/0D905
 ; CURRENT APPLICATION NUMBER: US/09/249,585A
 ; CURRENT FILING DATE: 1999-02-11
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1926
 ; TYPE: DNA
 ; ORGANISM: Epstein Barr Virus
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(1926)
 ; OTHER INFORMATION: template strand of EBNA-1 DNA
 US-09-249-585A-4

Query Match 1.1%; Score 49.8; DB 4; Length 1926;

Best Local Similarity 44.9%; Pred. No. 0.18; Mismatches 232; Indels 0; Gaps 0;

QY 1856 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1915
 Db 740 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 681
 QY 1916 CTGCAAGCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1975
 Db 680 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
 QY 1976 GAGGAATCTGATTCCTCTCATCAAGAGTGTGAGATTCGGGAGCTGAGGAGCCCA 2035
 Db 620 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 561
 QY 2036 CTTCTCCGCTTCCACACTGTCTCCATCTGAAAGCTCGAGCGCAAGAGCAAGGCTGA 2095
 Db 560 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 501
 QY 2096 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2155
 Db 500 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
 QY 2156 AAGCTTCTCCAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2215
 Db 440 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 381
 QY 2216 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2275

RESULT 9

US-09-130-114-2/c
 ; Sequence 2, Application US/09130114
 ; Patent No. 5976807
 ; GENERAL INFORMATION:
 ; APPLICANT: Hotlick, Robert A.
 ; APPLICANT: Damaj, Bassam B.
 ; APPLICANT: Robbins, Alan K.
 ; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
 ; FILE REFERENCE: 0867/1D903US1
 ; CURRENT APPLICATION NUMBER: US/09/130,114
 ; CURRENT FILING DATE: 1998-08-06
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: EBNA
 US-09-130-114-2

Query Match 1.1%; Score 49.8; DB 2; Length 1931;

Best Local Similarity 44.9%; Pred. No. 0.18; Mismatches 232; Indels 0; Gaps 0;

QY 1856 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1915
 Db 740 CGAGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 681
 QY 1916 CTGCAAGCTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1975
 Db 680 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
 QY 1976 GAGGAATCTGATTCCTCTCATCAAGAGTGTGAGATTCGGGAGCTGAGGAGCCCA 2035
 Db 620 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 561
 QY 2036 CTTCTCCGCTTCCACACTGTCTCCATCTGAAAGCTCGAGCGCAAGAGCAAGGCTGA 2095
 Db 560 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 501
 QY 2096 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2155
 Db 500 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
 QY 2156 AAGCTTCTCCAGGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2215
 Db 440 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 381
 QY 2216 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2275
 Db 380 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 321
 QY 2276 G 2276
 Db 320 G 320

RESULT 10

US-07-951-715A-6
 ; Sequence 6, Application US/07951715A
 ; Patent No. 5625136
 ; GENERAL INFORMATION:
 ; APPLICANT: Kozziel, Michael G.
 ; APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621 /product= "Full-length, maize
OTHER INFORMATION: Optimized cry1B"
OTHER INFORMATION: /note= "Disclosed in Figure 6."
US-07-951-715A-6
Query Match 1.1%; Score 49.4; DB 1; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

Qy 743 CTTCCAGCGCTGCTGAGCGAGCTTGAGCCCAAGCTGCTTACGATCTACGAGG 802
Db 2487 CTTCCAGTGAAGAGCCGAGCTGAGCTGAGCTGCGCGAGCGAGAGTGGCCACCA 2546
Qy 803 CAGCCACCGCGAGTGGTGAAGCTGCTTCCACAGCAGCGAGTGGCGCGACCTGGGT 862
Db 2547 CAGCGACGACTTCAGCTGGAGCATGAGGTGGCTGCAACCGACCTGCAAGAGAACTGGG 2606
Qy 863 CACTGGCTGCGCTACTGCTATGCGCGGAGATCAGCGACAGAGAGAGCTGGCTCGCGCCA 922

Db 2607 CGTGTGGGTGTGTCTTAAGATCAAGACCCAGAGAGGCGCAAGCCCTGTGGCAACTGGA 2666
Qy 923 GCGCAGCAGGAGCCAG--TGGCTGAAGCAGACGTTTGAAGAGCCGAGCAAGAGCGGGA 979
Db 2667 GTTCATGAGGAGAGAGCCCTGTGCTGGCGAGGCGCTGAGCCGGGTGAAGCGCCAGAA 2726
Qy 980 TGGAGCCTGAGCATTTGGCGAGAGTCCGTGAGCTGCTGCAACAGCTCAAGTGAAGCTGCC 1039
Db 2727 GAAGTGGCGCAGCAGAGCCGAGAAAGCTGAGCTGAGAGACCAAGCGGTGTACACCGAGC 2786
Qy 1040 CCGCAGAGGGGTGAAGCAGATGTTCAAGGAAAGCGGACACCGATGACCAACCAAGGAGCGCT 1099
Db 2787 CAAGAGAGCGGTGAGAGCCCTGTTTCGTGGAACAGCAGTACAGACCGCTGACGCGCAGAC 2846
Qy 1100 GGGTTTGAAGAGTTCTGTGCTTTTCAAGATGATGTCCACCCCGGAGGACTTAACT 1159
Db 2847 CAACATGGGATGATCCAGCCCGCGCAAGCTGTGTCACCGGATCCGGAGGCTTAACCT 2906
Qy 1160 GCTCATGCTGACCTACAGCAGCAACCAAGAGCAACCTGATGCCGCGAGCTGAGGCGCTT 1219
Db 2907 GAGCGAGCTGCCGTGATCTCCCGCGCTGAACCGCGAGATCTTGAGAGAGCTGAGGAGCA 2966
Qy 1220 CCT 1222
Db 2967 CAT 2969
RESULT 11
US-08-459-448A-6
Sequence 6, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621 /product= "Full-length, maize"
OTHER INFORMATION: optimized cry1B
OTHER INFORMATION: /note= "Disclosed in Figure 6."
US-08-459-448A-6

Query Match 1.1%; Score 49.4; DB 2; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

Qy 743 CTTCCAGGCGTACCTGAGCGGAGCTTGAACCCCACTGCTTCACTTCAACCG 802
Db 2487 CTTGAGTGAACCCCACTGAGCTGAGCTGCGGAGCGGAGGAGCGCCACCA 2546
Qy 803 CAGCCACCGGAGTGGTGAACCTGCTCCACGAGGAGGTGGCGGACCTGGGT 862
Db 2547 CAGCCACCTTCACTGAGCATGAGCTGAGCGGAGCTGAGCGGAGGAGGAG 2606
Qy 863 CACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
Db 2607 CGTGTGGT 2666
Qy 923 GCGCAGGAGGAGCGAG--TGCTGAAGCAGACGTTTGAACGAGCGGAGGAG 979
Db 2667 GTTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2726
Qy 980 TGGCAGCTGAGCACTTGGCGAGGCTTGGAGCTGCTGCAAGCTCAACCTG 1039
Db 2727 GAGTGGGCGGAGCAAGCGCGAGAGCTGAGCTGAGCAAGCGCGGTGTAC 2786
Qy 1040 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1099
Db 2787 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2846
Qy 1100 GGGTTTGAAGGTTCTGCTGCTTCAAGATGATGTCACCGCGCGGAGCTT 1159
Db 2847 CAACATCGGAGTATTCACCGCGCGGAGCAAGCTGTGACCGGAGGAGCT 2906
Qy 1160 GCTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
Db 2907 GAGCGAGCTGCGCGGAGTATTCGCGGAGGAGGAGGAGGAGGAGGAGG 2966
Qy 1220 CCT 1222
Db 2967 CAT 2969

RESULT 12
US-08-459-595A-6
Sequence 6, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.

APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John U.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutcliffe, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621 /product= "Full-length, maize"
OTHER INFORMATION: optimized cry1B
OTHER INFORMATION: /note= "Disclosed in Figure 6."
US-08-459-595A-6

Query Match 1.1%; Score 49.4; DB 3; Length 3624;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

Qy 743 CTTCCAGGCGTACCTGAGCGGAGCTTGAACCCCACTGCTTCACTTCAACCG 802
Db 2487 CTTGAGTGAACCCCACTGAGCTGAGCTGCGGAGCGGAGGAGCGCCACCA 2546

QY 803 CAGCACCGGAGTGGCTGAGACCTGCTCCACAGAGGAGTGGCGGACCTGGGT 862
 DB 2547 CAGCCACCACTTACAGCTGAGCATGAGCTGGGCTGACCGACCTGACAGAACTTGGG 2606
 QY 863 CACTGGCTTGGCTGCTCACTTGGCGGATCAGCGACGAGAGCAGCTGGCTGGCGGCA 922
 DB 2607 CGTGTGGGTGTGTTCMAAGATCAAGACCCAGAGGGGCAAGCCCGCTGGGCACTTGA 2666
 QY 923 GCGCACCGGAGGACGAG--TGCTGAAAGCAGAGCTTTCAGAGGCGGACAAAGCGGGGA 979
 DB 2667 GTTCATCGAAGAAAGGCGCTGCTGGGCGAGGCGCTGAGCGCGGTGAAGCGCGCGAGAA 2726
 QY 980 TGGCAGCTGAGGATTTGGCGAGGTCTGCGAGCTGCTGCAAGCTGAAGTGAACCTGTC 1039
 DB 2727 GAGTGGCGGAGCAAGCGGAGAGAGCTGAGCTGAGAGACCAAGCGGCTGTACACGAGGC 2786
 QY 1040 CCGGCAAGGGGTGAAGCAATGTTTCAGGGGAAAGCGGACAGGATGACCAACAAAGGACGT 1099
 DB 2787 CAGGAGGCGCTGAGAGCGCTGTTCTGTGAGCAGCCAGTACGACCGCTGCAAGGCGGAC 2846
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 QY 1220 CCT 1222
 DB 2967 CAT 2969

RESULT 13
 US-08-459-504B-6
 ; Sequence 6, Application US/08459504B
 ; Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Lannis, Karen L.
 APPLICANT: Rothenstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 6075185artis Corporation
 STREET: 1054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,504B
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/459,595
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3624 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Synthetic DNA"
 HYPOTHEICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3621
 OTHER INFORMATION: /product= "Full-length, maize
 OTHER INFORMATION: optimized cry1B"
 OTHER INFORMATION: /note= "Disclosed in Figure 6."
 US-08-459-504B-6

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 Best Local Similarity 45.3%; Pred. No. 0.25;
 Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

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 QY 1220 CCT 1222
 DB 2967 CAT 2969

RESULT 14
US-08-459-444-6
Sequence 6, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CCCL577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3621
OTHER INFORMATION: /product= "Full-length, maize
optimized cDNA"
/note= "disclosed in Figure 6."
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-459-444-6
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Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 219; Conservative 0; Mismatches 261; Indels 3; Gaps 1;
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DB 2487 CTTCCAGTGAAGCCGACCTGAGCTGACGCTGCCGACGCGAGAACTGCGCCACCA 2546
QY 803 CAGCCACCGGAGTGGCTGACCTGCTTCCACGACGAGGAGTGGCGCGACCTGGGT 862

DB 2547 CAGCCACCACTTTCAGCCTTGACATGACGTGGGCTGACCGACCTGACGAGAACTGGG 2606
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QY 1220 CCT 1222
DB 2967 CAT 2969
RESULT 15
US-09-053-549-7
Sequence 7, Application US/09053549
Patent No. 6121521
GENERAL INFORMATION:
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSSEE: No. 6121521artis Corporation
STREET: 3054 Cornwallis Rd.
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,549
FILING DATE: 01-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:

GenCore version 5.1.4 p5_4578
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Run on: March 28, 2003, 16:34:17 ; Search time 399 Seconds
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Title: US-09-927-112-1

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Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications NA:*

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SUMMARIES

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6	308.6	6.7	2709	10	US-09-804-969-20
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16	144.2	3.1	5273	10	US-09-728-952-78
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18	144.2	3.1	10172	10	US-09-822-635-1
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20	143.6	3.1	2171	10	US-09-908-664-4	Sequence 4, Appli
21	106.4	2.3	981	10	US-09-867-550-1333	Sequence 1333, Ap
22	106.4	2.3	1505	10	US-09-728-952-59	Sequence 59, Appl
23	105.8	2.3	2547	10	US-09-765-298A-9	Sequence 9, Appli
24	100	2.2	278	9	US-09-796-692-3034	Sequence 3034, Ap
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26	91	2.0	2139	10	US-09-828-447-7	Sequence 7, Appli
27	77.2	1.7	13953	9	US-10-096-961-3	Sequence 3, Appli
28	76	1.6	760	10	US-09-828-447-1	Sequence 1, Appli
29	76	1.6	2276	10	US-09-828-447-6	Sequence 6, Appli
30	73.6	1.6	285	10	US-09-867-701-5561	Sequence 5561, Ap
31	71.6	1.5	582	10	US-09-764-870-112	Sequence 112, App
32	71.6	1.5	582	10	US-09-764-860-50	Sequence 50, Appl
33	68.8	1.5	503	10	US-09-764-870-92	Sequence 92, Appl
34	68.4	1.5	2517	10	US-09-476-242-16	Sequence 16, Appl
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36	68.4	1.5	2523	10	US-09-476-242-15	Sequence 15, Appl
37	68.4	1.5	2529	10	US-09-476-242-14	Sequence 14, Appl
38	68.4	1.5	2535	10	US-09-476-242-13	Sequence 13, Appl
39	68.4	1.5	2541	10	US-09-476-242-9	Sequence 9, Appl
40	68.4	1.5	2541	10	US-09-476-242-10	Sequence 10, Appl
41	68.4	1.5	2541	10	US-09-476-242-11	Sequence 11, Appl
42	68.4	1.5	2541	10	US-09-476-242-12	Sequence 12, Appl
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44	57.2	1.2	1680	9	US-09-938-842A-787	Sequence 787, App
45	56.4	1.2	773	10	US-09-910-943-594	Sequence 594, App

ALIGNMENTS

RESULT 1
US-09-927-112-1
Sequence 1, Application US/09927112
Patient No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32544, a novel human phospholipase C and
FILE REFERENCE: 38155-20048.00
CURRENT APPLICATION NUMBER: US/09/927,112
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/246,808
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4635
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (435) ... (4058)
US-09-927-112-1

Query Match 100.0%; Score 4635; DB 10; Length 4635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4501 TACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4560

QY 4561 TCTGCCCCACCCACGCTGCTCCGAGTAGGAACTGAGAGCGGAGTAGACAGTAA 4620
DB 4561 TCTGCCCCACCCACGCTGCTCCGAGTAGGAACTGAGAGCGGAGTAGACAGTAA 4620
QY 4621 CGGGGCCCGAGCCCG 4635
DB 4621 CGGGGCCCGAGCCCG 4635

RESULT 2

US-09-927-112-3
; Sequence 3, Application US/09927112
; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-927-112-3

Query Match 78.2%; Score 3624; DB 10; Length 3624;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 ATGGCTTCCCGACAGCCGCGCCCTTCTTGCCAGCTTTCCGCTGAGAGACCCAGG 494
DB 1 ATGGCTTCCCGACAGCCGCGCCCTTCTTGCCAGCTTTCCGCTGAGAGACCCAGG 60
QY 495 CCGGATCCCGAGAGAGAGTGGCTTTCTTGAGGCGCAATTGCGCCGTGGTGAAGCG 554
DB 61 CCGGATCCCGAGAGAGAGTGGCTTTCTTGAGGCGCAATTGCGCCGTGGTGAAGCG 120
QY 555 TCGATGGGTGCTTCAAGAGAGGAGTGCAGATGTGAAGCTGGTGGCGCTCAAGAGG 614
DB 121 TCGATGGGTGCTTCAAGAGAGGAGTGCAGATGTGAAGCTGGTGGCGCTCAAGAGG 180
QY 615 CTGGTCCGCTTCTTACTACTGAGAGACCGCTCTGCAATCCGCTGAGAGCCCTTCAAG 674
DB 181 CTGGTCCGCTTCTTACTACTGAGAGACCGCTCTGCAATCCGCTGAGAGCCCTTCAAG 240
QY 675 AAGAAAGAGAGGCGCAAGATCTCCATCGACTCCATCCAGAGGTGAGAGGCGGCGAG 734
DB 241 AAGAAAGAGAGGCGCAAGATCTCCATCGACTCCATCCAGAGGTGAGAGGCGGCGAG 300
QY 735 TCGAGAGTCTTCCAGAGCTTCACTGAGAGGAGCTTCAAGAGGAGCTTCAAGAGCT 794
DB 301 TCGAGAGTCTTCCAGAGCTTCACTGAGAGGAGCTTCAAGAGGAGCTTCAAGAGCT 360
QY 795 TACCAAGGAGAGAGAGAGAGTGTGAGAGCTGTGCTCAAGAGAGAGAGTGTGAGAG 854
DB 361 TACCAAGGAGAGAGAGAGAGTGTGAGAGCTGTGCTCAAGAGAGAGAGTGTGAGAG 420
QY 855 ACCTGGGTCACTGGGCTTCACTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
DB 421 ACCTGGGTCACTGGGCTTCACTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 915 CGCCGCGAG 974
DB 481 CGCCGCGAG 540
QY 975 GGGAGATGAGAGCTGAGACTTGGAGAGGTCCTGAGAGCTGCTGCAAGAGCTCAAGCTGAAC 1034

DB 541 GGGAGATGAGAGCTGAGAGATTTGGAGAGTCTGAGAGCTGCTGCAAGAGCTCAAGCTGAAC 600
QY 1035 CTGCCCGGAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1094
DB 601 CTGCCCGGAGAGAGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 1095 ACGCTGGGTCTTGAAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1154
DB 661 ACGCTGGGTCTTGAAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 1155 TACCTGCTCATGCTGAG 1214
DB 721 TACCTGCTCATGCTGAG 780
QY 1215 CGCTTCTGAG 1274
DB 781 CGCTTCTGAG 840
QY 1275 ATGAGAGAGTGTGAG 1334
DB 841 ATGAGAGAGTGTGAG 900
QY 1335 TTCAACCACTACACAG 1394
DB 901 TTCAACCACTACACAG 960
QY 1395 CACCAAGAGATGAG 1454
DB 961 CACCAAGAGATGAG 1020
QY 1455 CTGGTGGGTGAG 1514
DB 1021 CTGGTGGGTGAG 1080
QY 1515 GCTGAGTGGGTGAG 1574
DB 1081 GCTGAGTGGGTGAG 1140
QY 1575 CACCATGGCTTCACTGAG 1634
DB 1141 CACCATGGCTTCACTGAG 1200
QY 1635 AATATGCTTCTTCAAG 1694
DB 1201 AATATGCTTCTTCAAG 1260
QY 1695 GTCAATCAAG 1754
DB 1261 GTCAATCAAG 1320
QY 1755 CTGATCAAG 1814
DB 1321 CTGATCAAG 1380
QY 1815 AAGATCTCTGAG 1874
DB 1381 AAGATCTCTGAG 1440
QY 1875 GAGGTGTCTGAG 1934
DB 1441 GAGGTGTCTGAG 1500
QY 1935 GATGATCAAG 1994
DB 1501 GATGATCAAG 1560
QY 1995 ATCAAGAGAGTGAAG 2054
DB 1561 ATCAAGAGAGTGAAG 1620
QY 2055 TCCCATCTGAG 2114

Db 1621 TCCCATCTGAAAGCTCGAGCGCAAGCAAGCTGAAGAGGACGTGAGTCTGGGGAG 1680
QY 2115 GATGCGGGGGCCGAGAGCCCAATGCGCGCTGTGTGGGAAGCTTCCAGGGCCAG 2174
Db 1681 GATGCGGGGGCCGAGAGCCCAATGCGCGCTGTGTGGGAAGCTTCCAGGGCCAG 1740
QY 2175 AAGAGGGGAGCAAGCTGAAGAGCGCGCAGCGTGAAGAGGAGATGAGGTTCAGAGC 2234
Db 1741 AAGAGGGGAGCAAGCTGAAGAGCGCGCAGCGTGAAGAGGAGATGAGGTTCAGAGC 1800
QY 2235 TCCCGGGAGGCGAGAGCCGAGGGCGAGCCCGCAGAGAGACCTGAAAGCTGTCCCG 2294
Db 1801 TCCCGGGAGGCGAGAGCCGAGGGCGAGCCCGCAGAGAGACCTGAAAGCTGTCCCG 1860
QY 2295 GCGCTCTCTGAACCTGTGGAAGTACACCAAGTCCGTGGCCCAACAGACATAGATGAG 2354
Db 1861 GCGCTCTCTGAACCTGTGGAAGTACACCAAGTCCGTGGCCCAACAGACATAGATGAG 1920
QY 2355 GCGGCGTCCAGCTGGAGAGTGTGTCTTTCAGCGAGACCAAGGCCCAACAGATTCGAG 2414
Db 1921 GCGGCGTCCAGCTGGAGAGTGTGTCTTTCAGCGAGACCAAGGCCCAACAGATTCGAG 1980
QY 2415 CAGAAAGCGGCGAGTACCTACCTGTAACCAAGAGAGTCTTCCCGCATTCACCTCC 2474
Db 1981 CAGAAAGCGGCGAGTACCTACCTGTAACCAAGAGAGTCTTCCCGCATTCACCTCC 2040
QY 2475 TCCCTACCTGTGAGCTCCAGCACTACCAACCGGAGCCCTTGTGAAGCGCGGTGCA 2534
Db 2041 TCCCTACCTGTGAGCTCCAGCACTACCAACCGGAGCCCTTGTGAAGCGCGGTGCA 2100
QY 2535 ATGGTTCCTCTGAACCTACAGTCAAGAGGGGCGAGTGTGAGCTGAACCGAGCCAAATTC 2594
Db 2101 ATGGTTCCTCTGAACCTACAGTCAAGAGGGGCGAGTGTGAGCTGAACCGAGCCAAATTC 2160
QY 2595 AGCGCCAAAGGT 2654
Db 2161 AGCGCCAAAGGT 2220
QY 2655 AACCCCAACTCGAGAGAGCCCGCTGCGGGGAGCTCAAGAGAGAGCTGTGTGTGTGTGTGT 2714
Db 2221 AACCCCAACTCGAGAGAGCCCGCTGCGGGGAGCTCAAGAGAGAGCTGTGTGTGTGTGTGT 2280
QY 2715 ATCAGTGGCGAGAGCTTCCCAACCGCGGAGCTCAATGTGTGTGTGTGTGTGTGTGTGT 2774
Db 2281 ATCAGTGGCGAGAGCTTCCCAACCGCGGAGCTCAATGTGTGTGTGTGTGTGTGTGTGT 2340
QY 2775 ATGCAAGCTTGT 2834
Db 2341 ATGCAAGCTTGT 2400
QY 2835 ACCGCGGT 2894
Db 2401 ACCGCGGT 2460
QY 2895 GTGCAATGCGGAGATGCGGT 2954
Db 2461 GTGCAATGCGGAGATGCGGT 2520
QY 2955 CGTGAATTCATTTGCGCAGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3014
Db 2521 CGTGAATTCATTTGCGCAGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
QY 3015 GTGTACCTAGAAAGGATGGAAGAGAGCTTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 3074
Db 2581 GTGTACCTAGAAAGGATGGAAGAGAGCTTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
QY 3075 AGCGGTAAAGTCAAGCAGAGCTTGTGGGCTTAAAGAGCTTCTTCCAGAGGCCCAAAGCCC 3134
Db 2641 AGCGGTAAAGTCAAGCAGAGCTTGTGGGCTTAAAGAGCTTCTTCCAGAGGCCCAAAGCCC 2700
QY 3135 GCGT 3194
Db 2701 GCGT 2760

QY 3195 ATCTGCGGCGCAGCGCCAGCGCCCGACCAAGAGCCAAAGAGCCGAGGCCCTTC 3254
Db 2761 ATCTGCGGCGCAGCGCCAGCGCCCGACCAAGAGCCAAAGAGCCGAGGCCCTTC 2820
QY 3255 CCGAGAGCTGT 3314
Db 2821 CCGAGAGCTGT 2880
QY 3315 CCCCCCGGAGCCCGAGCTGTCCGGAAGCCCAAGCCAGAGAGGGGCGGCGAGCGGAGC 3374
Db 2881 CCCCCCGGAGCCCGAGCTGTCCGGAAGCCCAAGCCAGAGAGGGGCGGCGAGCGGAGC 2940
QY 3375 CCCCCGAGTAAAGCGCGCAGCTGTGCGGTGCAAGAAAGCCCTGTGTGTGTGTGTGTGTGT 3434
Db 2941 CCCCCGAGTAAAGCGCGCAGCTGTGCGGTGCAAGAAAGCCCTGTGTGTGTGTGTGTGTGT 3000
QY 3435 CGTGTCTGT 3494
Db 3001 CGTGTCTGT 3060
QY 3495 GATCTGT 3554
Db 3061 GATCTGT 3120
QY 3555 CCTGCAAGCAGGCGAGGAGCCATTCGCAAGAGCCCGGGCTCGGGCTGATCTCATGTGGG 3614
Db 3121 CCTGCAAGCAGGCGAGGAGCCATTCGCAAGAGCCCGGGCTCGGGCTGATCTCATGTGGG 3180
QY 3615 GCGCCCTGT 3674
Db 3181 GCGCCCTGT 3240
QY 3675 GGTCTGT 3734
Db 3241 GGTCTGT 3300
QY 3735 AGCCGAGCAGCGCGGAGATCCCGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3794
Db 3301 AGCCGAGCAGCGCGGAGATCCCGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3360
QY 3795 CAAGCGGGGGCGCTGAGGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3854
Db 3361 CAAGCGGGGGCGCTGAGGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
QY 3855 AGAGTAAATCCCATGT 3914
Db 3421 AGAGTAAATCCCATGT 3480
QY 3915 CAGGCGCTGT 3974
Db 3481 CAGGCGCTGT 3540
QY 3975 CCGT 4034
Db 3541 CCGT 3600
QY 4035 CCTTGGCTGT 4058
Db 3601 CCTTGGCTGT 3624

RESULT 3

US-09-969-14
; Sequence 14, Application US/09804969
; Patent No. US20020081595A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomukichy, Boris
; APPLICANT: Donoho, Gregory
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abuln, Alejandro

; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US20020081595A1el Human Phospholipases and Polynucleotides En
 ; FILE REFERENCE: LEX-0148-USA
 ; CURRENT APPLICATION NUMBER: US/09/804,969
 ; CURRENT FILING DATE: 2001-03-13
 ; PRIOR APPLICATION NUMBER: US 60/188,885
 ; PRIOR FILING DATE: 2000-03-13
 ; PRIOR APPLICATION NUMBER: US 60/189,693
 ; PRIOR FILING DATE: 2000-03-15
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 2289
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-804-969-14

Query Match 6.7%; Score 308.6; DB 10; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 2.2e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

QY 744 TTCAGGCGCTACCTGACGCGACGCTTCAACCCCACTGCTGCTTCAAGCTTACCAACGCGC 803
 DB 229 TTGCTGTGATGCTTGGAGAGAGCTTCCCTGAGCAGGCGCTTCACTGTTTTCAT 288
 QY 804 AGCCACCGCGAGTGTGCTGACCTGTCTCCACGAGCAGGAGTGGCGGCACTGGATC 863
 DB 289 GCGCGCGCTCCAACTGACCTGATGGCCAAAGATGTTGAGAGGCGCCAGATATGATG 348
 QY 864 ACTGCGCTGCTCACTCATGCGCGCATGAGCAGAGACAGCTGCTGCGCGCCAG 923
 DB 349 CAGAGGCTCAGCTGTGGTGGATCTTGTCAACAGCATGAGCAGGAGGCGCT- 404
 QY 924 CGCAGCAGGAGCAGTGGCTGAAGCAGAGCTTGAAGAGCGGAGCGAGAGAGGAGTGC 983
 DB 405 -----GACCAATGCTGAGCAGCTTGTTCATGAGAGCAAAATAGAGATGAT 456
 QY 984 AGCCTGAGCATTTGGAGGCTGCTGACGCTGCTGACAGACTCAACGCTGAACCTGCCCCG 1043
 DB 457 AAGATGATGTTTCCAAAGATTTAGCGGTTATTTGCACTTATGATGATGAAATGAGACCA 516
 QY 1044 CAGAGGCTGAAGCATGTTTCAAGGAGGAGCAGACGAGATGACCAACGAGAGCGCTGCT 1103
 DB 517 GAATATGCTTCACTGCTTCTTCAAGGAGCAGACAG-TCCTGAGTCTGGAACCTTGGAA 573
 QY 1104 TTGAAGAGTCTGCTCTTCTACAGATGATGTCACCGCGCGGAGCTTACCTGCTC 1163
 DB 574 GAGAGAGATTTGTACAGATTTCTATGAGGCACTTGAACGATGAGTGAAGGAGACTG 633
 QY 1164 ATGCTGACCTTAAGCAACCAAGAGCACTGATGCGGAGCGGAGCTGAGCGCTTCTG 1223
 DB 634 TTTGAAAGTTTTCAGCTGATGGGAGAGGCTGAGCTGCTGGAATTTTGGATTTTCC 693
 QY 1224 CAGGTGAGACAGAAATGCGCGGTGAGACCTTCCAGAGCTGCCAGAGCATCTGAGAG 1283
 DB 694 CAGAGAGAGCAGAAAGAGAGAGAGCTGACCTTGAACCTTCTGGAATCTCAATTAACGC 753
 QY 1284 TTTGAGACCTAGCCCAAGAAAGAGTAAAGGGGCTGCGGAGTGAAGGCTTCAACCAAC 1343
 DB 754 TATGAACCTTTCAGAGAGTGGCAAACTGCGGAGATGTCGATGATGATGATGCTTCC 813
 QY 1344 TACACAGAGAGCGCTGCTGCTGATCTTCAACCTTGAAGACCAACCATGTCAGCAGAG 1403
 DB 814 TACCTGTGCTTAAGATGAGAGCATCTTCAACCTGAGCTGCTCCCATCTATAGAGAT 873
 QY 1404 ATGAGCAGACCGCTGAGCAGCATCTTCACTACCTGCTCCCAACCAACCTTCTGCTG 1463
 DB 874 ATGATCAACCCCTGTAACCACTTCACTTCTCTTCTCATTAACCACTTCTTCTGCTG 933
 QY 1464 GACCAAGCTATGCTCCAGTCAAGGAGGAGCATGATGCTTGGGCTCTGAGGCTGCTGC 1523

DB 934 GACCACTTTGGCGGACAGAGAGCGCTGAGGAGATATATACGGGCTTGAACGCGGCTGC 993
 QY 1524 CGTGTGCTGAGAGTGAAGTGTGAGATGGGCGGACGAGGAGCCATTTGTCACCAATGAGC 1583
 DB 994 CGCTGCGTGAAGTGTGATGATGAGATGAGACTGAGCGGAGAACCTTGTCTTACACGGA 1053
 QY 1584 TACACTGACTTCCAGATCTCTTCAAGAGCTCATTTGAACCATCAACATATATGCC 1643
 DB 1054 CACACCTGACCTCCCGATCTCTTCAAGATGTCGTGGCCACAGATAGACAGATATGCC 1113
 QY 1644 TTTCAAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1703
 DB 1114 TTTCAAGATCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 1173
 QY 1704 CAGAAAGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1763
 DB 1174 CAGCAGACCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1233
 QY 1764 GTGAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1823
 DB 1234 TTGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1293
 QY 1824 GTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1883
 DB 1294 GTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1353
 QY 1884 GATGAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1943
 DB 1354 CTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1413
 QY 1944 ACCAATGGAAGCTGTGAAGAAACCTGTAAGAGGAACTGTGATTCCTCAT 1996
 DB 1414 CAGAGAGCAACCTTCAAGATTAAGACAAAGAAAGAAATCCAGGCCATCTT 1466

RESULT 4
 US-09-908-664-3
 ; Sequence 3, Application US/09908664
 ; Patent No. US20020115178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura
 ; APPLICANT: Tsai, Fong Yin
 ; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
 ; FILE REFERENCE: 38155-20022.00
 ; CURRENT APPLICATION NUMBER: US/09/908,664
 ; CURRENT FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: US 60/218,675
 ; PRIOR FILING DATE: 2000-07-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 2289
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-908-664-3

Query Match 6.7%; Score 308.6; DB 10; Length 2289;
 Best Local Similarity 54.2%; Pred. No. 2.2e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;

QY 744 TTCAGGCGCTACCTGACGCGACGCTTCAACCCCACTGCTGCTTCAAGCTTACCAACGCGC 803
 DB 229 TTGCTGTGATGCTTGGAGAGAGCTTCCCTGAGCAGGCGCTTCACTGTTTTCAT 288
 QY 804 AGCCACCGCGAGTGTGCTGACCTGTCTCCACGAGCAGGAGTGGCGGCACTGGATC 863
 DB 289 GCGCGCGCTCCAACTGAGCTGATGGCCAAAGATGTTGAGAGGCGCCAGATATGATG 348
 QY 864 ACTGCGCTGCTCACTCATGCGCGCATGAGCAGAGACAGCTGCTGCGCGCCAG 923

Db 349 CGAGGCTCCAGCTGTTGGATCTTTGACACGATGAGACCATGAGGCGCT---- 404
 Qy 924 CGCACCAGGAGCAGTGGCTGAAAGACCTTTGACGAGCGCAGAAACGGGATGCG 983
 Db 405 -----GGACCAATGGCTGAGCGCATTTGGTTCAACGTGAGAACAAAATCAGATGCT 456
 Qy 984 AGCTGAGCATTTGGCCAGGCTCTGAGCTGCTGACAGCTGCAACCTGAACTGCGCCGG 1043
 Db 457 AGATGATGTTCCAGAAAGTTGACGGGTATTTGACCTTAATGATGGAAATGACCAA 516
 Qy 1044 CAGAGGTGAAGCAGATGTTCAAGGAAAGCAGGATGACCAAGGAGCGTGGT 1103
 Db 517 GAATATGCTTCACTGCTTTTTCAGGACGAGACAG---TCCAGTCTGGAACCTTGAA 573
 Qy 1104 TTTGAAGATTCTGTGCTTTCTCAAGATGATGCTCAACCCCGGAGCTTACCTGCTC 1163
 Db 574 GGAGAAATTCGATCAGTTCTATTAAGGCACTTAAGAGTCTGAGGAGGAGAACTG 633
 Qy 1164 ATGCTGACCTACGACCAACCAAGGACCACTGGATGCGCGCAGCTGACGCTTCTG 1223
 Db 634 TTTGAAAGTTTTCAGCTGATGGGACAGAGCTGACTGCTGGAATTTTGGATTTCTC 693
 Qy 1224 CAGGTGAGCAGAAAGATGCGGGGTGTGACCTCGAGAGCTGCAAGACATCATGAGCAG 1283
 Db 694 CAGAGGAGCAGAAAGAGAGAGACTGCACTGAGCTTGTCTGGAACCTCATTTGACCG 753
 Qy 1284 TTTGAGCCATGCCAGAAAACAGATGAAGGGGTGCTGCGGCACTTGTGCTTCAACCA 1343
 Db 754 TATGAACTTTCAGACAGTGGCAACCTGCGATGTGCTGATGATGATGATGCTTCTGAC 813
 Qy 1344 TACACCGAGGAGCCTGCGGTGATCATCTTCAACCTGAGACCAACATGTCAGACAGAC 1403
 Db 814 TACCTGCTTAAAGATGAGACATCTTCAACCACTGCTGCTTCACTTACAGAT 873
 Qy 1404 ATGACGAGCGCTGAGACCACTTACTATCACTGTGCTCAACCACTTACTGCTGCTGCT 1463
 Db 874 ATGACTAACCTTGAACCACTTACTTCTGCTTCTTCACTTCACTTACTGCTGCTGCTG 933
 Qy 1464 GACCACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1523
 Db 934 GACCACTTTCGCGCAGAGAGAGGCTGAGGATTTATACGGGCTTGAAGCGGGGCTG 993
 Qy 1524 CGCTGCGTGGAGTGGATGCTGCTGAGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGG 1583
 Db 994 CGCTGCGTGGAGTGGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1053
 Qy 1584 TACACTGCTTCCAGATGCTTCTTCAAGAGGCTTATGAACCTTCAACCAATATGCT 1643
 Db 1054 CACACCTGACCTCCGCTGCTGCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113
 Qy 1644 TTTCACTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1703
 Db 1114 TTTCACTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
 Qy 1704 CAGAAAGAAATGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1763
 Db 1174 CAGCAGACCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
 Qy 1764 GTGACAGTGAAGATGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1823
 Db 1234 TTTGATGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
 Qy 1824 GTGAGGAGGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1883
 Db 1294 GTGAGGAGGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
 Qy 1884 GATGAGGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1943
 Db 1354 CCGTGAAGTGAAGATGCAAAATTTGGGCTGAGGCTGCAAGTTGAGACTGAGGCTGAG 1413
 Qy 1944 ACCAATGGAAGGCTGAGAAACACTGCTTAAAGAGAACTGGAATTCCTCAT 1996
 Db 1414 CAGAGCAGAACTTCAAGATTAAGACAAAAGAAATTCACACCTATCTT 1466

RESULT 5
 US-09-908-664-1
 ; Sequence 1, Application US/09908664
 ; Patent No. US20020115178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura
 ; APPLICANT: Tsai, Pong Yin
 ; TITLE OF INVENTION: 16818 AND 16839, NOVEL HUMAN
 ; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 38155-20022.00
 ; CURRENT FILING DATE: US/09/908, 664
 ; PRIOR APPLICATION NUMBER: US 60/218, 675
 ; PRIOR FILING DATE: 2000-07-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2629
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (257)...(2545)
 US-09-908-664-1
 Query Match 6.7%; Score 308.6; DB 10; Length 2629;
 Best Local Similarity 54.2%; Pred. No. 2.3e-65;
 Matches 679; Conservative 0; Mismatches 559; Indels 15; Gaps 2;
 Qy 744 TTCACGCTTACCTGACGAGCAGCTTTCAGACCCCACTGCTGCTGAGCATTCACACGCG 803
 Db 485 TTGCTGCTGAGCTTGGCAGAGAGCTCCCTCGAGAGAGGCTTACCATTTGCTTCAT 544
 Qy 804 AGCACCAGGAGTGGCTGAGCTGCTTTCACACAGAGAGAGTGGCGGACCTGGGTC 863
 Db 545 GGGCGCGCTCCAACTGAGACCTGATGAGCAAGTGTGAGAGAGGCGGCAATATGATG 604
 Qy 864 ACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
 Db 605 CGAGGCTCCAGCTGTTGATGATCTTTCACAGATGAGACCATGAGAGCTT----- 660
 Qy 924 CGACACAGGAGCAGTGGCTGAGAGCAGCTTTCAGAGGCGGAGGAGGAGGAGGAGGAG 983
 Db 661 -----GGACCAATGGCTGAGCGATTTGCTTCAACGTGAGACAAAATGAGATGCT 712
 Qy 984 AGCTGAGCATTTGGCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
 Db 713 AGATGATTTCCAGAAAGTTGACGCGTTATTGCACTTAATGATGATGATGATGATGAT 772
 Qy 1044 CAGAGGTGAAGATGTTTCAGAGGAGGAGCAGAGAGACCAACCAAGGAGCGTGGT 1103
 Db 773 GAATATGCTTCAAGTCTTTTTCAGGAGCAGACAG---TCCAGTCTGAAACCTTGAA 829
 Qy 1104 TTTGAAGATTCTGTGCTTCTTCAAGATGATGCTCACCGCGGAGCTTCACTGCTC 1163
 Db 830 GGAGAAATTTCTGATGATTTTAAGGATGATCAAAAGTGTGAGGTGAGGAACTG 889
 Qy 1164 ATGCTGACTTACAGCAACCAAGAGCACCTGAGATGCGGACAGCTGAGCGCTTCTG 1223
 Db 890 TTTGAAAGTTTTCAGCTGATGGGAGAAAGCTGACTCTGGAATTTTGGATTTCTC 949
 Qy 1224 CAGGTGAGCAGAAAGATGCGGGGTGTGACCTTGAAGAGCTGCGAGACATTCAGAGAG 1283
 Db 950 CAGAGGAGCAGAAAGAGAGAGACTGCACTTCTGACTTCTGGAATCTATGACCGG 1009
 Qy 1284 TTTGAGCCATGCCAGAAAACAGATGAAGGGGTGCTGCGGCACTTATGATGCTTCAACCA 1343
 Db 1010 TATGAACTTTCAGACAGTGGCAAACTGCGGCAATGCTGCTGATGATGATGATGCTTCT 1069

QY	1344	TACACAGAGCCGCTGAGTGAATCTTCAACCTGAGACACCAATGTCACAGAC	1403
Db	1070	TACCTGTCTTAAGAGATGAGACATCTTCAACCCACCTGCTCCCATCTATCAGAT	1122
QY	1404	ATGAGCGAGCCGCTGAGCATCTACTTCACTCGTCCCAACAACCTTACTCGTGGT	1463
Db	1330	ATGACTCAACCCCTGAACACCTACTCTTATCTGCTCTTCTATTAACCTACTTAAGTGGG	1189
QY	1464	GACCACTCATGTCCCAATCAAGGATGACATGATGCTTGGGTCTGAGAGCTGAGTGC	1523
Db	1190	GACCACTTTTCGGCGAGAGCAGCGTGAAGGATATATACGGGCTCTGAAGGGGGGTGC	1249
QY	1524	CGCTCCGTGAGAGTGGACCTGCTGGGAGAGGGCCGACGGGGAGGCCATTGTGACATGGC	1583
Db	1250	CGCTCCGTGAGAGTGAATGTAATGGGAATGGAACCTGAGCGGGGAACCTGTCTTTTACACGGA	1309
QY	1584	TACACTGTGACTTCCAAAGATCTCTTCAAAAGCGTCAATGAAACCATCAACAAATATGCC	1643
Db	1310	CACACCTTGACCTCCGACATCTGTTCAAAAGATGTCGTGGCCACAGTACACAGTATGCC	1369
QY	1644	TTTCATCAAGATGTGATCCCAAGTATCTCTGCAATGGAAAACAATGCAAGTGTCAATCAG	1703
Db	1370	TTCCAGACATAGACTACCAAGTCAATTTGTCTGGAAGCCACATGCAAGCTGGAGAG	1429
QY	1704	CAGAAAGAAATGSCCCAGTATCTTGACTGACATCTTTGGGGAACAAGTGAACCTGTCA	1783
Db	1430	CAGAGACCAATGGCCCTCTCATCTGACTGAGATCTTGGGGGAACAAGTGTGAGCACACC	1489
QY	1764	GTGAGCAGTGAAGATGTCACACACATCCCTCTCCACAAGTCTCAAGGGCAAGATCTCTC	1823
Db	1490	TTGGATGGGGTGTGCTGCCCATCTAGAGTCTCCCTCGCTGAGAGACTTCGAGAGAAAGATCTTG	1549
QY	1824	GTGAAGGGGAAGAGCTTCCAGCCAAATCAGCGAGATGCGAGAAAGCGAGGTGTCT	1883
Db	1550	GTGAAGGGGAAGAGATTAACTTGGAGAAACCTTGGAATATGAGAAAGAGAGACGAA	1609
QY	1884	GATGAGACAGTGTGATGATTTGACGATGACTGCAAGCTCCTCAATGGGGATGACATCC	1943
Db	1610	CCTGAGTTGGAAAGATCAGAAATTTGGGCTGAGATCCCAATTTGABAATGAGACTGAGACC	1669
QY	1944	ACCAATCGAAAGCTGTGAAAAACATGCTTAAGAGAAATGGAATTCCTCAT	1996
Db	1670	CAGGACGAAACCTTCAGAATTAAGGACAAAAAGAAATTCACACCATCTT	1722

RESULT	6
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/ Sequence 20, Application US/09804969
/ Patent No. US20020081595A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Yi
/ APPLICANT: Nepomnichy, Boris
/ APPLICANT: Donomichy, Gregory
/ APPLICANT: Hilbun, Erin
/ APPLICANT: Turner, C. Alexander Jr.
/ APPLICANT: Abuin, Alejandro
/ APPLICANT: Friedrichz, Glenn
/ APPLICANT: Zambrowicz, Brian
/ APPLICANT: Sands, Arthur T.
/ TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides
/ FILE REFERENCE: LEX-0148-USA
/ CURRENT APPLICATION NUMBER: US/09/804,969
/ CURRENT FILING DATE: 2001-03-13
/ PRIOR APPLICATION NUMBER: US 60/188,885
/ PRIOR FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: US 60/189,693
/ PRIOR FILING DATE: 2000-03-15
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 2709
/
/ TYPE: DNA
/ ORGANISM: homo sapiens

```

US-09-804-969-20

Query Match	6.7%	Score 308.6;	DB 10;	Length 2709;
Best Local Similarity	54.2%;	Pred. No. 2.3e-65;		
Matches 679;	Conservative 0;	Mismatches 559;	Indels 15;	Gaps 2;

OY	744	TTCCAGCGCTACCTCGACGGGAGCTTGGAACCCCAACTGGCTTACACATCTACACGCGC	803
Db	486	TTGCTGCGTAGCTGGCAGAGAGACTCCCTTGGAGCAGAGGCTTTCACCATTTGCTTCAT	545
OY	804	AGCCACCGGAGTGGCTGGACTTGGTCTCCACGACGAGAGTGGCGGACCTTGGTTC	863
Db	546	GGCCCCCGCTCCAACTTGGACTGATGGCCAAAGTGTGAGAGGGCCGAGATATGATG	605
OY	864	ACTGCGCTGGCGTACCTCATGGCCGGGATCAGGCGACGAGGACAGCTGGCTGGCCGCGCAG	923
Db	606	CGAGGGCTTCAGCTGTGTGTGTGAATCTTGTCAACGACATGACCATCAGAGGCGCTT----	661
OY	924	CGCACCGAGAACAGTGGCTGAAACGATTTGACGAGGCGGACAAAGACGGGAGTGGC	983
Db	662	-----GGACCAATGGCTGAGGCAATTTGGTTTCAACGTGGAGACAAAATATCAGATGGG	713
OY	984	AGCCTGAGCACTTGGCGAGGCTCTGGACCTGCTGCAAGCTCAACGTGAACCTGCCCCGG	104
Db	714	AMAGTAGTCTTCAAGAACTTCAACGGCTTATTGCACTTAATGAATGGAAATGAGACAA	773
OY	1044	CAGAGGCTGAAGCAGATGTTCAAGGAAACGGACACGAGATGACCAAGGACGCTGGGT	110
Db	774	GAAATATGCTTCACTCTTTTTCAGGGCAGCAGACG---TCCAGTCTGGAACCTTGAA	830
OY	1104	TTTGAAGGTTCTTGCCCTTCAACAGATGATATGTCCACCCGCGGGACCTTACCTGCTC	116
Db	831	GGAGAAATTCCTGACAGCTTCTATAGGCACTTAATTAAGTGTGAGGTCGACGAACTG	890
OY	1164	ATGCTGACTTACAGCAACCAAGAGCAACCTTGATCCGCGACCTGACGCGCTTCTG	122
Db	891	TTTGAAGTTTTCAGCTGATGGGACGAAGCTGACTCTGTGGAAATTTTGGATTTCCCTC	950
OY	1224	CAGGTGAGCAGAAAGATGGGGGTGTGACCTCGAGAGCTGCGACAGACATCATCCAGCAG	128
Db	951	CAAGGAGCAGAAAGGAGAGAGACTGCACTCTGACCTTGTGGAACTCATATGACGCG	1010
OY	1284	TTTGAAGCATGCCCCAGAAAACAAGATGAAGGGCTCTGGGCAATGATGGCTTCAACAAC	134
Db	1011	TATGAACCTTACAGACAGTGGCAAACTGCGGCATGTCTGATGATGATGGCTTCCCTACAGC	1070
OY	1344	TAGACCAAGAGCCCTGTGGTGTGACATCTTCAACCTCGAGACACCATGTGACCAAGAC	140
Db	1071	TACTTGTCTTAAAGATGAGACATCTTCAACCAAGCCTGCTCCCACTATACAGAT	1130
OY	1404	ATGACGAGCGCGCTGAGCACTTATCATCCTGCTCCACAAACACTTACTCTGGGT	146
Db	1131	ATGACTCAACCCCTGAACCACTACTTCACTGTGCTTTCATTAACCACTACTAGTGGGG	1190
OY	1464	GACAGCTCATGTCCAGTTCACGGGTGACATGTATGCTTTGGGTCTGTGAGGCTGGCTGC	152
Db	1191	GACCACTTTTGGCGCCAGAGACACGTCGAGGATATATATCGGSCCTTGAAAGGGGGGTGC	1250
OY	1524	CGCTGCTGAGGTGATGCTGTGGATGTGGACCCGACGGGAGACCCATTGTGACCATATGC	1583
Db	1251	CGCTGCTGAGGTGATGTATGTGATGACCTTACGGGGAACTGTGTGTTTACACAGGA	1310
OY	1584	TATCACTGTGACTTCCAAAGATCTCTTCAAAAGCTGTATTGAAACCATCAACAATATGCC	1634
Db	1311	CACACCTTGACTTCCGCACTCTGTTCAAAGATGTGTCGACACAGTATGCC	1370
OY	1644	TTTATCAAGATAGTATACCAAGATCTGTCTCATTCGAAAAACACTGAGTGTATCTCAG	1703
Db	1371	TTTCAAGCATCAAGATCAACCAATCATCTTGTCCCTGGAGAACCACTGACGCTGGAGAG	1430
OY	1704	CAGAAAGAAATGGCCCAAGTATCTGACTGACATCTTTGGGACACAGCTGAACTGTCTATCA	1763
Db	1431	CAGGAGCAATGGCCCGTCTATCTGACTGAGATCTTGGGGAGCAAGCTCTGAGCACACCC	1490

QY 1764 GTGAGCAGTGAATGATCCACCACTCCCTCTCCACAGATGCTCAAGGGCAAGATCTTC 1823
DB 1491 TTGGATGGGGTGTCTGCTCCACTCAGTGCCTCGCTGAGAGCTTTGAGAGAAATCTCG 1550
QY 1824 GTGAGGGGGAAGAGCTCCAGCCCAATCAGCAGGAGTCCGAGAGAAAGCGAGTGTCT 1883
DB 1551 GTGAGGGGGAAGAGTAACTTACACTTGGAGAAAGCTGGAATATGAGAGAAAGAGAGAA 1610
QY 1884 GATGAGCAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
DB 1611 CTGAGATTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1670
QY 1944 ACCAATGGAAGCTGTGAAGAAACCTGCTAAGAGAACTGATTCCTTCAT 1996
DB 1671 CAGAGCAGAACTTCAAGATTAAGACAAAAGAAATCCAGCCCATCTT 1723

RESULT 7

US-09-835-996A-7
Sequence 7, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyun
APPLICANT: Qian, Xiahong
APPLICANT: Mang, Dunrui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835, 996A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 1840
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (140)..(1840)
US-09-835-996A-7

Query Match 6.6%; Score 307; DB 10: Length 1840;
Best Local Similarity 54.1%; Pred. No. 5.2e-65;
Matches 678; Conservative 0; Mismatches 560; Indels 15; Gaps 2;
QY 744 TTCCAGCGCTACCTGACGCGAGCTTTCAGACCCCACTGCTCTTCAAGCATCTACACGGC 803
DB 368 TTGCTGCGTGAAGCTGAGAGAGAGCTCCCTCGAGAGAGGCTTCAACATTTGCTTTCAT 427
QY 804 AGCCACCGGAGTCCGTGAGCTGTCTTCACACGAGAGAGTGGCGGACCTCGGCTC 863
DB 428 GGCGCGCTCCCACTGAGCTGATGGCAACAGTGTGAGAGAGGCCCAATATGATG 487

QY 864 ACTGCTCGCTTACCTCATAGCCGCGATCAGCGAGAGAGACAGCTTGGCTCGCCGAC 923
DB 488 CGAGGGCTCCAGCTGTGTGTGATCTTGTCAACAGCATGACCATCAGAGCGCT---- 543
QY 924 CGCACGAGGACCGATGCTTAAGACAGACTTTTACAGAGCCGCAAGAAACGGGATGCG 983
DB 544 -----GGAACCAATGCTGAGGATTTGTTTCAAGTGAACAAAATCAAGATGCT 595
QY 984 AGCCGACATTTGGGAGAGTCTGAGCTGCTGACCAAGCTCAAGCTGAACCTGCGCG 1043
DB 596 AAGATGATTTTCAAGAGTTCAGCGGTTATTGACCTTAATGAATGTGAATGAGCA 655
QY 1044 CAGAGGTGAAGCAGATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
DB 656 GAATATGCTTCACTTTTTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
QY 1104 TTTGAAGTCTGTGCTTTTCAAGAGATGATGTCACCCGCGGAGCTTACCTGCTC 1153
DB 713 GAGAGAAATTCATCAAGTTCATTAAGGCAATGACTAAAGTCTGAGTGAAGAGAACTG 772
QY 1164 ATGCTGACCTACAGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
DB 773 TTTGAAGTCTTTTCAAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
QY 1224 CAGTGAAGCAG 1283
DB 833 CAG 892
QY 1284 TTTGAAGTGTGAG 1343
DB 893 TATGAACCTTCAG 952
QY 1344 TACACAG 1403
DB 953 TACCTGTCTTAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1012
QY 1404 ATGAGCAG 1463
DB 1013 ATGACTCAACCCCTGAACACACTTCACTGCTCTTCTCAACACCTTACTTATGAGG 1072
QY 1464 GACAGCTATGCTCCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
DB 1073 GACAGCTTGTGAG 1132
QY 1524 CGTGTGAG 1583
DB 1133 CGTGTGAG 1192
QY 1584 TACACTGTGACTTCAAGATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
DB 1193 CACACCTGACCTCCGCACTCTGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1252
QY 1644 TTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1703
DB 1253 TTCCAGACATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1312
QY 1704 CAGAGAAATGAG 1763
DB 1313 CAG 1372
QY 1764 GTGAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1823
DB 1373 TTGGATGGGGTGTGCTCCACTCAGCTGCTGCTGCTGAGAGAGAGAGAGAGAGAG 1432
QY 1824 GTGAG 1883
DB 1433 GTGAG 1492
QY 1884 GATGAGCAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1943
DB 1493 CTGAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1552

FEATURE:
NAME/KEY: CDS
LOCATION: (153) ... (2360)
US-09-800-971-1

Query Match 5.5%; Score 301.8; DB 10; Length 3425;
Best Local Similarity 54.0%; Pred. No. 1.1e-63;
Matches 743; Conservative 0; Mismatches 607; Indels 27; Gaps 5;

545 GGTGAGCGGTGATGGTCCATGCAAGAGGATGCAAGTGTGAAGTCTGTCGCG 604
Db 164 GAGAGAGAGAGAGTGTGGCCATGCTGGGGCTCCGGCTCCGCAAGATCGCTCGCG 223
QY CTCCAGAGGCTGTGCTGCTTCTTACTACTGAGAGAGC-----CGCTCCGATCCG 658
Db 224 CACGTGCAACAAGAGCGGCTGTACCGCTGCAAGAGAGAGGCTGTGTGTTC 283
QY CTGAGGCGCTTCAACGAGAGAGAGAGGCAAGATCTTCATGCACTCCAGAGAGT 718
Db 284 GCGCGCATCCCGTGGTGGCCATGCAAGACATCTTCTGTGAGACATCGAGGGGT 343
QY GAGTGAAGGCGGCGAGTGGAGGCTTTCAGCGCTTCAAGCGAGCTTTCAGCCCA 778
Db 344 CCGGAGAGGCGACAGTCCAGAGGCTGCGGCGCTTC---GGGGTGTCTTTCGCGCAGC 400
QY CTGCTGCTTACGATCTTACCAAGCGGACCCGAGATGCTGTGAGCTTCCACAG 838
Db 401 GCGCTGCTTCAACATCCCTTTCAGAGGCGCGCAAGACCTGAGACCTGGCGGCTCC 460
QY CAGGAGGTGCGCGGCACTGGGTCACTGCGCTGCTTCACTGCGCGGATCAGCGA 898
Db 461 GCGTGAAGAGCGAGCGCTGGGTGGCGGCTTCAAGAGCTCCGCGCGGCTTGAAGC 520
QY CAGAGACAGCTGTGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 958
Db 521 CATGAGCGGCGGCGGCGGCT-----AGACCACTGAGATCACTCTTATCGCA 568
QY CGAGGCGGCAAGAGCGGCGGATGCGAGCTTGGAGGCTTGGAGGCTTGGAGGCT 1018
Db 569 CCGGCTTACTTCAACGAGAGAGAGATGCTTCAAGAGATCAAGAGCTTGTGAG 628
QY CAAGCTCAAGCTGAAGCTGCGCGGCGGAGAGGAGTGTTCAGAGAGCGGAGC 1078
Db 629 AATGATCAAGCTGAGATGAAGAGATGAGCTTCTCTTCAAGAGAGTGTGAG-- 686
QY GAGTGAACCAAGAGAGCGTGGGTTTGAAGATTTGTGCTTCTTCAAGAGATGATC 1138
Db 687 -CACTCAACCAAGAGAGCGTGTAGAGGGGCTGAGATGAGAGATGCTGCGCGGCTGCT 745
QY 1139 CACCGCGCGGAGCTTCACTGCTCATGCTGACCTAAGCAACCAAGAGACCACTGGA 1198
Db 746 GAGGCGGCGGAGCTGAGAGAGATTTTCATATGATCTGGCGGAGAGACCGCTGTAG 805
QY 1189 TCCCGCAGCTGAGCGCTTCTGAGGTGAGAGAGATGCGGGGTGTGAGCTTGA 1238
Db 806 TCCCTTGAAGCTGTGAGATCT--GAGAGACAGGCGGAGGCGGCGGCGGCGG 862
QY 1259 GAGCTGCGGAGATGAGAGAGATTTTGAAGCATGCGGCAAGAAAAGAGTAAAGGGCT 1318
Db 863 CCGCGCGCGAGCTTCAAGACCTATGAGCTCAAGAGAGAGAGAGAGAGAGAGT 922
QY 1319 GCGTGGCATTTGATGCTTCAACCACTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
Db 923 GATGACATGATGATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 982
QY 1379 TGAGACCAACATGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
Db 983 CACCGACAGCTGTGTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1042
QY 1439 GTCCCAACCACTTACTGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1498
Db 1043 CTCACCAACCACTTACTGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102

QY 1499 TGTGTGAGCTTGTGAGAGCTGAGCTGCGCTGCTGAGAGTGTGATGCTGAGAGTGGCCCGA 1558
Db 1103 TGTAGGGCTTGTGCGGAGGATGCGCTGCTGAGAGTGTGAGTGTGAGAGAGGCGGAGG 1162
QY 1559 CCGGAGAGCTTGTGAG 1618
Db 1163 AGGGAGAGCTGATCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1222
QY 1619 CATTTAAGCACTCAACCAATATGCTTTCATCAAGAGAGAGAGAGAGAGAGAGAGAG 1678
Db 1223 GGTCCAGAGCTGAG 1282
QY 1679 CGAAG 1738
Db 1283 GAG 1342
QY 1739 TGGGAG 1798
Db 1343 GGGGAG 1402
QY 1799 ACAGATGCTCAAG 1858
Db 1403 AG 1462
QY 1859 GAGTGGAG 1915
Db 1463 GATGGCGCGGCTGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519

RESULT 10

US-09-880-107-3293
Sequence 3293, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIORITY APPLICATION NUMBER: US 60/211,379
PRIORITY FILING DATE: 2000-06-14
PRIORITY APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3293
LENGTH: 2627
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 U09117
US-09-880-107-3293

Query Match 6.3%; Score 289.8; DB 10; Length 2627;
Best Local Similarity 54.2%; Pred. No. 8.2e-61;
Matches 744; Conservative 0; Mismatches 587; Indels 42; Gaps 6;

QY 564 GCCATGCAAG 623
Db 155 GCGCTGCTGAAG 214
QY 624 TTCTACTACTGAG 674
Db 215 TTCTAAGAGTGTGAG 274
QY 675 AAG 734
Db 275 ACCCGAGAGTCCAGCTGTCTTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
QY 735 TGGAGAGCTTTCAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794

Db	335	ACGGAGGCTCTGGAGAAATTCCCCCGTATGTGCCCCGAGAACCGCTCTCTTCATTTGTC	394
Qy	795	TACCAAGGACGCCACCGCGAGTGCCTGGACCTGTGTTCCACACAGACGAGGTGGCGCG	854
Db	395	TTCCAAAGAA---CCAGCGCAATACATTAACCTCATCCGCCCATCGCAGCTGATGCCAG	451
Qy	855	ACCTGGGTCACTGGACCTCGGTACTCCTCATTTGGCCGGCATTCAGCCAGCAGACCTGGCT	914
Db	452	CACCTGGGTCTGGGGCTGCACAAAGTATCTCCACCACTCAGCTTCATATGACACAGCTCAG	511
Qy	915	CGCCGCGACGCAACAAGGACCAAGTGGCTGAAGCAAGTTTGACAGAGCGCCACAAGAAC	974
Db	512	AAGCTACACACACTGAGATTTCATCTGCTTGGCAA-----AAGTGAACAAAAC	559
Qy	975	GGGGATGGAGGCTTAGCAATTGGCGAGGTCCTGACGTGCTGCACAAAGTCAACGTGAAC	1034
Db	560	AAGGACAAACAATATAGAGCTTCAAGGAGCTGCAGAACTTCTTGAAGAGCTCAACATCCAG	619
Qy	1035	CTGCCCCGACAGAGGATGAAGCAGATGTTTCAGGGAACGGACACAGATGACCAACCAAGG	1094
Db	620	GTGGACGACAGCTATGCCCGGAAGTCTTCAAGGAGGTATC---CATCTCCAGACAGAC	676
Qy	1095	AGCGTGGGTTTGAAGAGTTCTGTGCTCTTCTACAAATGATGTCCACCCGCGGAGCTTC	1154
Db	677	TCCCTTGGAGAGCAGAGGAATTTGAAGGCTTCTTCAAGATGTCTGACCCAGCGGTTGAGATC	736
Qy	1155	TACCTGTATGCTGATCACTTACAGCAACCAAGGACCACTGGATGTCGCGCCAGCCCGAG	1214
Db	737	GACCGGACCTTGCAGGAGCCGCGGGGCCCAGGGAGACTGTGTGCTGATCAAGTTAAGTC	796
Qy	1215	CGCTTCTGCAAGTGGAGAGAGAATGGCGGGTGTGACCTCTGAGAGCTGCCAGGACATC	1274
Db	797	AGCTTCTGCAAGCACACAGACACGGGAAGAGCGGACAGGGCTGCGCTGCGCTCTCTCCTC	856
Qy	1275	ATCGAGCAAGTTTGAAGCCATGCGCCAGAAAACAAGATGAAGGGGCTGTGTGGCACTTGAATGC	1334
Db	857	ATTGAGCCGCTAGAGCCACGAGAGACTTCCAAAGCCGAGGGAGATGACCAAGGACGGC	916
Qy	1335	TTCCACCAACTACACAGAGAGCCCTGTGCTGTAATCTTCAACCTTGAGCACCACCATATG	1394
Db	917	TTCCCAAGTACTTAATCTACTGTGGCTGAGCGGACGGCCTTACAGCTGGCACACCGCGGTTC	976
Qy	1395	CACCAAGCATGAGCGAGCGGCTGAGGCACTACTTTCATCACTCGTCCCAACAACCTTAC	1454
Db	977	TACCAAGACATGGGCGAGCCACTTAGCCACTTACCTGGTCTCTTCAACAACAACCTTAC	1036
Qy	1455	CTCGTGGGTGACAGCTCATGTGCCATCTCAGGGTGAATGATGCTTGGTCTCTGCAG	1514
Db	1037	CTGCTGGAGGACCAAGTACCGGGCCAGAGCACTGAAGCCTTAATCCGGCACTGTGC	1096
Qy	1515	GCTGGCTGCGGCTCGGAGAGTGGATCTGTGGATGGGCCCCGAGCGGAGCCCATTTGTG	1574
Db	1097	AAAGGCTGCGCATCTCGAGGCTTGAATGTGTGGAGAGGGGCCCAACACAGAACCATATCTC	1156
Qy	1575	CACCATGGCTACACTCTGACTTCCAAAGTCTTTCAAAAGAGTCATTGAAACCATCAAC	1634
Db	1157	TACCAACGGCTATCTTTCACCTTCAAGATCTCTTCTGGAATGTCTCAAGGCAATCCGG	1216
Qy	1635	AAATATGCTTTCATCAAGAAATGAGTACCAAGTATCTGTCCATGGAACCACTGCAGT	1694
Db	1217	GACTATGCTTCAAGGGTCCCTTACCTGTATCTTAATCTTGAGAAACACTGCAACA	1276
Qy	1695	GTCAATCAGCAGAAATATGCGCCAGTATCTGACATCTTTGGGGAACAACCTGAGAC	1754
Db	1277	CTGGAGCAGACGAGCGGTGATGGGCGGCACTGTCATCTGTGGGCCCATGCTGTGG	1336
Qy	1755	CTGTATCTAGTGAAGCTGAAGTGCACCACTTCCCTCTTCCAAGATGCTCAAGGGC	1814
Db	1337	AACCGACCACTG---GATGGGGTCCACCAACAGCTGTCCTCCCTGAGCAACTGAAGGG	1393
Qy	1815	AAGATCTCGGAAAGGGGAAGAGCTTCCAGGCCAATCTAGGAGAGTGCAGAGAAAGGC	1874

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Db      1394 AAGATCTGTCTGAAGGGGAAAGAACTTCGGGGGGGCTCTCCCGCCCTTGAAGGGAGGGTGGC 1453
QY      1875 -----GAGGTGTCTGATGAGACACATGCTGATGATGATGATGATGA 1915
Db      1454 CCTGAGGCGCACGTGTGGTGTCTCAGACGAAAGACGAGGCTGTGAGATGAGAGATGA 1506

RESULT 11
US-09-728-952-35
; Sequence 35, Application US/09728952
; Patent No. US20020111302A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Yamazaki, Vicki
; APPLICANT: Ujwal, Manusha L.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020111302a1el Nucleic Acids and
; FILE REFERENCE: 799
; CURRENT APPLICATION NUMBER: US/09/728,952
; CURRENT FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: pc_Fl_genes Version 2.0
; SEQ ID NO 35
; LENGTH: 3068
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2512)
US-09-728-952-35

Query Match      6.0%; Score 276.8; DB 10; Length 3068;
Best Local Similarity 53.4%; Pred. No. 1,2e-57;
Matches 743; Conservative 0; Mismatches 607; Indels 42; Gaps

QY      545 GGTGAGCGGTGTCATGAGTGCATCAAGAGGGGATGCAATGTGAAGCTGCGTGGCG 604
Db      298 GGAGGACGAGGACGTGCGCGGCATCTCGCGGGCTCCCGGCTCGCAAGATCCGCTCGCG 357
QY      605 CTCCAAGGGGCTGTGTCGCGCTTACTTACTGTGAGCGAGC-----GGCTCTCGATCCG 658
Db      358 CACGTGTGCAACAGAGACCGGCTGTACCGGCTGACGAGAGACGGCTTGAGCGTGTGTTCA 417
QY      659 CTGAGAGCCCTTCAGCAAGAAAGAGAGAGCCCAAGATCTTCATCGATCTTCATCCAGAGGT 718
Db      418 GCGGGGCAATCCCGCTGCGGCATCGCAGACATCTTCTTGTCGAGCAGATCGAGGGCGGT 477
QY      719 GAGTAGAGGGGGGCGGACGTGAGAGGTCTTCAACGGCTTACCCCTACCGGACGCTTCGACCCAA 778
Db      478 CCGCAAGGGCCACCAAGTCCGAGGAGGCTCGCGGGCTTC--GAGGATGCTTTCGCGCAGC 534
QY      779 CTGCTGCTTCAAGCATCTTCAACGCGAGGCCACCGGAGAGTGTGCTGAGACCTGATCTTCCACG 838
Db      535 GCGGTGCTTCAACATCGCTTCAAGGGGCGCGCGCAAGAACTTGAACTCGGGCGGCGCCAC 594
QY      839 CAGCGAGGTGGCGCGCAACCTGGGTTCATGTGCGCTGCGCTACTTCAATGCGCGGATCAGCGA 898
Db      595 GGCCTAGGAAGCGCAGCGCTGTGGGTGCGCGCTTCAACCAAGTTCGCGCGCGGCTGGAAGC 654
QY      899 CGAGGACAGCTGTGCTGCGCGCCAGCGCAGCAGCAAGGAGCAAGTGTGTAAGAGAGACGTTGA 958
Db      655 CATGAGCGAAGGCGAGCGGCTA-----GACCACTGATTCATCTTATCTTCA 702
QY      959 CGAGGCGCAAGAAACGGGGATGCGACGCTGAGCATTTGGCGAGGTCTTCGAGCTGTGCA 1018
Db      703 CCGGGCTGATCTTCAACAGGACAGCAAGATGAGCTTCAAGAGATCAAGAGCTGTGAG 762

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QY 1019 CAAGCTCAACGTGAACCTGCCCCGAGAGGGGTGAAGACAGATGTTCAAGGAAACGACAC 1078
Db 763 AATGTCATAGTGAATGACATGACACATGTAAGCTTACCTCTTCAAGAGATGTGAC-- 820
QY 1079 GGATGACCAACCAAGGAGACGCTGGGTTTGAAGAATTCTGTGCTTCTTCAAGATGATGTC 1138
Db 821 -CACTCCAAACAAAGACCGTCTAGAGGGGGGTAGATCGAGAGATTCCTCGGGGGCTGCT 879
QY 1139 CACCCGCGGGGACCTTACTGCTCATGCTGACCTTACAGAACCAACAAGACCACTGGA 1198
Db 880 GAAGCGGCGGAGACTGAGAGAGATCTTCAATCAGTACTCGGGGAGAGACCGCTGCTGAG 939
QY 1199 TGCCGCGAGCTGTCAGAGCGCTTCTGACAGGTGAGAGAAAGATGGCGGTGTGACCTTCA 1258
Db 940 TGCCCTTGAAGCTGTGAGATTTCT--GAGAGACCAAGGGGAGAGAGGCGCCACACTGGC 996
QY 1259 GAGCTGCGAGACATCATCATGAGAGATTGAGCCATGCGCAAAACAAAGATGAGGGCT 1318
Db 997 CCGGGCCAGACAGCTCATTCAGACCTATGAGCTCAACAGACAGCCAGCAGCATGAGCT 1056
QY 1319 GCTGGGATGATGAGCTTCACTCACTACACAGAGAGCCCTGTGTGATCATCTTCAACC 1378
Db 1057 GATGACACTGATGAGCTTCACTGATGATGATCTGTTGCGCGAGAGGGGCTGCTTGAACA 1116
QY 1379 TGAGCACACCATGATGACACAGGACATGACGACGCGCTGAGCCACTTCACTCACTC 1438
Db 1117 CACCCACACGTGTGTGTTCACAGACATGAAACAGCCCTTGCCCACTCACTTCACTCTTC 1176
QY 1439 GTCCCAACAACCTACTCTGTGTGTGACACAGCTCATGTCCCACTCACTGAGGTGACATGTA 1498
Db 1177 CTCCCAACAACCTATCTGACTGACTCCAGATCGGGGGGCCAGACGACCCAGAGCTTA 1236
QY 1499 TGCT-----TGGGTCTGACAGGCTGTGCGCGTGTGAGGAGGAGCTG 1543
Db 1237 TGTAAAGTACTGTAAGAGGGGGGCTTTGCCCCAGAGATGCGGCTGTGAGAGCTG 1296
QY 1544 CTGGAGATGGGCGGAGGAGGAGCCATTTGACACATGCTACACTCTGATCTTCAAGAT 1603
Db 1297 CTGGAGAGGGGCGAGAGAGGAGGAGCCCTCATCTATCACTGCGCATACCTTCACTCAAGAT 1356
QY 1604 CCTCTTCAAGAGCTCATTTGAACCATCAACAAATATGCTTCACTCAAGATGATGATGCC 1663
Db 1357 TCTCTTCCGGGAGCTGTGTCMAAGCCGTGCGGACCATGCTTCACTGCTGCTCCCTTATCC 1416
QY 1664 AGTATCTCTGCTCATCAAAAACCATGCAATGCTCATCAAGAGAGAAATGAGCCAGTA 1723
Db 1417 TGTATCTCTTATCTCTGAGAACCACTGGGGCTGAGAGAGAGGCTTCCATGCGCCCA 1476
QY 1724 TCTGACATGACATCTTGGGGGACCAAGCTGACCTGTCTCATGATGACAGTGAAGATGCGAC 1783
Db 1477 CCTCTGACACATCTTGGGGGACATGCTGTGTGACACAGGCGGTGAGACTCCCAATATCCGA 1536
QY 1784 CACACTCCCTCTCTCAAGATGCTCAAGGGGCAAGATCTCTGTGAAGGAGAAAGCTGCC 1843
Db 1537 GAGAGCTGCACTCCCAAGAGAGCTGAAGGGGCGGGGTCTCTGTGAAGGAGAAAGAGCTGCC 1596
QY 1844 AGCCAACTCAAGCAGGATGAGGAGAGAGGAGGAGGTGTCTGATGAGGACAGTGTCTGTA 1903
Db 1597 CGCTGCTCGAGCAGGATGAGCGGGCTCTGTGATGAGGAGAGAGAGAGATGA 1656
QY 1904 GATTGACGATGA 1915
Db 1657 CGAGGAGAGAGA 1668

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RESULT 12
US-09-728-952-64
Sequence 64, Application US/09728952
Patent No. US20020111302A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping

```

APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Yamazaki, Yuki
APPLICANT: Ujwal, Manusha U.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and
FILE REFERENCE: 799
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 64
LENGTH: 3068
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)..(2512)
US-09-728-952-64

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Query Match 6.0%; Score 276.8; DB 10; Length 3068;

Best Local Similarity 53.4%; Pred. No. 1.2e-57; Mismatches 607; Indels 42; Gaps 6;

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QY 545 GGTGAGCGGTGCATGAGGTGCGATGCAAGAGGAGATGAGATGAGTGAAGTGTGCGG 604
Db 298 GAGAGACAGAGACATGCGCGCATCTGCGGGGCTCCGGCTCCGCAAGATCCGTGCG 357
QY 605 CTCAAGGCGCTGTGTCGCTTCTACTACTTGAAGAGAC-----CGCTCTGATCCG 658
Db 358 CAGTGGACCAAGAGACGAGCTGTACCGGCTGAGAGAGAGCGCTGAGCTGTGATTC 417
QY 659 CTGAGAGCCCTTACCCCAAGAACAGAAAGCCCAAGATCTCCATGCACTCATCCAGAGAT 718
Db 418 GCGGCGCATCTCCGCGTGCCTATGCAAGACATCTTCTTGTGACGACATCGAGCGGT 477
QY 719 GAGTGAAGGGGCGGAGTGGAGGTCTTCAGCGCTACCTGACGCGACCTTTCAGACCCGA 778
Db 478 CCGGAGGCGCACAGTCCGAGAGGCTTGGGCGCTTC---GGGGGTGCTTGGGCGCAGC 534
QY 779 CTGCTGCTTCAAGCATCTTACACAGGACCAACCGGAGTGTGCTGATCTGTCTCAACAG 838
Db 535 GGGCTCTTCAACATGCTTCAAGGGCGCGCAAAACCTGAGACTGTGGCGGCCAC 594
QY 839 CAGCAGGTGGGCGGACCTGTGTCACTGTGCTGCTTACCTCATGAGCGGATGAGCGA 898
Db 595 GGTGAGAGAGGCGAGCGCTGTGGTGGCGGTGTGACCAAGCTCCGCGCGGCTTGAAGC 654
QY 899 CGAGACAGCTGTGCTGCGCGCAGCGCACAGGACAGAGTGTGAAGACAGACCTTTGA 958
Db 655 CATGAGCGACGCGGAGCGCTA-----GACCACTGAGATCCATCTTATCTGGA 702
QY 959 CGAGGCGCAAGAAACGGGAGTGGACCTTGAACATTTGGCGAGTGTCTGCACTGTGCA 1018
Db 703 CCGGCTGACTCCAAACAGAGAGCAAGATGAGCTTCAAGGAGATCAAGAGCTGCTGAG 762
QY 1019 CAAGCTCAACGTGAACCTGCCCCGAGAGGTGAAAGAGATTCAGGAGACGCGACAC 1078
Db 763 AATGTCATAGTGAATGACATGACACATGTAAGCTTACCTCTTCAAGAGATGTGAC-- 820
QY 1079 GGATGACCAACCAAGGAGACGCTGGGTTTGAAGAATTCTGTGCTTCTTCAAGATGATGTC 1138
Db 821 -CACTCCAAACAAAGACCGTCTAGAGGGGGGTAGATCGAGAGATTCCTCGGGGGCTGCT 879
QY 1139 CACCCGCGGGGACCTTACTGCTCATGCTGACCTTACAGAACCAACAAGACCACTGGA 1198
Db 880 GAAGCGGCGGAGACTGAGAGAGATCTTTCATCACTGAGGAGAGAGCGGCTGTGAG 939
QY 1199 TGCCGCGAGCTGTCAGAGCGCTTCTGACAGGTGAGAGAGATGAGGAGGATGACCTTCA 1258

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Db 940 TGCCCCCTGAGCTGTGAGATTCT--GAGAGACACAGGCGAGAGGGCCCACTGCGC 996
Qy 1259 GAGTGGCCAGACATCATCGACAGATTGAGCCATGCCAGAAAACAAAGTAAGGGGCT 1318
Db 997 CCGGGCCACAGAGCTCATTCAGACTATGAGCTCAACGAGACAGCCAGAGCATGAGCT 1056
Qy 1319 GCTGGGATGATGAGCTTTCACCACTACACAGAGAGCCCTGCTGGTACATTTCAACC 1378
Db 1057 GATGACACTGATGAGCTTTCATGATGATCTGTGTCCGAGAGGGGCTGCCCTTGACAA 1116
Qy 1379 TGAGCACACCATGATGACAGGACATGACGACCGCTAGCCACTTTCATCACTC 1438
Db 1117 CACCCACACGCTGTGTTCAGAGACATGAAACAGCCCTTGCCCACTACTTCTTTC 1176
Qy 1439 GTCCCAACACCTTACTCTGTGGTGAACAGCTCATGTCCAGTCAAGGTGACATGTA 1498
Db 1177 CTCCCAACACCTTATCTGACTGATCTCCAGATCGGGGGGCCAGAGACACGAGGCTTA 1236
Qy 1499 TGCT-----TGGGTCTGACAGGCTGGCTGGCTGGCTGGAGTGAAGTGA 1543
Db 1237 TGTTAGTACTGATGACAGGGGGGCTTTGGCCAGGAGATGCCGTGGAGCTGAGACTG 1296
Qy 1544 CTGGGATGGGCCCCGACGGGGAGCCCATTTGACACATGGCTACTGACTTCCAAGAT 1603
Db 1297 CTGGGAGGGGCGAGAGGGGAGCCCGTCACTATGATGGCCATACCTCACTCCAAAGAT 1356
Qy 1604 CCTCTTCAAGAGAGTCAATTGAAACCATCAACAAATATGCTTTCATCAAGATGATGCC 1663
Db 1357 TCTCTTCCGGAGAGTGTCCAAACCCGCGCCGACATGCTTACCTGCTCCCTTACCC 1416
Qy 1664 AGTATCTGTCTTCATGAAAACCATGACAGTGTATCTCAGACAGAAAATGGCCAGTA 1723
Db 1417 TGTCACTCTATCTCTGGAAGAACCATGCGGGCTGGAGCAGAGGCTGCCATGGCCGCA 1476
Qy 1724 TCTGACTGATCTTTGGGGGACAGCTGACCTGTATCATGAGGAGTGAAGATGCCAC 1783
Db 1477 CCTCTGACCATCTGGGGGACATGCTGTGACACAGGCGCTGAGACTCCCAATCCGA 1536
Qy 1784 CACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCTCTGGAAGGGAAAGTCTCC 1843
Db 1537 GAGCTGCCATCCCAAGAGAGCTGAAGGGCGGGTCTGTGTGAAGGAAAGAGTGGC 1596
Qy 1844 AGCCAAATCAGAGAGATGCGAGGAAAGCGAGTGTGTGATGAGACAGTGTGATGA 1903
Db 1597 CGCTGCTCGAGAGGAGATGGCGGGCTGTGTGATGGGAGAGAGAGAGATGA 1656
Qy 1904 GATTGACATGA 1915
Db 1657 CGAGGAGAA 1668

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RESULT 13
US-09-764-868-24

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; Sequence 24, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT332
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR APPLICATION DATA REMOVED - refer to PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c

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; NAME/KEY: SITE
; LOCATION: (238)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (542)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-24

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Query Match 4.2%; Score 195.4; DB 9; Length 567;

Best Local Similarity 70.9%; Pred. No. 4.7e-38; Matches 270; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

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Qy 699 ATGCATCTCATCCAGAGTGTGAGGGGCGGAGTCCGAGGTCTTCCA-GGCTACCC 757
Db 187 ATTGATTCATTTACAAAGTACTGAGGGCGGAGCTGAATATTCGNTTACAGC 246
Qy 758 TGACGGCAGCTTTCGACCCCACTGCTCTTACGATCTTACGAGGACCGGAGTC 817
Db 247 TGAGGGGAACCTTCGACCCCACTGCTCTTACCATCTACATGCGAACCATGAGTC 306
Qy 818 GCTGACCTGCTTCCACCAAGAGCGAGGTGGCGGACCTGGGTACCTGGCTGCGCTA 877
Db 307 CTTGACCTTATCTACCTTCCACCCCGAGAGGCCGACCTGATTCACAGGCTTCAAGTA 366
Qy 878 CCTATGCGCGGACATCAGCAGCAGAGCAAGCTGCTGCGCGGACGAGCAGGAGCA 937
Db 367 CCTATGCTGTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
Qy 938 GTGCTGAAGAGACCTTTGACGAGGCGGACAGAAAGGGGATGGACCTTGACATTGG 997
Db 427 ATGGGTAAAGAGACCTTTGAGAGAGCTGATTAAGATGTGAAGGCTTGTGTGATATTTGA 486
Qy 998 CGAGTCTGAGCTGCTGACAAAGCTCAAGTGAACCTGCCCGGACAGGAGTGAAGCA 1057
Db 487 AGAATATCATCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
Qy 1058 GATGTTACAGGAGCGGAGCAC 1078
Db 547 AATGTTTCANAGAGCCGACAC 567

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RESULT 14
US-09-955-999-31

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; Sequence 31, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; FILE REFERENCE: PT086P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (238)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (542)
; OTHER INFORMATION: n equals a,t,g, or c

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; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-31

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Query Match	4.2%	Score 195.4;	DB 9;	Length 567;
Best Local Similarity	70.9%;	Pred. No. 4.7e-18;		
Matches 270;	Conservative 0;	Mismatches 110;	Indels 1;	Gaps 1;

Qy	699	ATCAGCTCATATCCAGAGAGGTGAGTGAAGGGGCGGCGAGTCGAGAGGTCTTCCA - GCCTTACCC	757
Db	187	ATTGATTTGCATTTTACAAGAAGTGAAGGAGGGCGGCGAATCTGGAATAATTCNMNTTACAAAGC	246
Qy	758	TGACGGCAGCTTTCGACCCCACTGCTGCTTCAGCATCTACACGGCGACGACCGCGAGTC	817
Db	247	TGAGGGGGAACCTTCGACCCCGAGCTGTGCTTTCACCATCTCTACATGGCGAACCATATGAGAGTC	306
Qy	818	GCTGGAACCTGGTCTTCACACGACGACGAGGAGGGGCGGCGACCTGGGTCTACCTGGCGTACGCGCTA	877
Db	307	CTTGAGACCTTCACTCACCTTCACAAACCCGAGGAGGCGCGACCTGGATCTACAGGCTTAAAGTA	366
Qy	878	CCTCATGAGCGCGCATTCACGACACGACGACAGCTGTGCTGCGCGCAGCGACGACAGGAGCA	937
Db	367	CTTATGCTGTCGATCTAGATGATGATGAAGACTCTCCCTTGCCAAAAGGACAGAGGACCATAGACCA	426
Qy	938	GTCGCTGAAGACAGCGTTTACGAGGCGGACAAAGAAAGGAGATGGCAGCTTGAAGCATTTGG	997
Db	427	ATGGGTGAAGACAGACTTTTGAAGGAGGTGATGAAGATGGTGAAGCGCTTCTGTAATATTGA	486
Qy	998	CGAGGTCCTGCACTGCTGTGCACAAAGCTCAACGTGAACCTTGCCCGGACAGAGGTTGAAGA	1057
Db	487	AGGATATCATCTAGCTGTGATGTGATAAACTGATATGTTAATCTGCCCGGAAAGAAAGTCNGACA	546
Qy	1058	GATGTTCCAGGAGACGGACAC	1078
Db	547	AATGTTTCANGAAGCCGACAC	567

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RESULT 15
US-09-835-996A-18
Sequence 18, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Kyle
APPLICANT: Liu, Chenghua
APPLICANT: Aundt, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunwei
FILE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835,996A
PRIORITY FILING DATE: 2001-04-16
PRIORITY APPLICATION NUMBER: US 60/197,137
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: US 09/714,936
PRIORITY FILING DATE: 2000-11-17
PRIORITY APPLICATION NUMBER: US 09/667,298
PRIORITY FILING DATE: 2000-09-22
PRIORITY APPLICATION NUMBER: US 09/631,451
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: US 09/598,042
PRIORITY FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 18
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(1170)
US-09-835-996A-18

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Query Match	3.1%	Score 146;	DB 10;	Length 1490;
Best Local Similarity	51.7%;	Pred. NO. 5.3e-26;		
Matches 391;	Conservative 0;	Mismatches 350;	Indels 15;	Gaps 2;

Qy	744	TTCCAGGCGTACCTCTGACCGGCACTTTCGACCACCTGCTGTGCTTACAGATCTACACACGGC	803
Db	379	TTGTGCGGTAGCTCGGAGAGAGAGCTCCCTCCCTGGAGACAGGGTTTACCATTTGTCTTCAT	438
Qy	804	AGCCACCGCAGATGCTGCGACCTGCTGTCTCCACACGACGAGGTGGCGGCACTGSGTC	863
Db	439	GGCGCGCGCTCCAACTCGGACTGATGGCCCAACAGTGTGAGAGAGCCAGATATGATGATG	498
Qy	864	ACTGGCCTGGCGTACTCTCAATGGCCGGGCAATACGACACAGAGACAGCCTGCTGCCGACG	923
Db	499	CGAGGGCTCCAGCTGTGGTGATCTTGTACACGAGATGACCATCAGAGGGCTT---	554
Qy	924	CGCACACAGGACACAGTGGCTGGAAGACAGACGTTTGAACGAGGGCCGACAAAGAACGGGATGAC	983
Db	555	-----GGACCAATGGCTGAGCGATTTGGTTTCAACGTGGAGACAAATAATAGATAGT	606
Qy	984	AGCCTGAGCATTGGCGAGAGTCTCTGACGCTGTGCAACAGCTCAACGTGAACCTGCCCCG	1043
Db	607	AAGATGATGTTCCAAAGAAATTCAGCGGTTATTGGACCTAATGAATGTGGAATATGACCA	666
Qy	1044	CAGAGGTTGAAGCAGATGTTCAAGGAAAGGGACACGAGATGACACCAAGGAGCGTGGT	1103
Db	667	GAAATATCCTTCAGTCTTTTTCAGGGACGACACG--TCCCAATCTGGAACCTTGAA	723
Qy	1104	TTTGAAGATTCGTGCTCTCTCAAGATGATGATGCCACCGCGCGGACCTCTACCTGTC	1163
Db	724	GGAGAAAGATTTCTGACAGTTCTATTAAGGCAATTBACTTAACGTCGTGAGGTGAGAACTG	783
Qy	1164	ATGCTGACTTACAGCAACCAACAGACCAACTGAGTCCGCGACGCTGCAGCGCTTCTG	1223
Db	784	TTTGAAAGTTTTCAGCTGATGGGACGAAGAGTACTCTGCGAAATTTTGGATTTCTC	843
Qy	1224	CAGGTGAGCAGAAATGCGCGGTGTGACCTCTGAGAGCTGCCAGACATCATCGACAG	1283
Db	844	CAAGAGGAGCAGAAAGAGAGACCTGACCTCTGAGCTTCTGGAATCTCATTCACGCG	903
Qy	1284	TTTGAGCGCATGCCCAAAAAACAAGATTAAGGGGCGCTGGGCAATTGATGGCTTCAACAAC	1343
Db	904	TATGAACCTTTACAGCTGGCAAACTGGCGCATGTGCTGATGATGATGGCTTCTTCACG	963
Qy	1344	TACACACAGAGCCCTGTGCTGTGACATCTTCAACCCGTGAGCAACCAATATGTGACACGAGAC	1403
Db	964	TACTCTGCTCTAAGATATGAGATCTTCTCAACCCAGCGCTCTCCCATATATAGAT	1023
Qy	1404	ATGACGAGCCCGTGAACCACTTACTTCACTGCTGCCACAAACAACCTTACTCTGTGGT	1463
Db	1024	ATGACTCAACCCCTGAACCACTTACTTCTGCTCTTCATTAACAACCACTTACTAGTGGG	1083
Qy	1464	GACGAGCTCATGTCCAGTACAGGGGTGGACATGTAT	1499
Db	1084	GACCAAGCTTTGGCGCCAGACACAGTCGTAGGGATAT	1119

Search completed: March 28, 2003, 22:07:46
Job time : 449 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 21:31:24 ; Search time 13290 Seconds
(without alignments) 10149.850 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
Sequence: 1 tcgcagctcgaactagtcg.....gttaacggggcccccagccccc 4635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

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- 32: em_hgt_other:*
- 33: em_hgt_mus:*
- 34: em_hgt_pln:*
- 35: em_hgt_rod:*
- 36: em_hgt_mam:*
- 37: em_hgt_vrt:*
- 38: em_sy:*
- 39: em_hgt_hum:*
- 40: em_hgt_mus:*
- 41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3205	69.1	4237	6	AX304472	AX304472 Sequence
2	2274	49.1	4411	6	AK074149	AK074149 Homo sapi
3	2112	45.6	2243	6	AX402958	AX402958 Sequence
4	1579	34.1	6551	6	AX392826	AX392826 Sequence
5	1446	31.2	6946	9	AB007919	AB007919 Homo sapi
6	1446	31.2	154736	9	AL139246	AL139246 Human DNA
7	861	18.6	2480	9	BC019679	BC019679 Homo sapi
8	242	5.2	106323	9	AL513477	AL513477 Human DNA
9	97	2.1	245	11	H5776M4T	AL442031 H. sapiens
10	62	1.3	976	10	MMU0296951	AJ269591 Mus muscu
11	62	1.3	190494	2	AL831788	AL831788 Mus muscu
12	29	0.6	67142	2	AC120432	AC120432 Mus muscu
13	28	0.6	621	9	HSA338904	AJ338904 Homo sapi
14	24	0.5	176291	2	AC023583	AC023583 Homo sapi
15	23	0.5	77863	2	AC121463	AC121463 Rattus no
16	23	0.5	174647	2	AC094559	AC094559 Rattus no
17	22	0.5	1525	9	AF110821	AF110821 Homo sapi
18	22	0.5	2419	9	HSM800908	AL110247 Homo sapi
19	22	0.5	2512	4	OCPLCMR	Z49747 O. cuniculus
20	22	0.5	2614	17	AF111852	AF111852 Homo sapi
21	22	0.5	3111	9	HSG6PT2	AF116863 Homo sapi
22	22	0.5	4408	9	HUMPLCA	M34667 Human phosp
23	22	0.5	4457	9	AF078163	AF078163 Homo sapi
24	22	0.5	5196	9	AF078163	AF097831 Homo sapi
25	22	0.5	9204	9	HSA17864	Y17864 Homo sapien
26	22	0.5	128899	9	AL391139	AL391139 Human DNA
27	22	0.5	142694	2	AF481053	AF481053 Mus muscu
28	22	0.5	146547	2	HSS11B24	AL022394 Human DNA
29	22	0.5	158634	2	AP000909	AP000909 Homo sapi
30	22	0.5	162996	9	AP000877	AP000877 Homo sapi
31	22	0.5	165394	2	AC112440	AC112440 Rattus no
32	22	0.5	171749	2	AC005696	AC005696 Homo sapi
33	22	0.5	177411	9	AC005696	AC003392 Homo sapi
34	22	0.5	178341	9	AP003392	AC110145 Rattus no
35	22	0.5	179270	2	AC108350	AC108350 Rattus no
36	22	0.5	179818	2	AC126653	AC126653 Rattus no
37	22	0.5	182362	2	AP000833	AP000833 Homo sapi
38	22	0.5	190762	2	AP000833	AC127633 Rattus no
39	22	0.5	191708	2	AP000854	AP000854 Homo sapi
40	22	0.5	196511	2	AC129979	AC129979 Mus muscu
41	22	0.5	198171	9	AC009061	AC009061 Homo sapi
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VERSION	AX304472.1				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Das, D., Reddy, R., Yao, M.G., Nguyen, D.B., Lu, Y., Tribouley, C.M.,				
	Yue, H., Khan, F.A., Gandhi, A.R., Au-Young, J., Lai, P., Kearney, L.,				
	Ellicott, V.S., Ding, L. and Thornton, M.				

TITLE Lipid metabolism enzymes
JOURNAL Patent: WO 0185955-A 10.15-NOV-2001;
Incyte Genomics, Inc. (US)
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Matches 3405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 REFERENCE
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 Griffith, J.A., Patterson, C., Gandhi, A.R., Lu, Y., Yao, M.G.,
 Baughn, M.R., Walla, N.K., Hatfield, A.J., Ding, L., Tribouley, C.M.,
 Das, D., Thornton, M., and Lal, P.
 TITLE
 Lipid metabolism enzymes
 JOURNAL
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Qy 3341 AGCCCAAGCCCAAGAGGAGGAGCCGAGGAGGAGCCGAGGAGGAGGAGGAGGAGGAGGAG 3400
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Qy 3401 GGCAGAGAGAGCCCTGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 3460
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Db 4898 GGGCTTCAAGAGGAGGAGGAGCCGAGGAGGAGGAGCCGAGGAGGAGGAGGAGGAGGAGGAG 4957
Qy 3581 CCAGAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3640
Db 4958 CCAGAGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5017
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Db 5018 CGGTATCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5077
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ACCESSION AB007919.1 GI:3413861
VERSION KIAA0450 protein.
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SOURCE plus clone:HG0217.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE
1 (sites)
Seki, N., Ohira, M., Nagase, T., Ishikawa, K., Miyajima, N.,
Nakajima, D., Nomura, N. and Ohara, O.
Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
JOURNAL DNA Res. 4 (5), 345-349 (1997)
MEDLINE 9811662
REFERENCE 2 (bases 1 to 6946)
Ohara, O.
Direct Submission
Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yama 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@fokkazusa.or.jp, Tel: +81-438-52-3913,
Fax: +81-438-52-3914)

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LOCUS				
DEFINITION	Human DNA sequence from clone RP-355M20 on chromosome 1p26.11-36.33, complete sequence.			
ACCESSION	AL139246			
VERSION	AL139246.20	GI:16973797		
KEYWORDS	HTG.			
SOURCE	human.			

REFERENCE 1 (bases 1 to 154736)
AUTHORS Moore, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,

COMMENT

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPep; Information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Ch1>

RP3-395M20 is from the library RPCT-3 constructed by the group of Pletier de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-395M20 The true left end of clone RP4-755G5 is at 90075 in this sequence. The right end of clone RP4-755G5 is at 90078 in this sequence. The true right end of clone RP11-361M21 is at 135438 in this sequence.

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus					
1 (bases 1 to 190494)					
Plumb, B.					
Direct Submission					
Submitted (12-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humguery@sanger.ac.uk					
On Jul 14, 2002 this sequence version replaced gi:21727735.					
----- Genome Center					
Center: Wellcome Trust Sanger Institute					
Center code: SC					
Web site: http://www.sanger.ac.uk					
Contact: humguery@sanger.ac.uk					
----- Project Information					
Center project name: DM173K14					
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Assembly program: XGAP4; version 4.5					
Chemistry: Dye-terminator; 100% of reads					
Consensus quality: 165080 bases at least Q40					
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Consensus quality: 167481 bases at least Q20					
Insert size: 188194; sum-of-contigs					
Insert size: 206960; 2.0% error; agarose-fp					
Quality coverage: 4.43x in Q20 bases; sum-of-contigs Quality coverage: 4.41x in Q20 bases; agarose-fp					

* NOTE: This is a 'working draft' sequence. It currently					
* consists of 24 contigs. The true order of the pieces					
* is not known and their order in this sequence record is					
* arbitrary. Gaps between the contigs are represented as					
* runs of N, but the exact sizes of the gaps are unknown.					
* This record will be updated with the finished sequence					
* as soon as it is available and the accession number will					
* be preserved.					
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                  /note="assembly fragment:00228
                  fragment_chain:6"
BASE COUNT      45591 a 48780 c 48760 g 45059 t 2304 others
ORIGIN

```

```

Query Match      1.3%; Score 62; DB 2; Length 190494;
Best Local Similarity 100.0%; Pred.No. 3.7e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1422 CACTACTTCACCTGCTGCCACACACCTACTGCGGTGACGACGCTCATGTCCAG 1481
Db 143233 CACTACTTCACCTGCTGCCACACACCTACTGCGGTGACGACGCTCATGTCCAG 143292

OY 1482 TC 1483
Db 143293 TC 143294

```

```

RESULT 12
AC120432/c      67142 bp DNA linear HTG 06-MAY-2002
LOCUS           Mus musculus clone RP24-553K14, LOW-PASS SEQUENCE SAMPLING.
ACCESSION      AC120432
VERSION        AC120432.1 GI:20455766
KEYWORDS       HTG; HTGS_PHASE0.
SOURCE         Mus musculus.
ORGANISM       Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE          1 (bases 1 to 67142)
JOURNAL        Birtten,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE      Mus musculus, clone RP24-553K14
AUTHORS        Unpublished
TITLE          2 (bases 1 to 67142)
JOURNAL        Birtten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
REFERENCE      Anderson,S., Batra,N., Bastien,V., Bloom,T., Boguslavsky,L.,
AUTHORS        Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
REFERENCE      Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
AUTHORS        Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
REFERENCE      Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
AUTHORS        Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
REFERENCE      Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
AUTHORS        Kanat,A., Karatas,A., Kelle,C., LaRoque,K., Lamazares,R.,
REFERENCE      Lander,E., Lehotzky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
AUTHORS        Maclean,C., MacDonald,P., Major,U., Marquis,N., Matthews,C.,
REFERENCE      McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,J.,
AUTHORS        Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
REFERENCE      Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
AUTHORS        Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
REFERENCE      Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
AUTHORS        Roman,U., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
REFERENCE      Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
AUTHORS        Strauss,N., Subramanian,A., Talamas,U., Testaye,S., Theodore,J.,
REFERENCE      Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
AUTHORS        Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
REFERENCE      Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
JOURNAL        Direct Submission
TITLE          Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome
JOURNAL        Research, 320 Charles Street, Cambridge, MA 02141, USA

```

COMMENT

```

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L26051
Center clone name: 553_K_14
-----
* NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
1 691: contig of 691 bp in length
* 692 791: gap of 100 bp
* 792 1524: contig of 733 bp in length
* 1525 1624: gap of 100 bp
* 1625 2355: contig of 731 bp in length
* 2356 2455: gap of 100 bp
* 2456 3135: contig of 680 bp in length
* 3136 3235: gap of 100 bp
* 3236 3928: contig of 693 bp in length
* 3929 4028: gap of 100 bp
* 4029 4730: contig of 702 bp in length
* 4731 4830: gap of 100 bp
* 4831 5532: contig of 702 bp in length
* 5533 5632: gap of 100 bp
* 5633 6372: contig of 740 bp in length
* 6373 6472: gap of 100 bp
* 6473 7212: contig of 740 bp in length
* 7213 7312: gap of 100 bp
* 7313 8009: contig of 697 bp in length
* 8010 8109: gap of 100 bp
* 8110 8631: contig of 722 bp in length
* 8632 8931: gap of 100 bp
* 8932 9631: contig of 700 bp in length
* 9633 9731: gap of 100 bp
* 9732 10448: contig of 717 bp in length
* 10449 10548: gap of 100 bp
* 10549 11268: contig of 720 bp in length
* 11269 11368: gap of 100 bp
* 11369 12087: contig of 719 bp in length
* 12088 12187: gap of 100 bp
* 12188 12931: contig of 744 bp in length
* 12932 13031: gap of 100 bp
* 13032 13780: contig of 749 bp in length
* 13781 13880: gap of 100 bp
* 13881 14576: contig of 696 bp in length
* 14577 14676: gap of 100 bp
* 14677 15410: contig of 734 bp in length
* 15411 15510: gap of 100 bp
* 15511 16248: contig of 738 bp in length
* 16249 16348: gap of 100 bp
* 16349 17053: contig of 705 bp in length
* 17054 17153: gap of 100 bp
* 17154 17836: contig of 683 bp in length
* 17837 17936: gap of 100 bp
* 17937 18651: contig of 715 bp in length
* 18652 18751: gap of 100 bp
* 18752 19477: contig of 726 bp in length
* 19478 19577: gap of 100 bp
* 19578 20282: contig of 705 bp in length
* 20283 20382: gap of 100 bp

```

```

* 20383 21125: contig of 743 bp in length
* 21126 21225: gap of 100 bp
* 21226 21974: contig of 749 bp in length
* 21875 22074: gap of 100 bp
* 22075 22783: contig of 709 bp in length
* 22784 22883: gap of 100 bp
* 22884 23584: contig of 701 bp in length
* 23585 23684: gap of 100 bp
* 23685 24409: contig of 725 bp in length
* 24410 24509: gap of 100 bp
* 24510 25220: contig of 711 bp in length
* 25221 25320: gap of 100 bp
* 25321 26029: contig of 709 bp in length
* 26030 26129: gap of 100 bp
* 26130 26849: contig of 720 bp in length
* 26850 26949: gap of 100 bp
* 26950 27674: contig of 725 bp in length
* 27675 27774: gap of 100 bp
* 27775 28509: contig of 735 bp in length
* 28510 28609: gap of 100 bp
* 28610 29341: contig of 732 bp in length
* 29342 29441: gap of 100 bp
* 29442 30176: contig of 735 bp in length
* 30177 30276: gap of 100 bp
* 30277 31015: contig of 739 bp in length
* 31016 31115: gap of 100 bp
* 31116 31844: contig of 729 bp in length
* 31845 31944: gap of 100 bp
* 31945 32639: contig of 695 bp in length
* 32640 32739: gap of 100 bp
* 32740 33484: contig of 745 bp in length
* 33485 33584: gap of 100 bp
* 33585 34322: contig of 738 bp in length
* 34323 34422: gap of 100 bp
* 34423 35120: contig of 698 bp in length
* 35121 35220: gap of 100 bp
* 35221 35918: contig of 698 bp in length
* 35919 36018: gap of 100 bp
* 36019 36720: contig of 702 bp in length
* 36721 36820: gap of 100 bp
* 36821 37539: contig of 719 bp in length
* 37540 37639: gap of 100 bp
* 37640 38360: contig of 721 bp in length
* 38361 38460: gap of 100 bp
* 38461 39198: contig of 738 bp in length
* 39199 39298: gap of 100 bp
* 39299 40038: contig of 740 bp in length
* 40039 40138: gap of 100 bp
* 40139 40882: contig of 744 bp in length
* 40883 40982: gap of 100 bp
* 40983 41707: contig of 725 bp in length
* 41708 41807: gap of 100 bp
* 41808 42513: contig of 706 bp in length
* 42514 42613: gap of 100 bp
* 42614 43325: contig of 712 bp in length
* 43326 43425: gap of 100 bp
* 43426 44133: contig of 708 bp in length
* 44134 44233: gap of 100 bp
* 44234 44954: contig of 721 bp in length
* 44955 45054: gap of 100 bp
* 45055 45786: contig of 732 bp in length
* 45787 45886: gap of 100 bp
* 45887 46618: contig of 732 bp in length
* 46619 46718: gap of 100 bp
* 46719 47455: contig of 737 bp in length
* 47456 47555: gap of 100 bp
* 47556 48296: contig of 741 bp in length
* 48297 48396: gap of 100 bp
* 48397 49125: contig of 729 bp in length
* 49126 49225: gap of 100 bp
* 49226 49974: contig of 749 bp in length
* 49975 50074: gap of 100 bp
* 50075 50768: contig of 694 bp in length

```

```

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 67142;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3015 GTGTACTAGAGGATGGAAGGCTC 3043
Db 20050 GTGTACTAGAGGATGGAAGGCTC 20022

RESULT 13
LOCUS HSA338904/c 621 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
ACCESSION AJ338904
VERSION AJ338904
KEYWORDS NLI-VF5R.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Kutsenko, A.S., Gizaev, I.I., R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
AUTHORS Podolskiy, R.M., Matukhin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodkov, A.I., Kashuba, V.I.,
TITLE Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zharovsky, E.R.
Noli flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 621)
AUTHORS Zharovsky, E.R.
TITLE Direct Submision
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NLI-VF5R"
BASE COUNT 152 a 217 c 172 g 80 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 28; DB 9; Length 621;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 519 TTCTTGGAGGCGCAATCTGCGGTG 546
Db 621 TTCTTGGAGGCGCAATCTGCGGTG 594

RESULT 14
LOCUS AC023583
AC023583 176291 bp DNA linear HTG 24-AUG-2002

```

DEFINITION Homo sapiens chromosome 19 clone RP11-294120 map 19, WORKING DRAFT
SEQUENCE, 38 unordered pieces.
AC023583
VERSION AC023583.2 GI:7139848
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 176291)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 19, clone RP11-294120
REFERENCE 2 (bases 1 to 176291)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Bouckgeert, B., Brown, A., Burkett, G., Campoliano, A., Castle, A.,
Chongel, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,
Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
Fenstermaker, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heath, A., Horton, L.,
Howard, J., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Largocque, K., Lehoczy, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marguis, N., McCarthy, M.,
McEwan, P., McGuirk, A., McKernan, K., McPheters, R., Meldrim, J.,
Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,
Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M.,
Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, S., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testfaye, S., Theodore, J., Tirelli, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.

TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS 3 (bases 1 to 176291)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouckgeert, B., Brown, A., Burkett, G.,
Campoliano, A., Castle, A., Chongel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heath, A., Horton, L.,
Howard, J., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., McPheters, R.,
McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McPheters, R.,
Meldrim, J., Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, S., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testfaye, S., Theodore, J., Tirelli, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 2000 this sequence version replaced gi:697825.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

Center Project name: L6622
Center Clone name: 294_1_20
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15757 bases at least Q40
Consensus quality: 165762 bases at least Q30
Consensus quality: 165979 bases at least Q20
Insert size: 172591; sum-of-coverage
Quality coverage: 4.3 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	1112:	contig of 1112 bp	in length
*	1113	1212:	gap of 100 bp
*	1213	2643:	contig of 1431 bp in length
*	2644	2743:	gap of 100 bp
*	2744	3807:	contig of 1064 bp in length
*	3808	3907:	gap of 100 bp
*	3908	5199:	contig of 1292 bp in length
*	5200	5299:	gap of 100 bp
*	5300	6456:	contig of 1157 bp in length
*	6457	6556:	gap of 100 bp
*	6557	8373:	contig of 1817 bp in length
*	8374	8473:	gap of 100 bp
*	8474	9630:	contig of 1157 bp in length
*	9631	9730:	gap of 100 bp
*	9731	11039:	contig of 1309 bp in length
*	11040	11138:	gap of 100 bp
*	11140	12869:	contig of 1730 bp in length
*	12870	12969:	gap of 100 bp
*	12970	14713:	contig of 1744 bp in length
*	14714	14813:	gap of 100 bp
*	14814	16251:	contig of 1438 bp in length
*	16252	16351:	gap of 100 bp
*	16352	18265:	contig of 1914 bp in length
*	18266	18365:	gap of 100 bp
*	18366	21235:	contig of 2870 bp in length
*	21236	21335:	gap of 100 bp
*	21336	23647:	contig of 2312 bp in length
*	23648	23747:	gap of 100 bp
*	23748	26775:	contig of 3028 bp in length
*	26776	26875:	gap of 100 bp
*	26876	29829:	contig of 2954 bp in length
*	29830	29929:	gap of 100 bp
*	29930	33977:	contig of 4048 bp in length
*	33978	34077:	gap of 100 bp
*	34078	37757:	contig of 3680 bp in length
*	37758	37857:	gap of 100 bp
*	37858	42751:	contig of 4894 bp in length
*	42752	42851:	gap of 100 bp
*	42852	47106:	contig of 4255 bp in length
*	47107	47206:	gap of 100 bp
*	47207	50568:	contig of 3362 bp in length
*	50569	50668:	gap of 100 bp
*	50669	56184:	contig of 5516 bp in length
*	56185	56284:	gap of 100 bp
*	56285	60604:	contig of 4320 bp in length
*	60605	60704:	gap of 100 bp
*	60705	64623:	contig of 3921 bp in length
*	64626	64725:	gap of 100 bp
*	64726	70005:	contig of 5280 bp in length
*	70006	70105:	gap of 100 bp
*	70106	74085:	contig of 3980 bp in length
*	74086	74185:	gap of 100 bp
*	74186	79664:	contig of 5479 bp in length


```

* 79665 79764: gap of 100 bp
* 79765 85612: contig of 5848 bp in length
* 85613 85712: gap of 100 bp
* 85713 91034: contig of 5322 bp in length
* 91035 91134: gap of 100 bp
* 91135 96686: contig of 5552 bp in length
* 96687 96786: gap of 100 bp
* 96787 104241: contig of 7455 bp in length
* 104242 104341: gap of 100 bp
* 104342 111850: contig of 7509 bp in length
* 111851 111950: gap of 100 bp
* 111951 119512: contig of 7562 bp in length
* 119513 119612: gap of 100 bp
* 119613 129856: contig of 10244 bp in length
* 129857 129956: gap of 100 bp
* 129957 138156: contig of 8200 bp in length
* 138157 138256: gap of 100 bp
* 138257 147577: contig of 9321 bp in length
* 147578 147677: gap of 100 bp
* 147678 161828: contig of 14151 bp in length
* 161829 161928: gap of 100 bp
* 161929 176291: contig of 14363 bp in length.

```

FEATURES

Source

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1. 176291
/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="19"
/map="19"

```

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/clone="RP11-294120"
/clone_lib="RP11 Human Male BAC"

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```

misc_feature
1. 1112
/note="assembly_fragment"

misc_feature
1213. 2643
/note="assembly_fragment"

misc_feature
2744. 3807
/note="assembly_fragment"

misc_feature
3908. 5199
/note="assembly_fragment"

misc_feature
5300. 6456
/note="assembly_fragment"

misc_feature
6557. 8373
/note="assembly_fragment"

misc_feature
8474. 9630
/note="assembly_fragment"

misc_feature
9731. 11039
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misc_feature
11140. 12869
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misc_feature
12970. 14713
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misc_feature
14814. 16251
/note="assembly_fragment"

misc_feature
16352. 18265

```

```

Query Match      0.5%; Score 24; DB 2; Length 176291;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3579 CGCCAGCAGCCCGGCGCGCT 3602

DB 37682 CGCCAGCAGCCCGGCGCGCT 37705

```

RESULT 15
AC121463/C
LOCUS
DEFINITION AC121463 77863 bp DNA linear HTG 24-JUN-2002
50 unordered pieces.
ACCESSION AC121463
VERSION AC121463.2 GI:21909415
KEYWORDS HTG; HTGS PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus

```

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 77863)

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TITLE

Unpublished

REFERENCE

2 (bases 1 to 77863)

AUTHORS

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TITLE

Direct Submision

REFERENCE

Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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TITLE

Direct Submision

COMMENT

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

On Jul 19, 2002 this sequence version replaced gi:20976415.

AUTHORS

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AUTHORS

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TITLE

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AUTHORS

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REFERENCE

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

AUTHORS

Worley,K.C.

Consensus quality: 19063 bases at least Q20

NOTE: Estimated insert size may differ from sequence length.
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1029 1128: gap of unknown length
1129 2640: contig of 1512 bp in length
2641 2740: gap of unknown length
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3796 3895: gap of unknown length
3896 5418: contig of 1523 bp in length
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5519 6696: contig of 1178 bp in length
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8334 8434: gap of unknown length
8435 9542: gap of unknown length
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69251 70807: contig of 1557 bp in length
70808 72341: contig of 1434 bp in length
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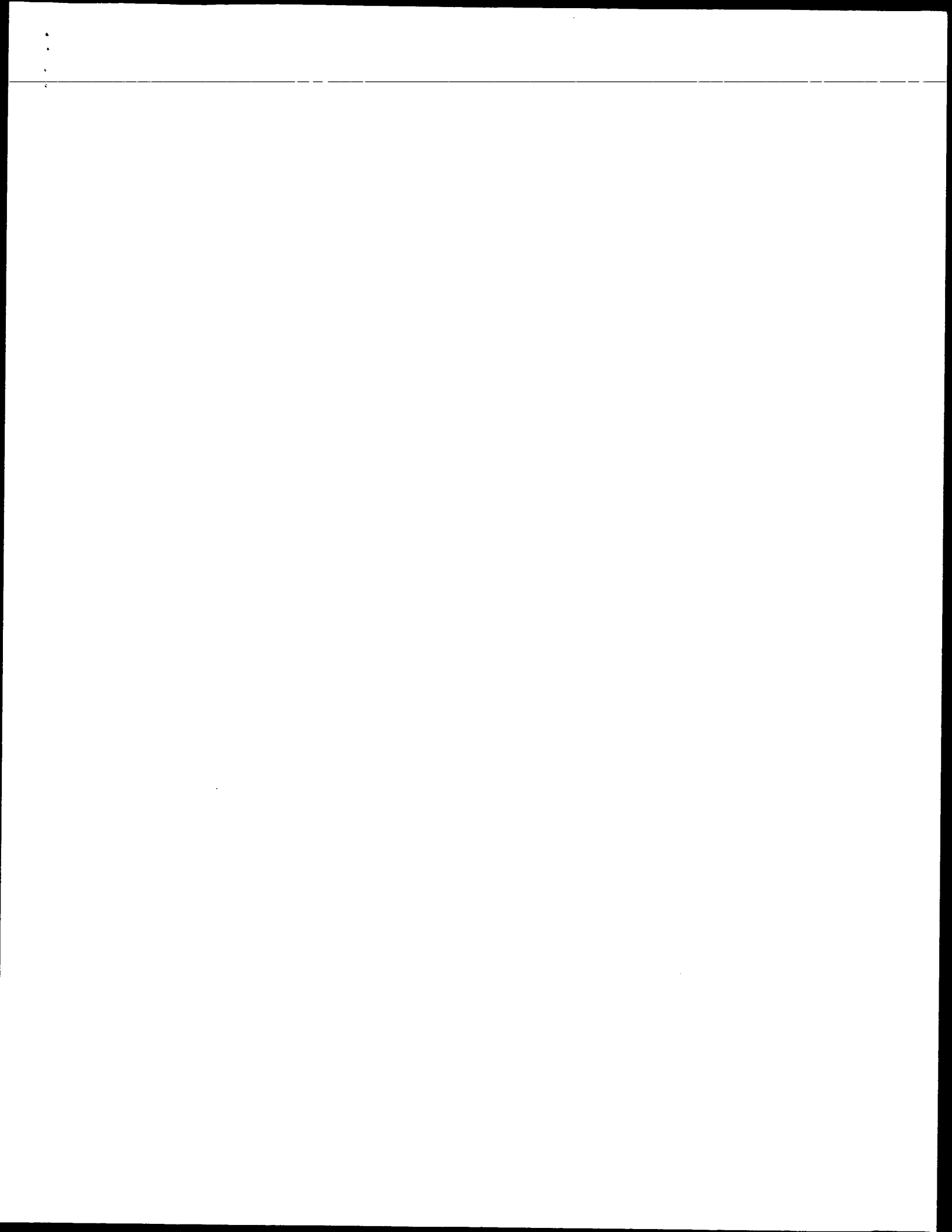
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GACCTTACTGCTCATGCTGAC 1171
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Job time: 16606 secs



GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 18:26:44 ; Search time 1028 Seconds

(without alignments)
10153.708 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
Sequence: 1 tcgcgactctagactagctg.....gttaacgggcccacagcccg 4635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3205	69.1	4237	24	ABA96005
2	2112	45.6	2243	24	ABA94696
3	1579	34.1	6551	24	ABK12390
4	60	1.3	60	24	ABN36694
5	56	1.2	233	21	AAC30759
6	44	0.9	534	24	ABK71572
7	21	0.5	896	24	AAD33703
8	21	0.5	1365	16	AAO87044
9	21	0.5	1365	16	AAO87772

10	21	0.5	4242	24	ABK84021	Human CDNA differe
11	21	0.5	4242	24	ABK84532	Human CDNA differe
12	21	0.5	4519	24	ABK84127	Human CDNA differe
13	20	0.4	324	23	AA591012	DNA encoding novel
14	20	0.4	426	24	ABK64733	Human benign prost
15	20	0.4	426	24	ABK66602	Lung cancer relate
16	20	0.4	642	23	AA580837	DNA encoding novel
17	20	0.4	870	22	AA193967	Human neuroblastom
18	20	0.4	894	24	AAD24359	Human Stat6 (signa
19	20	0.4	1062	17	AAT09951	High-affinity meia
20	20	0.4	1245	23	AA591014	DNA encoding novel
21	20	0.4	1530	23	AA554350	Pseudomonas aerugi
22	20	0.4	1840	22	AA019219	Human CG121 (or C5
23	20	0.4	1856	20	AA227941	Canine CT1A4 prote
24	20	0.4	1856	20	AA227942	Canine CT1A4 gene
25	20	0.4	2289	22	AAD17564	Novel human phosph
26	20	0.4	2289	22	AAD23721	Human phospholipas
27	20	0.4	2377	24	ABA94880	Mouse melatonin 1a
28	20	0.4	2462	24	AAD23723	Human phospholipas
29	20	0.4	2520	24	ABD60544	Human lipid metabo
30	20	0.4	2540	24	AAD23722	Human phospholipas
31	20	0.4	2573	24	ABK63432	Rat sequence diffe
32	20	0.4	2629	24	ABK10063	Human phospholipas
33	20	0.4	2709	22	AA017567	Novel human phosph
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36	20	0.4	3441	20	AAH80044	Human PRO243 nucle
37	20	0.4	3441	21	AAA49552	Human PRO243 CDNA
38	20	0.4	3441	24	AAA40258	DNA encoding huma
39	20	0.4	3441	24	ABK28570	Human DNA359-1207
40	20	0.4	3594	24	ABA94695	Human lipid metabo
41	20	0.4	3806	22	ABA08946	Human insulin rece
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43	20	0.4	4235	22	AAFC8399	Human lung tumour
44	20	0.4	4235	24	ABK84751	Human CDNA differe
45	20	0.4	4235	24	ABK83110	CDNA encoding clon

ALIGNMENTS

RESULT 1	ABA96005	standard; cDNA; 4237 BP.
ID	ABA96005;	
AC	ABA96005;	
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DT	04-MAR-2002	(first entry)
XX		
DE	Human lipid metabolism enzyme-5 (LME-5) cDNA.	
XX		
KW	Human; LME-5; lipid metabolism enzyme-5; cytostatic; neuroprotective;	
KW	immunopressive; anti-inflammatory; cardiovascular; gene therapy;	
KW	enzyme therapy; cancer; neurological disorder; autoimmune disorder;	
KW	inflammatory disorder; cardiovascular disorder; ss.	
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OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	99..3818
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PN	WO200185956-A2.	
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PD	15-NOV-2001.	
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PF	11-MAY-2001; 2001WO-US15210.	
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PR	11-MAY-2000; 2000US-203511P.	
PR	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	

XX (INCC-) INCYTE GENOMICS INC.
PA
PI Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-Young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;
XX
XX MPI: 2002-089794/12.
DR P-PSDB; ABB08205.
PT New lipid metabolism enzymes useful for diagnosing, treating and
PT preventing cancer, neurological disorders, autoimmune/inflammatory
PT disorders, and cardiovascular disorders
XX
XX Claim 5; Page 121-122; 122pp; English.
XX
XX The sequence encodes a novel human lipid metabolism enzyme (LME-5) of
CC the invention. The invention relates to novel human LME's, and the
CC polynucleotides which identify and encode them. The enzymes of the
CC invention have cytosolic, neuroprotective, immunosuppressive,
CC anti-inflammatory, and cardiovascular activity. The polypeptides and
CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
CC metabolism enzymes are useful in the diagnosis, treatment and prevention
CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
CC cardiovascular disorders, and in the assessment of the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
CC for compounds that modulate the activity of LME. Polynucleotides encoding
CC LME may be used for somatic or germline gene therapy, to detect and
CC quantify gene expression in biopsied tissues in which expression of LME
CC may be correlated with disease, to generate a transcript image of a
CC tissue or cell type, to generate hybridization probes useful in mapping
CC the naturally occurring genomic sequence, and for screening libraries of
CC compounds in drug screening techniques. The polypeptide sequences may be
CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
CC primers derived from polynucleotide sequences encoding LME may be used to
CC detect single nucleotide polymorphisms.
XX
XX Sequence 4237 BP; 816 A; 1327 C; 1370 G; 724 T; 0 other;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 3467 GCGCGCCACATGATGAATGT 3526
Db 3227 GCGCGCCACATGATGAATGT 3286
Qy 3527 GCAAG 3586
Db 3287 GCAAG 3346
Qy 3587 GCGCGCGGGGCTGTGATCATCTGTGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3646
Db 3347 GCGCGCGGGGCTGTGATCATCTGTGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3406
Qy 3647 CCGCGGAG 3706
Db 3407 CCGCGGAG 3466

Qy 3707 TAGCGGCTCCATGTCTCTCGAGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 3766
Db 3467 TAGCGGCTCCATGTCTCTCGAGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 3526
Qy 3767 CCGCGGCTGTGAG 3826
Db 3527 CCGCGGCTGTGAG 3586
Qy 3827 CTGTGTGCTCAAAAGCTGTGAG 3886
Db 3587 CTGTGTGCTCAAAAGCTGTGAG 3646
Qy 3887 GCGGCTCTTGTGCGGTGTGTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3946
Db 3647 GCGGCTCTTGTGCGGTGTGTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3706
Qy 3947 TGCTGTGCTTGTGCGGT 4006
Db 3707 TGCTGTGCTTGTGCGGT 3766
Qy 4007 GTGGACATGTCTCGGT 4066
Db 3767 GTGGACATGTCTCGGT 3826
Qy 4067 CTCTGTGCTGTGAG 4126
Db 3827 CTCTGTGCTGTGAG 3886
Qy 4127 GGAAGAAACAGAGCTGTCTTGT 4186
Db 3887 GGAAGAAACAGAGCTGTCTTGT 3946
Qy 4187 GCGGCTCTGAG 4246
Db 3947 GCGGCTCTGAG 4006
Qy 4247 CCGTGTGCTTGTCTGTGAG 4306
Db 4007 CCGTGTGCTTGTCTGTGAG 4066
Qy 4307 GCAAGCTCAAG 4366
Db 4067 GCAAGCTCAAG 4126
Qy 4367 GTCCTGTGAG 4426
Db 4127 GTCCTGTGAG 4186
Qy 4427 GCGCCAG 4475
Db 4187 GCGCCAG 4235

RESULT 2
ABA94696
ID ABA94696 standard; cDNA; 2243 BP.
XX
AC ABA94696;
XX
DT 23-APR-2002 (first entry)
XX
DE Human lipid metabolism molecule (LMW) cDNA (ID: 2965233CH1).
XX
XX Lipid metabolism molecule; LMW; cytosolic; neuroprotective;
KW anticompulsant; immunosuppressive; anti-inflammatory; dermatological;
KW cardiovascular; antiHIV; antileptic; antidiabetic; hypertensive; human;
KW cancer; gene therapy; protein therapy; ss.
OS
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 321..2189

```

FT      /+tag= a
FT      /product= "LMM"
XX
XX      MO200204490-A2.
XX
XX      17-JAN-2002.
XX
PF      06-JUL-2001; 2001MO-US21432.
XX
XX      07-JUL-2000; 2000US-216801P.
XX      07-JUL-2000; 2000US-216803P.
XX      14-JUL-2000; 2000US-218233P.
XX      21-JUL-2000; 2000US-22046P.
XX      26-JUL-2000; 2000US-220739P.
XX      04-AUG-2000; 2000US-222824P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
XX      Tang YT, Azimzai Y, Das D, Thornton M, Lu DM, Tribouley CM,
XX      Yue H, Gandhi AR, Wallia NK, Khan FA, Lu Y, Yao MG, Hafalia AD;
XX      Elliott VS, Patterson C, Lal P, Rankumar J, Nguyen DB, Baugh MR;
XX      WPI; 2002-164631/21.
XX      P-PSDB; ABB07493.
XX
XX      Lipid metabolism molecules useful in diagnosing, treating or preventing
XX      cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
XX      skin and cardiovascular disorders -
XX
XX      Claim 5; Page 123-124; 128pp; English.
XX
XX      The invention provides human lipid metabolism molecule (LMM) polypeptides
XX      and polynucleotides. The LMM polypeptides can be expressed by standard
XX      recombinant methodology. The LMM polypeptides are useful for diagnosing
XX      or treating a condition or disease associated with the expression of LMM,
XX      or screening for compounds that specifically bind to or modulate the
XX      activity or expression of LMM. They are also used to generate antibodies
XX      and assess the toxicity of test compounds. The LMM polypeptides,
XX      modulators and antibodies are specifically useful for diagnosing,
XX      treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
XX      melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
XX      cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/
XX      inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
XX      or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
XX      esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
XX      disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
XX      disorders (e.g. hypertension, arterial dissections, vascular tumours, or
XX      thrombolysis). The present sequence represents a human LMM polynucleotide
XX      sequence.
XX
XX      Sequence 2243 BP; 499 A; 678 C; 691 G; 375 T; 0 other;
XX
XX      Query Match      45 6%; Score 2112; DB 24; Length 2243;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY      112 GGCCTGAGGCTGAGGGGCTGAGTGTCTCATTCAGCGGCTCGGGGAAACCGGAGCTGGGA 171
DB      1 GGGCTGAGGCTGAGGGGCTGAGTGTCTCATTCAGCGGCTCGGGGAAACCGGAGCTGGGA 60
QY      172 GACCCATGCTTGGGGGTGAGGCTTGAGGCCAGGGCAGTGGGTGAGAGGCTCCGGAGAGA 231
DB      61 GACCCATGCTTGGGGGTGAGGCTTGAGGCCAGGGCAGTGGGTGAGAGGCTCCGGAGAGA 120
QY      232 GGGCTGGGACCAACAGGCTTGGGTGTGTGATGCGCTGTGGCCAGGCTAACCCCGAAC 291
DB      121 GGGCTGGGACCAACAGGCTTGGGTGTGTGATGCGCTGTGGCCAGGCTAACCCCGAAC 180
QY      292 AAGGGAACACCGGGGGCTTGGGAGCAGAGAGACTTCAGAGAGAGCTTCTCTCTCTCTG 351
DB      181 AAGGGAACACCGGGGGCTTGGGAGCAGAGAGACTTCAGAGAGAGCTTCTCTCTCTCTG 240
QY      352 TGGACGGCGGGCCCAAGCTGTGTATCCAGCAATCCAGCTTTTGAATTGCTGCCCCAC 411

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DB      241 TGGACGGCGGGCCCAAGCTGTGTATCCAGCAATCCAGCTTTTGAATTGCTGCCCCAC 300
QY      412 CGACAGTCTCAGTCCCTCCATGATGAGCTCCCGAGAGCGGCGCCCTTCTTGAGCCAG 471
DB      301 CGACAGTCTCAGTCCCTCCATGATGAGCTCCCGAGAGCGGCGCCCTTCTTGAGCCAG 360
QY      472 CTCTTCGCGCTGAGGACCCAGAGGCTCGATCCGAGAGAGAGTGTCTTTCTTGAGCCCA 531
DB      361 CTCTTCGCGCTGAGGACCCAGAGGCTCGATCCGAGAGAGAGTGTCTTTCTTGAGCCCA 420
QY      532 ACATTCGCGCTGAGGAGGAGGAGTGCATGAGTGCATGACAAAGAGGAGTGCATGAGTGA 591
DB      421 ACATTCGCGCTGAGGAGGAGGAGTGCATGAGTGCATGACAAAGAGGAGTGCATGAGTGA 480
QY      592 AGTGTGCTGCGGCTCCAGAGGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 651
DB      481 AGTGTGCTGCGGCTCCAGAGGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
QY      652 GCATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 711
DB      541 GCATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY      712 AGAGGTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 771
DB      601 AGAGGTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY      772 ACCCAACTGCTGCTTACAGATCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831
DB      661 ACCCAACTGCTGCTTACAGATCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY      832 CCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891
DB      721 CCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY      892 TCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 951
DB      781 TCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY      952 CGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1011
DB      841 CGTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY      1012 TGTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071
DB      901 TGTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY      1072 CGGACAGGATGACCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1131
DB      961 CGGACAGGATGACCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY      1132 TGAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1191
DB      1021 TGAATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY      1192 ACCTGATGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1251
DB      1081 ACCTGATGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY      1252 CCTCGAGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1311
DB      1141 CCTCGAGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY      1312 AGGGGCTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1371
DB      1201 AGGGGCTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY      1372 TCAACCTGAGCAACCAATGTCACCAAGAGCATGACGAGCGCTGAGCCACTTCA 1431
DB      1261 TCAACCTGAGCAACCAATGTCACCAAGAGCATGACGAGCGCTGAGCCACTTCA 1320
QY      1432 TCACTGTGTCACCAACCAATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1491

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QY 2381 CTTGAGGAGACCAAGGCCACCAAGATTCTGACAGAGAAAGCCGGCCAGTACCTT 2440
 DB 3759 CTTGAGGAGACCAAGGCCACCAAGATTCTGACAGAGAAAGCCGGCCAGTACCTT 3818
 QY 2441 CAACGACGACAGTCTCCCGCATCTACCCCTCTCTACCGGTGAGACTCCAGCAACTA 2500
 DB 3819 CAACGACGACAGTCTCTCCCGCATCTACCCCTCTCTACCGGTGAGACTCCAGCAACTA 3878
 QY 2501 CAACCCGACAGCTTCTGGAACGCCGCTGACCAATGTTGCCCTGAACCTACAGTACAG 2560
 DB 3879 CAACCCGACAGCTTCTGGAACGCCGCTGACCAATGTTGCCCTGAACCTACAGTACAG 3938
 QY 2561 GGGGCGGATGCTGACAGTGAACCGAGCCAAAGTTACAGCCCAAGGTGGCTGGGCTACGT 2620
 DB 3939 GGGGCGGATGCTGACAGTGAACCGAGCCAAAGTTACAGCCCAAGGTGGCTGGGCTACGT 3998
 QY 2621 ACTCAAGCTGAGTGCATGTGACAGGAGCGTGTCAACCCCACTGGAGAGACCCCTGAC 2680
 DB 3999 ACTCAAGCTGAGTGCATGTGACAGGAGCGTGTGTCAACCCCACTGGAGAGACCCCTGAC 4058
 QY 2681 CGGCGAGCTCAAGAGACAGCTGTGCTCCGATCATCAATGAGCCAGCACTTCCAGAGCC 2740
 DB 4059 CGGCGAGCTCAAGAGACAGCTGTGCTCCGATCATCAATGAGCCAGCACTTCCAGAGCC 4118
 QY 2741 GCGCGACTCAGTGTGGGGGACCGTGGGAGATCATCAACCCCTTGTGTGAGTGAAT 2800
 DB 4119 GCGCGACTCAGTGTGGGGGACCGTGGGAGATCATCAACCCCTTGTGTGAGTGAAT 4178
 QY 2801 CATTGGGCTCCCTGTGAGCTGACAGAGAGAGACCCGCTGTGTGAAGAGAGAGGTT 2860
 DB 4179 CATTGGGCTCCCTGTGAGCTGACAGAGAGAGACCCGCTGTGTGTGAAGAGAGAGGTT 4238
 QY 2861 CAACCCACCTGGAGAGAGACCTGTGTTTTCATGTGACATATGCGGAGATGCGCTGCT 2920
 DB 4239 CAACCCACCTGGAGAGAGACCTGTGTTTTCATGTGACATATGCGGAGATGCGCTGCT 4298
 QY 2921 CCGCTTCTCTGCTGTGGAGACAGATCCCAATCCGGGCGTGACTTCAATTTGGCAAGAGACGT 2980
 DB 4299 CCGCTTCTCTGCTGTGGAGACAGATCCCAATCCGGGCGTGACTTCAATTTGGCAAGAGACGT 4358
 QY 2981 GGCCTTCAAGCAGATGATCCAGGCTTACAGACAGTGTACTTGAAGAGGATGAAAGAGC 3040
 DB 4359 GGCCTTCAAGCAGATGATCCAGGCTTACAGACAGTGTACTTGAAGAGGATGAAAGAGC 4418
 QY 3041 CTCACATCTCGTGCATGTGCTGATGATCATCAAGCGGTAAAGTCAAGCAGGCTCTGGG 3100
 DB 4419 CTCACATCTCGTGCATGTGCTGATGATCATCAAGCGGTAAAGTCAAGCAGGCTCTGGG 4478
 QY 3101 CCTAAAAGGCTCTTCTCTCCAGAGCCCAAGCCCGGCTGCTGACAGTCAATGCTGTGG 3160
 DB 4479 CCTAAAAGGCTCTTCTCTCCAGAGCCCAAGCCCGGCTGCTGACAGTCAATGCTGTGG 4538
 QY 3161 GCGGCCCCCGGCGCCCTCTCGTTAGCCAGGATCTCTGCGGCGCACGCGCCAGGCCCC 3220
 DB 4539 GCGGCCCCCGGCGCCCTCTCGTTAGCCAGGATCTCTGCGGCGCACGCGCCAGGCCCC 4598
 QY 3221 GACCAAGAGCCGAGAGCCGGGCGGAGGCGCTTCCCGAGCTGTGCTGGGTACACAGGGA 3280
 DB 4599 GACCAAGAGCCGAGAGCCGGGCGGAGGCGCTTCCCGAGCTGTGCTGGGTACACAGGGA 4658
 QY 3281 CAAGGCTTCAAGAGGCGGTGACAGATGTGTGCCCCCGGCGCCGAGACCTGCTCGGA 3340
 DB 4659 CAAGGCTTCAAGAGGCGGTGACAGATGTGTGCCCCCGGCGCCGAGACCTGCTCGGA 4718
 QY 3341 AGCCCGACCCGAGAGGGGCGCGGAGCGGACGCCCCGAGGTAAAGCGCAAGTCCGCT 3400
 DB 4719 AGCCCGACCCGAGAGGGGCGCGGAGCGGACGCCCCGAGGTAAAGCGCAAGTCCGCT 4778
 QY 3401 GGCAGAGAGAGCCCTGTGAGTGCAGGCGCCCGGCTGCTGAGAGGCGCCCGGCGCTGC 3460
 DB 4779 GGCAGAGAGAGCCCTGTGAGTGCAGGCGCCCGGCTGCTGAGAGGCGCCCGGCGCTGC 4837

QY 3461 TGGATGCGCGCCACATGATGAAGTGTGTGTGGATCTCTGCGCGCGCTGGAACCCGG 3520
 DB 4838 TGGATGCGCGCCACATGATGAAGTGTGTGTGGATCTCTGCGCGCGCTGGAACCCGG 4897
 QY 3521 GGGCTGTGAGAGGAGGAGGCGCCACCCAGCCCGGGGCTGTGAGAGAGAGCAGCATTTCG 3580
 DB 4898 GGGCTGTGAGAGGAGGAGGCGCCACCCAGCCCGGGGCTGTGAGAGAGAGCAGCATTTCG 4957
 QY 3581 CCAGCAGCCCGGCGCGCGGCTGACTCACTGAGGAGGCGCCCTGCTGTGTGAGCCTGCA 3640
 DB 4958 CCAGCAGCCCGGCGCGCGGCTGACTCACTGAGGAGGCGCCCTGCTGTGTGAGCCTGCA 5017
 QY 3641 CGCTATCCCGGAGAGAGCAGAGAGGCTCCCAAGGTCCTGAGGAGGAGGAGGCTTC 3700
 DB 5018 CGCTATCCCGGAGAGAGAGCAGAGAGGCTCCCAAGGTCCTGAGGAGGAGGAGGCTTC 5077
 QY 3701 AGGCGGTAGAGGCGCTCAATGTCTCGACTGCTCAGCAGCGCCAGAGCCCGGCGCATCCCGA 3760
 DB 5078 AGGCGGTAGAGGCGCTCAATGTCTCGACTGCTCAGCAGCGCCAGAGCCCGGCGCATCCCGA 5137
 QY 3761 AAGTCCCGCGCTGAGGAGGCTGCTGAGGAGGCTGAGGAGGAGGAGGAT 3820
 DB 5138 AAGTCCCGCGCTGAGGAGGCTGCTGAGGAGGCTGAGGAGGAGGAGGAT 5197
 QY 3821 GAGTCCCTTGTGTTGCTCAAAAGCTGAGAGAGATCAGAGTAAATCCCATGTTCTCCG 3880
 DB 5198 GAGTCCCTTGTGTTGCTCAAAAGCTGAGAGAGATCAGAGTAAATCCCATGTTCTCCG 5257
 QY 3881 CG 3882
 DB 5258 CG 5259

RESULT 4
 ABN36694
 ID ABN36694 standard; DNA; 60 bp.
 XX
 AC ABN36694;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:9442.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 PS Example 1; SEQ ID 9442; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 60 BP; 14 A; 15 C; 19 G; 12 T; 0 other;

Query Match 1.3%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4446 TTGGGCTGAGACCCCTAGAGGGTGTCTCTTACCTGAGGAGGACATACAC 4505
1 TTGGGCTGAGACCCCTAGAGGGTGTCTCTTACCTGAGGAGGACATACAC 60

RESULT 5
AAC0759
ID AAC0759 standard; cDNA; 233 BP.

XX AAC0759;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 34834.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

PA Dumas Milne Edwards J, Duclet A, Giordano J;

DR WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX Claim 1; SEQ ID 34834; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)

of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

Sequence 233 BP; 41 A; 80 C; 72 G; 33 T; 7 other;

Query Match 1.2%; Score 56; DB 21; Length 233;
Best Local Similarity 100.0%; Pred. No. 8.5e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 254 GGTGTGATATGCGCTGCGCCAGGCTACACCCCGACAGGAGACCGGGGGCCC 309
DB 21 GGTGTGATATGCGCTGCGCCAGGCTACACCCCGACAGGAGACCGGGGGCCC 76

RESULT 6

ABK71572
ID ABK71572 standard; cDNA; 534 BP.

AC ABK71572;

DT 30-JUL-2002 (first entry)

DE Human dithp polynucleotide #38.

XX Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KW inflammatory disorder; viral infection; bacterial infection; seizure;
KW fungal infection; parasitic infection; developmental disorder; breast;
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KW skin; testis; thymus.

XX Homo sapiens.

PN WO200220754-A2.

PD 14-MAR-2002.

PF 29-AUG-2001; 2001WO-US27127.

XX 05-SEP-2000; 2000US-229747P.
PR 05-SEP-2000; 2000US-229748P.
PR 05-SEP-2000; 2000US-229749P.
PR 05-SEP-2000; 2000US-229750P.
PR 05-SEP-2000; 2000US-229751P.
PR 05-SEP-2000; 2000US-230583P.
PR 06-SEP-2000; 2000US-230585P.
PR 06-SEP-2000; 2000US-230514P.
PR 06-SEP-2000; 2000US-230515P.
PR 06-SEP-2000; 2000US-230517P.
PR 06-SEP-2000; 2000US-230518P.
PR 06-SEP-2000; 2000US-230519P.
PR 06-SEP-2000; 2000US-230595P.
PR 06-SEP-2000; 2000US-230597P.
PR 06-SEP-2000; 2000US-230598P.
PR 06-SEP-2000; 2000US-230599P.
PR 06-SEP-2000; 2000US-230610P.
PR 06-SEP-2000; 2000US-230865P.
PR 06-SEP-2000; 2000US-230988P.
PR 07-SEP-2000; 2000US-230951P.
PR 07-SEP-2000; 2000US-231163P.
PR 07-SEP-2000; 2000US-231167P.
XX (INCY-) INCYTE GENOMICS INC.

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PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright JL, Rietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiyama MG, Bradley JL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerdin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
XX WPI: 2002-383054/41.
DR P1PSDB; ABG59980.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics -
XX
XX Claim 1; Page 424-425; 686pp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dthp)
XX polynucleotides and their associated polypeptides (dthp polypeptides).
XX The sequences of the invention are used in the treatment and diagnosis of
XX cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
XX (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
XX cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
XX thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
XX psoriasis, osteoporosis), viral infections, bacterial infections, fungal
XX infections, parasitic infections, developmental disorders (e.g. anaemia,
XX epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
XX endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
XX (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
XX amyotrophic lateral sclerosis), multiple sclerosis), gastrointestinal
XX disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
XX (e.g. myoclonic dystrophy, cataplexy, peripheral neuropathy). Sequences
XX ABK71535-ABK71809 represent human dthp polynucleotides of the invention.
XX
XX Sequence 534 BP; 125 A; 154 C; 140 G; 115 T; 0 other;
SQ
Query Match 0.9%; Score 44; DB 24; Length 534;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1440 TCCGACACACTTACTGCTGGTGTACGAGCTGATGCCAGTC 1483
Db 334 TCCGACACACTTACTGCTGGTGTACGAGCTGATGCCAGTC 377
RESULT 7
AAD33703
ID AAD33703 standard; CDNA; 896 BP.
XX
XX AAD33703;
XX
XX 01-JUN-2002 (first entry)
XX
XX Human secreted protein-encoding gene 12 cDNA clone HCOMM91, SEQ ID NO:22.
XX
XX Human; secreted protein; immune disorder; anti-allergic; anti-rheumatic;
XX rheumatoid arthritis; breast neoplasia; breast cancer; anti-leukemic;
XX neurological disease; Alzheimer's disease; Parkinson's disease; trauma;
XX Tourette syndrome; encephalitis; cytosolic; haemostatic; anaemia; mania;
XX anti-inflammatory; ophthalmological; dermatological; immunostimulatory;
XX immunomodulatory; immunosuppressive; antibacterial; antiparasitic;
XX gene therapy; autoimmune disease; Huntington's disease; meningitis;
XX demyelinating disease; peripheral neuropathy; congenital malformation;
XX spinal cord injury; peripheral neuropathy; ischaemia; perception;
XX multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia;
XX depression; panic disorder; learning disability; ALS; feeding disorder;
XX hyperproliferative disorder; sleep pattern; cardiovascular disorder;
XX reproductive disorder; digestive system disorder; behavioural disorder;
XX gene; ss.
XX
XX Homo sapiens.
XX
XX
XX Location/Qualifiers
XX Key 542..817
XX CDS /*tag= a
XX /product= "Human secreted protein"
XX /transl_except= (pos:791..793, aa:Xaa)

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FT FT /note= "Xaa equals any of the naturally occurring
FT FT L-amino acids"
FT sig_peptide 542..634
FT /*tag= b
FT mat_peptide 635..814
FT /*tag= c
FT /product= "Human mature secreted protein"
XX
XX W0200216390-A1.
XX
XX 28-FEB-2002.
XX
XX 17-JAN-2001; 2001WO-US01435.
XX
XX 18-AUG-2000; 2000US-226282P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Komatsu G, Baker KP, Birse CE, Soppet DR, Olsen HS;
XX Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
XX Ni J;
XX
XX WPI: 2002-304113/34.
XX
XX P-PSDB; AAE21202.
XX
XX An isolated nucleic acid molecule (1) comprising a polynucleotide which
XX encodes a polypeptide useful in the diagnosis and treatment of
XX disorders e.g. immune disorders -
XX
XX Claim 1; Page 447; 534pp; English.
XX
XX AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
XX protein genes, and AAE21191-AAE21235 represent the proteins they encode.
XX AAE21236-AAE21280 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 21 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX immune or autoimmune diseases e.g. AIDS (acquired immune deficiency
XX syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
XX and breast cancer, neurological diseases e.g. Alzheimer's disease,
XX Parkinson's disease, Huntington's disease, Tourette syndrome,
XX meningitis, demyelinating disease, peripheral neuropathies, neoplasia,
XX trauma, congenital malformations, spinal cord injuries, toxic
XX neuropathies induced by neurotoxins, peripheral neuropathies, multiple
XX sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania,
XX altered behaviours e.g. disorders in feeding, sleep patterns, balance
XX and perception, encephalitis, disorders in cardiovascular, neural/
XX sensory, reproductive and digestive systems, behavioural disorders and
XX hyperproliferative disorder. The present sequence represents a human
XX secreted protein-encoding cDNA of the invention.
XX
XX Sequence 896 BP; 200 A; 213 C; 297 G; 180 T; 6 other;
SQ
Query Match 0.5%; Score 21; DB 24; Length 896;
Best Local Similarity 100.0%; Pred. NO. 43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4561 TCTGCCCCCACCACCGCTTGC 4581
Db 823 TCTGCCCCCACCACCGCTTGC 843
RESULT 8
AAQ87044/C
ID AAQ87044 standard; CDNA; 1365 BP.
XX
XX AAQ87044;
XX

```

DT	10-DEC-1995	(first entry)	
XX			
DE	Pig interleukin-10 cDNA.		
XX			
KM	Swine; interleukin-10; cytokine; lymphokine; protein; stem cell;		
KM	haematopoiesis; ss.		
XX			
OS	Sus scrofa.		
XX			
FH	Key	location/Qualifiers	
FT	CDS	73..651	
XX		/*tag= a	
PN	W09513363-A1.		
XX			
PD	18-MAY-1995.		
XX			
PF	01-NOV-1994;	94WO-US12522.	
XX			
PR	10-NOV-1993;	93US-0150739.	
XX			
PA	(GEHO) GEN HOSPITAL CORP.		
XX			
PI	Emery DW, Le GUERN CA, Sachs DH, leguern CA;		
XX			
DR	WPI; 1995-194083/25.		
XX	P-PSDB; AAR73018.		
PT	New purified haematopoietic stem cells - isolated from swine cord		
PT	blood, used in transplantation, inducing immune tolerance and immune		
PT	system reconstitution		
XX			
PS	Disclosure; Page 45; 58pp; English.		
XX			
CC	This sequence encoding pig interleukin-10 may be expressed		
CC	recombinantly in swine cord blood haematopoietic stem cells. These		
CC	engineered stem cells may then be introduced into a recipient animal		
CC	so that the stem cells express IL-10. These recombinant cells may		
CC	be used in the induction of immunological tolerance, tissue		
CC	transplantation and reconstitution of the immune system without		
CC	having to use broad spectrum immune suppressants.		
XX			
SQ	Sequence 1365 BP; 366 A; 322 C; 313 G; 344 T; 0 other;		
XX			
Query Match	0.5%;	Score 21;	DB 16; Length 1365;
Best Local Similarity	100.0%;	Pred. No. 42;	
Matches 21; Conservative	0;	Mismatches	0; Indels 0; Gaps 0
QY	3334 CTCGGAGAGCCCGAGCCGAG	3354	
DB	1066 CTCGGAGAGCCCGAGCCGAG	1046	
XX			
RESULT 9			
AAQ85772/c			
ID	AAQ85772 standard; cDNA; 1365 BP.		
XX			
AC	AAQ85772;		
XX			
DT	09-OCT-1995 (first entry)		
XX			
DE	Porcine interleukin-10 (IL-10) cDNA.		
XX			
KM	Interleukin-10; cytokine; immune response; ss.		
XX			
OS	Sus scrofa.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	73..600	
FT		/*tag= a	
PN	W09506657-A.		
XX			

[illegible]

DR WPI, 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression

PT of genes associated with granulocyte activation, which serves as

PT diagnostic markers that is useful for monitoring disease states and

XX drug toxicity -

XX

PS Claim 1: SEQ ID No 592; 114pp; English.

XX

XX The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing

CC the expression level to an expression level in an unactivated

CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GCA by contacting GC with an agent

CC that alters the expression of at least one gene in Gs; (2) screening (M3)

CC for an agent capable of modulating GCA or an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease using the

CC gene expression profile; (3) detecting (M4) an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease, by detecting the

CC level of expression in a sample of the tissue of gene(s) from Gs, where

CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,

CC an allergic response in a subject, exposure of a subject to a pathogen

CC or sterile inflammatory disease, by contacting a tissue having

CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for

CC modulating GCA; M3 is useful for screening an agent capable of modulating

CC GCA preferably in an inflammation in a tissue; M4 is useful for

CC detecting an inflammation (especially chronic) in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,

CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal

CC reperfusion injury, ARDS, adult respiratory distress syndrome,

CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,

CC periodontal disease, also bacterial infection, viral infection,

CC parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present

CC sequence represents a gene differentially expressed in granulocytes.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX

XX Sequence 4242 BP; 1116 A; 1097 C; 1127 G; 902 T; 0 other;

XX

XX

XX Query Match 0.5%; Score 21; DB 24; Length 4242;

XX Best local Similarity 100.0%; Pred. No. 40;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1661 CCCAGTGATCCTGTCATCGA 1681

DB 1349 CCCAGTGATCCTGTCATCGA 1369

RESULT 11

ABKR84532

XX ABR84532 standard; cDNA; 4242 BP.

XX

XX ABR84532;

XX

XX 14-NUG-2002 (first entry)

XX

XX Human cDNA differentially expressed in granulocytic cells #1103.

XX

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW	Crohn's disease; ulcerative colitis; periodontal disease;
KW	granulocyte activation; chronic inflammation; allergy.
XX	
XX	Homo sapiens.
OS	
XX	
XX	WO200228999-A2.
XX	
XX	11-APR-2002.
XX	
XX	03-OCT-2001; 2001WO-US30821.
XX	
XX	03-OCT-2000; 2000US-237189P.
XX	
XX	(GENE-) GENE LOGIC INC.
XX	
XX	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX	WPI, 2002-435328/46.
XX	
XX	Detecting granulocyte activation by detecting differential expression
XX	of genes associated with granulocyte activation, which serves as
XX	diagnostic markers that is useful for monitoring disease states and
XX	drug toxicity -
XX	
PS	Claim 1; SEQ ID No 1103; 114pp; English.
XX	
CC	The invention relates to detecting (M1) granulocyte (GC) activation
CC	(GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC	DNA chip analysis as given in the specification, and comparing
CC	the expression level to an expression level in an unactivated
CC	GC, where differential expression of Gs is indicative of GCA.
CC	Also included are modulating (M2) GA by contacting GC with an agent
CC	that alters the expression of at least one gene in Gs; (2) screening (M3)
CC	for an agent capable of modulating GCA or an inflammation (especially
CC	chronic) in a tissue, an allergic response in a subject, exposure of a
CC	subject to a pathogen or sterile inflammatory disease using the
CC	gene expression profile; (3) detecting (M4) an inflammation (especially
CC	chronic) in a tissue, an allergic response in a subject, exposure of a
CC	subject to a pathogen or sterile inflammatory disease, by detecting the
CC	level of expression in a sample of the tissue of gene(s) from Gs, where
CC	the level of expression of the gene is indicative of inflammation;
CC	(4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC	an allergic response in a subject, exposure of a subject to a pathogen
CC	or sterile inflammatory disease, by contacting a tissue having
CC	inflammation with an agent that modulates the expression of gene(s)
CC	from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC	modulating GA; M3 is useful for screening an agent capable of modulating
CC	GCA preferably in an inflammation in a tissue; M4 is useful for
CC	detecting an inflammation (especially chronic) in a tissue, an allergic
CC	response in a subject, exposure of a subject to a pathogen or sterile
CC	inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC	glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC	reperfusion injury, ARDS, adult respiratory distress syndrome,
CC	inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC	periodontal disease, also bacterial infection, viral infection,
CC	parasitic infection, protozoal infection, fungal infection and M5 is
CC	useful for treating one of the above conditions. The present
CC	sequence represents a gene differentially expressed in granulocytes.
CC	Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic
CC	format directly from WIPO at
CC	ftp.wipo.int/pub/published_pat_sequences.
XX	
XX	Sequence 4242 BP, 1116 A; 1097 C; 1127 G; 902 T; 0 other;
XX	
XX	Query Match 0.5%; Score 21; DB 24; Length 4242;
XX	Best Local Similarity 100.0%; Pred. No. 40;
XX	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX	
XX	1661 CCGAGTGATCTGTCCATCGA 1661
XX	
XX	1349 CCGAGTGATCTGTCCATCGA 1369

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIR0
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 324 BP; 97 A; 61 C; 79 G; 87 T; 0 other;
Query Match 0.4%; Score 20; DB 23; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2181 GGCAGCAAGCTGAAGAGGC 2200
DB 160 GGCAGCAAGCTGAAGAGGC 179
RESULT 14
ABK64733/c
ID ABK64733 standard; DNA; 426 BP.
XX
AC ABK64733;
XX
DT 18-JUN-2002 (first entry)
DE Human benign prostatic hyperplasia gene #628.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
FN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISR) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 339; 444p; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for

CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 426 BP; 149 A; 78 C; 87 G; 112 T; 0 other;
Query Match 0.4%; Score 20; DB 24; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3044 CATCTTCGTGATGTGGCTG 3063
DB 234 CATCTTCGTGATGTGGCTG 215
RESULT 15
ABL66602/c
ID ABL66602 standard; DNA; 426 BP.
XX
AC ABL66602;
XX
DT 15-MAY-2002 (first entry)
DE Lung cancer related gene sequence SEQ ID NO:4939.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytosaratic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
FN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234933P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236422P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 03-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.

PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

XX
 PA (AVAL-) AVALON PHARM.

XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;

XX
 DR MPI; 2002-188264/24.

XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -

XX
 PS Claim 1; SEQ ID 4939; 44p; English.

XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.

XX
 SQ Sequence 426 BP; 149 A; 78 C; 87 G; 112 T; 0 other;

Query Match 0.4%; Score 20; DB 24; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3044 CATTTCGTCATGTGGCTG 3063

DB 234 CATTTCGTCATGTGGCTG 215

Search completed: March 28, 2003, 22:25:35
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587	12.7	759	12 BG472146	BG472146 602513869
2	548	11.8	561	10 BE255177	BE255177 601115717
3	512	11.0	1016	12 BG394794	BG394794 602457129
4	473	10.2	14	BM903836	BM903836 AGENCOURT
5	365	7.9	436	12 BE908459	BE908459 601503091
6	340	7.3	663	12 BG819793	BG819793 602781835

7	293	6.3	395	10	BE244972	BE244972 TCBA3E16
8	172	3.7	801	13	BE255354	BE255354 601115369
9	156	3.4	684	13	BI756147	BI756147 603030048
10	57	1.2	839	17	AO741196	AO741196 HS-2273-A
11	38	0.8	509	12	BF463298	BF463298 UI-M-CGP
12	38	0.8	656	10	BB430723	BB430723 BB430723
13	38	0.8	711	12	BG299246	BG299246 602395735
14	38	0.8	889	14	BQ946757	BQ946757 AGENCOURT
15	38	0.8	930	14	BO960462	BO960462 AGENCOURT
16	35	0.8	427	12	BE988680	BE988680 UI-M-CGP
17	35	0.8	645	14	BO571436	BO571436 UI-M-FCO-
18	35	0.8	733	14	BM950299	BM950299 UI-M-EHDP
19	32	0.7	543	17	AZ503328	AZ503328 1M0343105
20	32	0.7	667	10	BB624082	BB624082 BB624082
21	32	0.7	702	17	AZ805180	AZ805180 2M0066013
22	32	0.7	714	10	BB652903	BB652903 BB652903
23	32	0.6	300	13	BG955666	BG955666 CM4-CT065
24	29	0.6	514	10	BB283947	BB283947 BB283947
25	29	0.6	577	14	BM932679	BM932679 UI-M-CGP
26	29	0.6	664	10	BB642639	BB642639 BB642639
27	29	0.6	678	10	AV361753	AV361753 AV361753
28	27	0.6	226	10	BB047756	BB047756 BB047756
29	27	0.6	308	13	BG946330	BG946330 PM3-KT004
30	25	0.5	885	13	BI737630	BI737630 603358539
31	23	0.5	109	17	BH089788	BH089788 RRCI-24-3
32	23	0.5	314	13	BG945796	BG945796 PM3-KT004
33	23	0.5	624	12	BG682479	BG682479 602623577
34	22	0.5	230	10	AM889403	AM889403 RC6-NT002
35	22	0.5	233	12	BF944313	BF944313 RC5-NN116
36	22	0.5	245	12	BF804488	BF804488 OVA-C1015
37	22	0.5	276	12	F00147	F00147 HSB35B091-S
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39	22	0.5	400	13	BI816577	BI816577 1031046D0
40	22	0.5	485	14	BQ243736	BQ243736 TA815010A
41	22	0.5	487	10	AV621575	AV621575 AV621575
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43	22	0.5	512	10	AV392820	AV392820 AV392820
44	22	0.5	553	9	AA892330	AA892330 EST196133
45	22	0.5	555	17	AZ599264	AZ599264 IM0414D02

ALIGNMENTS

RESULT 1
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LOCUS 602513869F1 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:4645721 5',
DEFINITION mRNA sequence.
ACCESSION BG472146
VERSION BG472146.1 GI:13404520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 759)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov
Plate: L1CM1419 row: 1 column: 18
High quality sequence stop: 683.
Location/Qualifiers
1..759
/organism="Homo sapiens"

FEATURES

source

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/clone="IMAGE:4645721"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notice="Organ: eye; Vector: pOTB1; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. _directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH_MGC library."

```

BASE COUNT	148 a	248 c	256 g	107 e
ORIGIN				

Query March	12.7%;	Score 587;	DB 12;	Length 759;
Best Local Similarity	100.0%;	Pred. No. 8e-260;		
Matches 587;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2195	GGAATCAATTTGGAGTCCCTGTGGA	CTCAGACAGGAGAGCAACCCGGGTGGACACAA	285
Db	2	GGAGTCATTTGGGCTCCCTGTGGA <td>CTCAGACAGGAGCAACCCGGGTGGACACAA</td> <td>61</td>	CTCAGACAGGAGCAACCCGGGTGGACACAA	61
QY	2855	CGGGTTCAACCCCACTGGAGAGAGAC <td>CCCTGGTTTTATGTGTCACATGCCGAGATGCG</td> <td>291</td>	CCCTGGTTTTATGTGTCACATGCCGAGATGCG	291
Db	62	CGGGTTCAACCCCACTGGAGAGAGAC <td>CCCTGGTTTTATGTGTCACATGCCGAGATGCC</td> <td>121</td>	CCCTGGTTTTATGTGTCACATGCCGAGATGCC	121
QY	2915	GCTGTCGCGTTTCTCGTCTGGAGACAC <td>AGATCCCATCGGGCGTGAATTTATTTGGCCAGAG</td> <td>297</td>	AGATCCCATCGGGCGTGAATTTATTTGGCCAGAG	297
Db	122	GCTGTCGCGTTTCTCGTCTGGAGACAC <td>AGATCCCATCGGGCGTGAATTTATTTGGCCAGAG</td> <td>181</td>	AGATCCCATCGGGCGTGAATTTATTTGGCCAGAG	181

QY	2915	GAGCCTGGCCCTTCAGCAGCATGTATGCCAGGCTACAGACAGTGTACTTCGAAAGGATGGA	3033
Db	182	GACCTGGCCCTTCAGCAGCATGTATGCCAGGCTACAGACAGTGTACTTCGAAAGGATGGA	241
QY	3035	AGAGGCTCCCATCTTCGTGATGTGGCTGTCAATGACATCAGGGGTAAAGTCAAGAGGC	3099
Db	242	AGAGGCTCCCATCTTCGTGATGTGGCTGTCAATGACATCAGGGGTAAAGTCAAGAGGC	301

[illegible]

QY	3775	ACGGGACACAGGCTCCCAAGGGGGTGTGCACAACAATGTGTGTGTGCCCTCCCGGGCCTGGACTTCG	3334
Db	482	ACGGGACACAGGCTCCCAAGGGGGTGTGCACAACAATGTGTGTGTGCCCTCCCGGGCCTGGACTTCG	541
QY	3335	TTCGGGAAGCCCCAAGCCCAAGAAGGGGCCCGGACAGCGGCACTCCCAG	3381
Db	542	TTCGGGAAGCCCCAAGCCCAAGAAGGGGCCCGGACAGCGGCACTCCCAG	588

RESULT 2	BE255177	561 bp	mrna	linear	EST 13-JUL-2000
LOCUS	BE255177				
DEFINITION	601115717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356069 5',				

ACCESSION	BE255177	
VERSION	BE255177.1	GI:9125614
KEYWORDS	EST	

SOURCE ORGANISM	human.
	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 561)	NIH-MGC http://mgc.ncbi.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Struhsberg, Ph.D.			
	robstruhs@ncbi.nlm.nih.gov			

CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: InCite Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CML1 row: b column: 06
High quality sequence stop: 559.

FEATURES	LOCATION/QUALITY
source	1. .561

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:3356069"
/clone_1lb="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: POTB; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT      101 a      185 c      191 g      84 t

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Query Match	11.8%	Score 548;	DB 10;	Length 561;
Best Local Similarity	100.0%;	Pred. No. 7.9e-242;		
Matches 548;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2828 GAGAGCAGACCCGGTGTGTGAGACGACAAAGGGTTCAACCCACCTGGGAGGAGACCCGTG 2887

Db 14 GAGAGCAGACCCGGTGTGTGAGACGACAAAGGGTTCAACCCACCTGGGAGGAGACCCGTG 73

QY 2888 TTTCATGTGTGCATGTCCGGAGATCGCCCTGTGCTCTTCCCTGTCTGGAGACACGATCC 2947

Db 74 TTTCATGTGTGCATGTCCGGAGATGTGGCTGTGCTCTTCCCTGTCTGGAGACACGATCC 133

QY 2948 CATTCGGCGGTACTTTCATTTGGCCAGAGGACGCTGAGCTTTCAGCAGCATGATGCCAGGCTA 3007

Db 134 CATTCGGCGGTACTTTCATTTGGCCAGAGGACGCTGAGCTTTCAGCAGCATGATGCCAGGCTA 193

[illegible]

Db	314	AAAGCCGCGCTCGTGGACAGTCAATGCTGTGGCGGCGCCCGGCGCCCTCCGTTAG	373
Qy	3188	CCAGCGGATCTCTGGCGCGCAGGCGCAGCGGCCGACCAAGAGCCAGAGCGGGCGCAG	3247
Db	374	CCAGCGGATCTCTGGCGCGCAGGCGCAGCGGCCCGCCACCAAGCAGCAGAGCGGGCGCAG	433
Qy	3248	GGGCTTCCCGGAGCTGTCCTGGGGAACAAGGATCTTCAAGAGGGTGTGGCAACGA	3307

Db 434 GGGCTTCCCGAAGCTGGTCTTGGGTACACGGAGACACAGGCTTCAAGGGGGTGGCAGACGA 433

QY 3308 TGTGTGCCCCCGAGGACCTGTCGGGAAGCCAGCCAGAGGGGCCCGGACAG 336

Db 494 TGTGTGCCCCCGGCGCCGAGACTCTCTCGGAAGCCAGCCAGAGGGGCCCGGACAG 553

QY 3368 CGGACGCC 3375
DB 554 CGGACGCC 561

RESULT 3
BG394794 1016 bp mRNA linear EST 12-MAR-2001
LOCUS 602457129F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4579663 5',
DEFINITION mRNA sequence.
ACCESSION BG394794
VERSION BG394794.1 GI:13288242
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1016)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L12M1297 row: 1 column: 08
High quality sequence stop: 599.

FEATURES
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1. 1016
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4579663"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: POT8; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 324 a 302 c 247 g 143 t
ORIGIN

Query Match 11.0%; Score 512; DB 12; Length 1016;
Best Local Similarity 99.8%; Pred. No. 3.8e-225;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1287 GAGCATTGCCAGAAAACAAGTAAGGGCTGTGGGCAATTGATGGCTTACCAACTAC 1346
DB 9 GAGCATTGCCAGAAAACAAGTAAGGGCTGTGGGCAATTGATGGCTTACCAACTAC 68

QY 1347 ACCAGAGCCCTGTGTGATCATCTTCAACCTGAGACCAACATGTGACCCAGGACATG 1406
DB 69 ACCAGAGCCCTGTGTGATCATCTTCAACCTGAGACCAACATGTGACCCAGGACATG 128

QY 1407 ACCGAGCCGTGAGCCACTACTCATCTGCTCCACAACACTACCTGTGGGTGAC 1466
DB 129 ACCGAGCCGTGAGCCACTACTCATCTGCTCCACAACACTACCTGTGGGTGAC 188

QY 1467 CAGCTCATGTCACAGTACAGGATGATGATGCTGGTCTCTGACAGCTGCTGCGC 1526
DB 189 CAGCTCATGTCACAGTACAGGATGATGATGCTGGTCTCTGACAGCTGCTGCGC 248

QY 1527 TGGCTGAGGTGATCTGCTGGATGGGCGGAGGAGGAGCCATTGGCACTATGGCTAC 1586
DB 249 TGGCTGAGGTGATCTGCTGGATGGGCGGAGGAGGAGCCATTGGCACTATGGCTAC 308

QY 1587 ACTCTGACTTCCAAAGATCTCTTCCAAAGACGTGATGAAACATCAACAAATATGCTTC 1646
DB 309 ACTCTGACTTCCAAAGATCTCTTCCAAAGACGTGATGAAACATCAACAAATATGCTTC 368

QY 1647 ATCAAGATAGTATCCAGATGATCTGTCATGGAAGAACACGACGATGATCCAGCAG 1706
DB 369 ATCAAGATAGTATCCAGATGATCTGTCATGGAAGAACACGATGATCCAGCAG 428

QY 1707 AAGAAATGCGCCAGTATCTGATGATGATCTGGGAGCAAGCTGACCTGTATGATG 1766
DB 429 AAGAAATGCGCCAGTATCTGATGATGATCTGGGAGCAAGCTGATGATGATG 488

QY 1767 AGCAGTAAATGTCACCACTCTCTTCCACAGATGCTCAAGGCAAGATCTCTG 1826
DB 489 AGCAGTAAATGTCACCACTCTCTTCCACAGATGCTCAAGGCAAGATCTCTG 548

QY 1827 AAGGGAAGAACTCCAGCCAA 1849
DB 549 AAGGGAAGAACTCCAGCCAA 571

RESULT 4
BM903836 1002 bp mRNA linear EST 12-MAR-2002
LOCUS BM903836
DEFINITION AGENCOURT_6695882 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5492312
5', mRNA sequence.
ACCESSION BM903836
VERSION BM903836.1 GI:19353598
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1002)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L12M1214 row: d column: 09
High quality sequence stop: 428.

FEATURES
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1. 1002
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5492312"
/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: PCWV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 220 a 299 c 343 g 140 t
ORIGIN

Query Match 10.2%; Score 473; DB 14; Length 1002;
Best Local Similarity 100.0%; Pred. No. 4e-207;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2066 AAAGCTGAGCGCAAGCAAGCTGAAGAGAGCTGAGTCTGAGAGAGATGCTGGGCG 2125
DB 1 AAAGCTGAGCGCAAGCAAGCTGAAGAGAGCTGAGTCTGAGAGAGATGCTGGGCG 60

QY 2126 CAGCAGAGCAATGCGCCCTCTGCTGGGAAGCTTCTCCAGGCGCAAGAAAGAGGCGAG 2185

Db 61 CAGCAGACGCAATGCGCGCTCTCTGGAAGCTTCTCCAGGCGCAAGAGAGGCGAG 120
 Qy 2186 CAAGCTGAAGAGCGCGCGCGCGCTGAGAGAGAGATGAGAGTCAAGACTCCCGGAGAG 2245
 Db 121 CAAGCTGAAGAGCGCGCGCGCGCTGAGAGAGAGATGAGAGTCAAGACTCCCGGAGAG 180
 Qy 2246 CCGAGCGCGAGCGCGCGCGCGCGCGAGAGAGAGATGAGAGTCTCCCGGCGCTCTCTGA 2305
 Db 181 CCGAGCGCGAGCGCGCGCGCGCGCGAGAGAGAGATGAGAGTCTCCCGGCGCTCTCTGA 240
 Qy 2306 CCGTGTGAAGTACCAAGAGTCCGTGCGCAACCGACATGAGATGAGAGCGCGCTCGAG 2365
 Db 241 CCGTGTGAAGTACCAAGAGTCCGTGCGCAACCGACATGAGATGAGAGCGCGCTCGAG 300
 Qy 2366 CTTGCGAGGTGTCTCTCTTCAAGCGAGACCAAGCGCCACAGATTTCTGACAGAGCGCGC 2425
 Db 301 CTTGCGAGGTGTCTCTCTTCAAGCGAGACCAAGCGCCACAGATTTCTGACAGAGCGCGC 360
 Qy 2426 GCAGTACCTACGCTTCAACAGAGAGAGAGTCTCCGATCTACCTCTCTACCGTGT 2485
 Db 361 GCAGTACCTACGCTTCAACAGAGAGAGAGTCTCCGATCTACCTCTCTCTACCGTGT 420
 Qy 2486 GCACTCAGCACTACCAAGCGCGCGCTTCTGGAAGCGCGCTGCGCAATGAG 2538
 Db 421 GCACTCAGCACTACCAAGCGCGCGCTTCTGGAAGCGCGCTGCGCAATGAG 473

RESULT 5 436 bp mRNA linear EST 20-OCT-2000
 BE908459
 LOCUS 601503091F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904894 5',
 DEFINITION mRNA sequence.
 ACCESSION BE908459
 VERSION BE908459.1 GI:10403059
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 436)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9711 row: e column: 23
 High quality sequence stop: 433.

FEATURES
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 Location/Qualifiers
 1..436
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 /db_xref="taxon:9606"
 /clone="IMAGE:3904894"
 /clone_lib="NIH_MGC_70"
 /tissue_type="epitheloid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.1 Kb. Library constructed by Life
 Technologies."

BASE COUNT 100 a 129 c 138 g 69 t
 ORIGIN

Query Match 7.9%; Score 365; DB 12; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2.7e-157;
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 937 AGTGCTGAACAGACGTTTGACGAGGCCGACCAAGAAAGCGAGATGCGAGCTTGACATTG 996
 Db 72 AGTGCTGAACAGACGTTTGACGAGGCCGACCAAGAAAGCGAGATGCGAGCTTGACATTG 131
 Qy 997 GCGAGTCTCTGACCTGTGTGACAGAGTCAAGGTGAACCTGCCCCGAGAGAGGTGAAGC 1056
 Db 132 GCGAGTCTCTGACCTGTGTGACAGAGTCAAGGTGAACCTGCCCCGAGAGAGGTGAAGC 191
 Qy 1057 AGATGTTCAAGGAAGCGGACACGAGATACCAAGAGGAGCGTGGTTTGAAGATTCT 1116
 Db 192 AGATGTTCAAGGAAGCGGACACGAGATACCAAGAGGAGCGTGGTTTGAAGATTCT 251
 Qy 1117 GTGCTTCTACAAATATATGTTCACCCCGGAGACTCTTCTGCTCATCTGACCTTACA 1176
 Db 252 GTGCTTCTACAAATATATGTTCACCCCGGAGACTCTTCTGCTCATCTGACCTTACA 311
 Qy 1177 GCAACCAAGAGACCACTGATGCGCGCAGCTGACGAGCTTCTGACAGTGAAGAGA 1236
 Db 312 GCAACCAAGAGACCACTGATGCGCGCAGCTGACGAGCTTCTGACAGTGAAGAGA 371
 Qy 1237 AGATGCGCGGTGTGACCTTCAAGAGCTGCGAGACATCATGAGCAAGTTTGAAGCATTGCC 1296
 Db 372 AGATGCGCGGTGTGACCTTCAAGAGCTGCGAGACATCATGAGCAAGTTTGAAGCATTGCC 431
 Qy 1297 CAGAA 1301
 Db 432 CAGAA 436

RESULT 6 663 bp mRNA linear EST 22-MAY-2001
 BG819793
 LOCUS 602781835F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4932488
 DEFINITION 5', mRNA sequence.
 ACCESSION BG819793
 VERSION BG819793.1 GI:14167380
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 663)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10658 row: f column: 09
 High quality sequence stop: 649.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:4932488"
 /clone_lib="NCI CGAP_Brm67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 Kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP library."

BASE COUNT 133 a 199 c 212 g 119 t
 ORIGIN

Query Match	7.3%	Score 340;	DB 12;	Length 663;
Best Local Similarity	99.8%;	Pred. No. 1.1e-145;		
Matches 460;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

QY	2596	GGCGCAACGGTGGGCTGGCGGCTACGATCACTCAAGCGCTGGGTGATGGCCAGGAGCGTTTCA	2655
Db	78	GGCGCAACGGTGGGCTGGCGGCTACGATCACTCAAGCGCTGGGTGATGGCCAGGAGCGTTTCA	137
QY	2656	ACCCCAACTCGGAGGAGACCCCTCGTCCCGGAGCTTCAAGAACGACGTGTCTCCGGATCA	2715
Db	138	ACCCCAACTCGGAGGAGACCCCTCGTCCCGGAGCTTCAAGAACGACGTGTCTCCGGATCA	197
QY	2716	TCGATGGCGACACA-GCTTCCCAAGCCGGGCACTCCATCGCTGGGGGACCGTGGGGAGATC	2774
Db	198	TCGATGGCGACAGTACTTCCCAAGCCGGGCACTCCATCGCTGGGGGACCGTGGGGAGATC	257
QY	2775	ATCGACCCCTTTGTGTGAGAGTGGAGATCATCTTTGGGCTCCCTGTGTGACTGTGACAGGAGAGCAG	2834
Db	258	ATCGACCCCTTTGTGTGAGAGTGGAGATCATCTTTGGGCTCCCTGTGTGACTGTGACAGGAGAGCAG	317
QY	2835	ACCCGCGTGGTGGATGCATCAACGGGTTTCAACCCCACTGGGAGAGAACCCCTGGTTTTCATG	2894
Db	318	ACCCGCGTGGTGGATGCATCAACGGGTTTCAACCCCACTGGGAGAGAACCCCTGGTTTTCATG	377
QY	2895	GTCGACATGCGGAGATGCGCTGGTTCGCTTCCGTCTGTGGGACCAAGATCCCATCCG	2954
Db	378	GTCGACATGCGGAGATGCGCTGGTTCGCTTCCGTCTGTGGGACCAAGATCCCATCCG	437
QY	2955	CGTGACTTCAATTGGCGAGAGACGCTGGCTTTCAGACAGATGATGCCAGGCTTACAGACAC	3014
Db	438	CGTGACTTCAATTGGCGAGAGACGCTGGCTTTCAGACAGATGATGCCAGGCTTACAGACAC	497
QY	3015	GTTGATCTAGAAAGGATGGAAGAGCCCTTCATCTTTCGTGCA	3055
Db	498	GTTGATCTAGAAAGGATGGAAGAGCCCTTCATCTTTCGTGCA	538

RESULT	7
LOCUS	BE244972
DEFINITION	395 bp mRNA linear EST 03-OCT-2001
ACCESSION	BE244972
VERSION	TCBAP16191
KEYWORDS	Pediatric pre-B cell acute lymphoblastic leukemia
SOURCE	Baylor-HSCC project=TCBA Homo sapiens CDNA clone TCBAP16191, mRNA sequence.
ORGANISM	BE244972
TITLE	BE244972.1 GI:3096637
JOURNAL	EST.
COMMENT	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 395) Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. Pediatric Leukemia CDNA Sequencing Project Unpublished (2000) Contact: Dr. Judith F. Margolin Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536 Fax: 832-825-4038 Email: clones@txccc.org Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seq primer: M13 primer.

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/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/notes=Vector: lambda psb; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAAGACTCAGAGCGCGCAGGAGG(17)VN
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGGCTCGGATCGCGCGCGCGCAATATATATAT(C) 3'1.
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamI and SalI sites of
lambda psb vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997")

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Query Match	6.3%;	Score 293;	DB 10;	Length 395;
Best Local Similarity	100.0%;	Pred. No. 5e-124;		
Matches 293;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2257	GGGCAACCCGGAGAAAGAAACATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTAACT	2316
Db	103	GGGCGACCCGGAGAAAGAACATGAAGCTGTCCCGGGCCCTCTCTGACCTGGTAACT	162
QY	2317	ACAACCAATCCGTGGCCACCGACATATGATGAGGCGGGGCTTCAGTGGCAGGTGT	2376
Db	163	ACAACCAATCCGTGGCCACCGACATATGAGTGAAGGGGGGCTTCACGCTGGCAGGTGT	222
QY	2377	CGACCTTCAGCGAGACCAAGGCCCAAGATTCTGCAGCAGAAAGCCGGCCAGTACTAC	2436
Db	223	CGTCTCTTCAGCGAGACCAAGGCCCAAGATTCTGCAGCAGAAAGCCGGCCAGTACTAC	282
QY	2437	GCTTCAACGAGCAGAGCTCTCCGGCATCTACCCCTCTCTTCAACGTGTGACTCCAGCA	2496
Db	283	GCTTCAACGAGCAGAGCTCTCCGGCATCTACCCCTCTCTTCAACGTGTGACTCCAGCA	342
QY	2497	ACATCAACCCGCGACCCCTCTGGAAGCGCGGGCTGCAAAATGGTTGGCCCTAAC	2549
Db	343	ACTATCAACCCGCGACCCCTCTTGAAGCGCGGGCTGCAAAATGGTTGGCCCTAAC	395

RESULT 8	BE255354	801 bp	mRNA	linear	EST 13-JUL-2000
LOCUS	BE255354				
DEFINITION	BE255354 601115359P1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:335589 5', mRNA sequence.				
ACCESSION	BE255354				
VERSION	BE255354.1	GI:9125792			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 801)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				

FEATURES

Source

Location/Qualifiers

1. .801

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3355889"

/clone_1ib="NIH MGC 16"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT

206 a 231 c 213 g 151 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.6e-68; Length 801;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GAGCCCTGCTGTGATCATCTTCAACCTGAGACACCATGTGACACGAGATGACGCA 1411

Db 55 GAGCCCTGCTGTGATCATCTTCAACCTGAGACACCATGTGACACGAGATGACGCA 114

QY 1412 GCGGCTAGCCACTACTTCACTACCTGCTGCCACACACCTACTGCTGAGTACAGCT 1471

Db 115 GCGGCTAGCCACTACTTCACTACCTGCTGCCACACACCTACTGCTGAGTACAGCT 174

QY 1472 CATGTCCAGTCACGGGTGACATGTATGCTGGGCTCTGACGAGCTGGCTGC 1523

Db 175 CATGTCCAGTCACGGGTGACATGTATGCTGGGCTCTGACGAGCTGGCTGC 226

RESULT 9

LOCUS B1756147 684 bp mRNA linear EST 25-SEP-2001

DEFINITION 603030048F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200378 5',

mRNA sequence.

ACCESSION B1756147

VERSION B1756147.1 GI:15747725

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.

1 (bases 1 to 684)

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL1501 row: p column: 11

High quality sequence stop: 535.

Location/Qualifiers

1. .684

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5200378"

/clone_1ib="NIH MGC_114"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dt

FEATURES

Source

primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library"

BASE COUNT

136 a 240 c 225 g 82 t 1 others

ORIGIN

Query Match

Best Local Similarity 99.5%; Pred. No. 1.1e-60; Length 684;

Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3676 GTCTCTGGGCGCTTGAGAGGAGGCTCAGCGGCTCATATCTCTGACATCCAGCA 3735

Db 79 GTCTCTGGGCGCTTGAGAGGAGGCTCAGCGGCTCATATCTCTGACATCCAGCA 138

QY 3736 GCCCAGACAGCCCGGAGCATCCCGGAAAGGTCCCGCTGAGCTGAGAGGCTGACAGC 3795

Db 139 GCCCAGACAGCCCGGAGCATCCCGGAAAGGTCCCGCTGAGCTGAGAGGCTGACAGC 198

QY 3796 AACCGGGGCGCTTGAGAGGAGATGAGTGGCTTTGCTCAAAAGCTGAGAGATCA 3855

Db 199 AACCGGGGCGCTTGAGAGGAGATGAGTGGCTTTGCTCAAAAGCTGAGAGATCA 258

QY 3856 GGAGTAAATCCCGCATGTTCTCCGCGC 3882

Db 259 GGAGTAAATCCCGCATGTTCTCCGCGC 285

RESULT 10

LOCUS A0741196 839 bp DNA linear GSS 16-JUL-1999

DEFINITION HS_2273_A2_G04_MR CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=2273 Col=8 Row=M, DNA sequence.

ACCESSION A0741196

VERSION A0741196.1 GI:5518718

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 839)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 2273 row: M column: 8

Seq primer: M13 Reverse

Class: BAC ends

High quality sequence stop: 839.

Location/Qualifiers

1. .839

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="plate=2273 Col=8 Row=M"

/clone_1ib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelorAC11; BAC Clones in E-Coli DH10B"

BASE COUNT

134 a 263 c 178 g 109 t 155 others

							/dev stage="nault"		
							/lab host="SOLR"		
							/note="Site_1: XhoI; Site_2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',		
							GAGAGAAGAAATCCCAAGACCTCTTTTTTTTTTTNN 3']	cDNA was prepared by using trianlose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'	
							GAGAGAAGATTCTCGAATTATTAAATTATCCCCCCCCCCC 3']"		
BASE COUNT		184 a	175 c	202 g	134 t	1 others			
ORIGIN									
	Query Match	0.8%	Score 38;	DB 10;	Length 696;				
	Best Local Similarity	100.0%;	Pred. No.	3.7e-06;					
	Matches 38;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
OY	1641 GCCTCATCAGAAATGATGCCAGATGCCTGGCAT	1678							
Dd	145 GCCTCATCAAGAAATGAATGCCAGATGTCTGTCAT	182							
RESULT 13									
LOCUS	BG299246	711 bp	mRNA	linear	EST 21-FEB-2001				
DEFINITION	602395735F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4507377 5,								
LOCUS	mRNA Sequence.								
ACCESSION	BG299246								
VERSION	BG299246.1 GI:13064707								
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baae) 1 to 711)								
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)								
AUTHORS	Contact: Robert Stransberg, Ph.D.								
TITLE	Email: csqab@remail.nih.gov								
JOURNAL	Tissue Procurement: The Cepko Laboratory CSDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN). DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:								
COMMENT	http://image.lln.gov Plate: LLM10384 row: e column: 10 High quality sequence start: 4 High quality sequence stop: 660. Location/Qualifiers								
FEATURES	source	1..711							
	/organism="Mus musculus"								
	/db_xref="taxon:10090"								
	/clone_image="IMAGE:4507377"								
	/clone_id="NIH_MGC_94"								
	/library_type="retinal"								
	/lab_host="MDH1OB (phage-resistant)"								
	/note="Organ: eye; Vector: pCMV-SPORE6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: This is a NIH_MGC Library."								
BASE COUNT	179 a	204 c	211 g	116 t	1 others				
ORIGIN									
Query Match	0.8%; Score 38;	DB 12;	Length 711;						
Best Local Similarity	100.0%;	Pred. No.	3.7e-06;						

Matches	38;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2466	TACCCCTCCTCTACCGTGTGAGCTTCACCACTACAA	2503						
Db	310	TACCCCTCCTCTACCGTGTGAGCTTCACCACTACAA	347						
RESULT 14									
LOCUS	B0946757								
DEFINITION	AGENCOURT_8924326 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466785								
ACCESSION	B0946757								
VERSION	B0946757.1	GI:22362235							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
TITLE	NIH-MGC http://mgc.nci.nih.gov/.								
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)								
COMMENT	Unpublished (1999)								
	Contact: Robert Strausberg, Ph.D.								
	Email: cgabs@remail.nih.gov								
	Tissue Procurement: The Cepko Laboratory								
	cDNA Library Preparation: Life Technologies, Inc.								
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)								
	DNA Sequencing by: Agencourt Bioscience Corporation								
	Clone distribution: MGC clone distribution information can be								
	found through the I.M.A.G.E. Consortium/LMNL at:								
	http://image.lnl.gov								
	Plate: L1AM1391 row: k column: 10								
FEATURES	High quality sequence stop: 676.								
source	Location/Qualifiers								
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	/db_xref="taxon:10090"								
	/clone="IMAGE:6466785"								
	/clone_1id="NIH MGC_94"								
	/tissue_type="retina"								
	/lab_host="DH10B (phage-resistant)"								
	/note="Organ: eye; Vector: pCMV-SKOR6; Site 1: NCI;								
	Site_2: Salt; Cloned unidirectionally; oligo-dt primed.								
	Average insert size 3.3 kb. Library enriched for								
	full-length clones and constructed by Life Technologies.								
	Note: this is a NIH MGC Library."								
BASE COUNT	193 a	268 c	272 g	155 t					
ORIGIN									
	Query Match	0.88;	Score 38;	DB 14;	Length 889;				
	Best Local Similarity	100.0%;	Pred. No. 3..9e-06;						
	Matches 38;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
Qy	2535	AVGGTTGCCCTGAACTACCACTCAGAGGGCGGATGCT	2572						
Db	24	ATGGTGGCCCTGAATCACTCAGAGGGCGGATGCT	61						
RESULT 15									
LOCUS	B0960462								
DEFINITION	AGENCOURT_8930277 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6466491								
ACCESSION	B0960462								
VERSION	B0960462.1	GI:22375940							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
	(Bases 1 to 930)								
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.								

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13990 row: c column: 04
High quality sequence stop: 634.
Location/Qualifiers

FEATURES
source
1. 930

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6466491"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 222 a 267 c 292 g 148 t 1 others
ORIGIN

Query Match 0.8%; Score 38; DB 14; Length 930;
Best Local Similarity 100.0%; Pred.No. 3.9e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2466 TACCCCTCCTACCGTGTGAGACTCCAGCACTACCA 2503
Db 431 TACCCCTCCTACCGTGTGAGACTCCAGCACTACCA 468

Search completed: March 29, 2003, 08:02:21
Job time : 6873 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:51:40 ; Search time 38 Seconds
(without alignments)
1865.249 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379

Sequence: 1 MAPPTAGPLPGPALPEDEGPPESRWLFSLANILPYVERCKAMQEGMAYKLGSGSKG 60

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6379	100.0	1207	10	US-09-927-112-2
2	1738	27.2	325	10	US-09-927-112-10
3	1441	22.6	762	10	US-09-804-969-15
4	1441	22.6	762	10	US-09-908-664-2
5	1281	20.1	744	9	US-10-096-961-4
6	1279.5	20.1	736	10	US-09-800-971-2
7	1279.5	20.0	736	9	US-10-096-961-2
8	1262	19.8	744	9	US-10-096-961-5
9	1085.5	17.0	608	10	US-09-908-664-5
10	1002	15.7	567	10	US-09-835-996A-8
11	840.5	13.2	1809	10	US-09-822-635-2
12	723.5	11.3	1054	10	US-09-828-447-11
13	685.5	10.7	628	10	US-09-828-447-12
14	522.5	8.2	340	10	US-09-835-996A-19
15	515	8.1	191	10	US-09-908-664-22
16	494	7.7	170	10	US-09-908-664-13
17	458	7.2	158	10	US-09-927-112-11
18	452.5	7.1	847	10	US-09-765-298A-10
19	452	7.1	182	10	US-09-800-971-7

20	444	7.0	119	9	US-09-764-868-637	Sequence 637, App
21	444	7.0	119	9	US-09-955-999-84	Sequence 84, App
22	426.5	6.7	153	10	US-09-822-635-5	Sequence 5, App
23	426.5	6.7	153	10	US-09-800-971-6	Sequence 6, App
24	426.5	6.7	153	10	US-09-927-112-7	Sequence 7, App
25	426.5	6.7	153	10	US-09-908-664-10	Sequence 10, App
26	426.5	6.7	153	10	US-09-908-664-19	Sequence 19, App
27	375	5.9	201	10	US-09-867-550-1334	Sequence 1334, App
28	335	5.3	119	10	US-09-800-971-9	Sequence 9, App
29	323.5	5.1	128	10	US-09-908-664-23	Sequence 23, App
30	320.5	5.0	272	10	US-09-804-969-19	Sequence 19, App
31	319.5	5.0	119	10	US-09-908-664-15	Sequence 15, App
32	290	4.5	128	10	US-09-800-971-8	Sequence 8, App
33	290	4.5	128	10	US-09-927-112-8	Sequence 8, App
34	290	4.5	128	10	US-09-927-112-8	Sequence 8, App
35	290	4.5	128	10	US-09-908-664-11	Sequence 11, App
36	284.5	4.5	181	10	US-09-908-664-20	Sequence 20, App
37	284.5	4.5	202	10	US-09-927-112-14	Sequence 14, App
38	264	4.1	158	10	US-09-908-664-14	Sequence 14, App
39	264	4.1	158	10	US-09-764-870-377	Sequence 377, App
40	263.5	4.1	102	10	US-09-764-860-342	Sequence 342, App
41	260.5	4.1	102	10	US-09-822-635-7	Sequence 7, App
42	255.5	4.0	134	10	US-09-764-870-357	Sequence 357, App
43	249	3.9	92	10	US-09-927-112-15	Sequence 15, App
44	228	3.6	1134	9	US-09-927-112-16	Sequence 16, App
45	193.5	3.0	535	9	US-10-001-873-50	Sequence 50, App
					US-10-043-487-306	Sequence 306, App

ALIGNMENTS

RESULT 1
US-09-927-112-2
Sequence 2, Application US/09927112
Patent No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32544, a novel human phospholipase C and
FILE REFERENCE: 38155-20048.00
CURRENT FILING DATE: US/09/927, 112
PRIOR FILING DATE: 2001-08-10
PRIORITY APPLICATION NUMBER: US 60/246,808
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1207
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-112-2

Query Match 100.0%; Score 6379; DB 10; Length 1207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAPPTAGPLPGPALPEDEGPPESRWLFSLANILPYVERCKAMQEGMAYKLGSGSKG 60
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DB 61 LVAFYTLDEHRSCTIRKPRKNEKAKISTDSIOEVSSEGSQSVFPRYPGSDPNCFSI 120
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DB 121 YHSHRESLDIVSTSEVARTWTGRLYLACISDESLARORTRDQWLKQTFDEADKN 180
OY 181 GDGSLISGEYLQLLHRLANLNPQRKYKQMFREADTDHGTGTFEFCAFYKMSRRDL 240
DB 181 GDGSLISGEYLQLLHRLANLNPQRKYKQMFREADTDHGTGTFEFCAFYKMSRRDL 240

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QY 241 YLMLTYSNKHDLDAASLOFLQVEOKMAGVTLSESCODIIEOEPCEPKSKGLGIDG 300
DB 241 YLMLTYSNKHDLDAASLOFLQVEOKMAGVTLSESCODIIEOEPCEPKSKGLGIDG 300
QY 301 FTNTRSPAGDIFNEHHHHVHODMTQPLSHYFTSSHNFTLVGDQLMSQSRVMYAVLQ 360
DB 301 FTNTRSPAGDIFNEHHHHVHODMTQPLSHYFTSSHNFTLVGDQLMSQSRVMYAVLQ 360
QY 361 AGCCVCVDCMDGDPGEPIYHGGTTLTKSLKLFKDVITETIKKAFINKEYVILISTENHCS 420
DB 361 AGCCVCVDCMDGDPGEPIYHGGTTLTKSLKLFKDVITETIKKAFINKEYVILISTENHCS 420
QY 421 VIOOKMAOYLTDLDGDKLDSVSSSEDATLTPSPQMLKGLIYVKGKILPANISEDAGEG 480
DB 421 VIOOKMAOYLTDLDGDKLDSVSSSEDATLTPSPQMLKGLIYVKGKILPANISEDAGEG 480
QY 481 EVSDESDADEIDDDCKLNDASTNKRKVENYAKRKLDLSIKESKIRDCEDPNFNSVSTL 540
DB 481 EVSDESDADEIDDDCKLNDASTNKRKVENYAKRKLDLSIKESKIRDCEDPNFNSVSTL 540
QY 541 SPGKILGRKKAEDVESGSDAGASRRNGLYVSPSRKKKSKLTKAASVEEGDEGOD 600
DB 541 SPGKILGRKKAEDVESGSDAGASRRNGLYVSPSRKKKSKLTKAASVEEGDEGOD 600
QY 601 SPGQSRGATROKTKMLSRALSDLVKTKSVATHDIEEAASSMQVSSFSETKAHQILQ 660
DB 601 SPGQSRGATROKTKMLSRALSDLVKTKSVATHDIEEAASSMQVSSFSETKAHQILQ 660
QY 661 OKRAOYLRFNOOQLSRIYSSVYVSDSNPNPOPFMAAGCOMALNTQSGRMLOINRAKE 720
DB 661 OKRAOYLRFNOOQLSRIYSSVYVSDSNPNPOPFMAAGCOMALNTQSGRMLOINRAKE 720
QY 721 SANGCGGYVLKPCMCQGVFNPNSEDPPLPGOLKOLYLRIISGOOLPKPRDMSLGDRCGI 780
DB 721 SANGCGGYVLKPCMCQGVFNPNSEDPPLPGOLKOLYLRIISGOOLPKPRDMSLGDRCGI 780
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DB 781 IDPFVVEIIGLPCDCSRQOTRYVNDNGNPNFTWETLVFMVMPETALVRLVMDHDPITG 840
QY 841 RDEFIGORTLAFSSMMPGYHYVLEGEAEASIFVHVASDISGKVOALGKGLFIRGPKP 900
DB 841 RDEFIGORTLAFSSMMPGYHYVLEGEAEASIFVHVASDISGKVOALGKGLFIRGPKP 900
QY 901 GSLDSHAAGRPAPRSVSQRIILRTASAPTKSQKPRGRGFPPELVLTGTRDTGSKGVAADV 960
DB 901 GSLDSHAAGRPAPRSVSQRIILRTASAPTKSQKPRGRGFPPELVLTGTRDTGSKGVAADV 960
QY 961 PPGPAPAPAPAOEGPGSGSPGKAPAAVAEKSPPVRRPRLVDSGPGAGMAATCMKCV 1020
DB 961 PPGPAPAPAPAOEGPGSGSPGKAPAAVAEKSPPVRRPRLVDSGPGAGMAATCMKCV 1020
QY 1021 GSCAGVNTGGLQREPRPSPGPASRQAALRQOPRARADSLGAPCCGLDHPHALPGSRREAPK 1080
DB 1021 GSCAGVNTGGLQREPRPSPGPASRQAALRQOPRARADSLGAPCCGLDHPHALPGSRREAPK 1080
QY 1081 GPGARQPGSGSGSSSSSPDSCPTGERSPRMEGACRPGALOGMSALFAOKLEEI 1140
DB 1081 GPGARQPGSGSGSSSSSPDSCPTGERSPRMEGACRPGALOGMSALFAOKLEEI 1140
QY 1141 RSKSPMFSAKRPDLPCVYLPHAPGAGGSPAAASAMTVSRVYLVALYPMHCLRTGLL 1200
DB 1141 RSKSPMFSAKRPDLPCVYLPHAPGAGGSPAAASAMTVSRVYLVALYPMHCLRTGLL 1200
QY 1201 PMLACGP 1207
DB 1201 PMLACGP 1207

```

```

; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Siles-Santiago, Inmaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 38155-20048..00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-10

```

```

Query Match 27.2%; Score 1738; DB 10; Length 325;
Best Local Similarity 99.7%; Pred No. 1.2e-97;
Matches 324; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 883 KYKQALGLKGLFLNGPKRGLSDSHAAGRPAPRSVSQRIILRTASAPTKSQKPRGRGFP 942
DB 1 QVKAOLGLKGLFLNGPKRGLSDSHAAGRPAPRSVSQRIILRTASAPTKSQKPRGRGFP 942
QY 943 LVLTGTRDTGSKGVAADVPPGAPAPAPAOEGPGSGSPGKAPAAVAEKSPPVRRP 1002
DB 61 LVLTGTRDTGSKGVAADVPPGAPAPAPAOEGPGSGSPGKAPAAVAEKSPPVRRP 1002
QY 1003 LDGPGPAGMAATCMKCVYVSGAGVNTGGLQREPRPSPGPASRQAALRQOPRARADSLGAP 1062
DB 121 LDGPGPAGMAATCMKCVYVSGAGVNTGGLQREPRPSPGPASRQAALRQOPRARADSLGAP 1062
QY 1063 CCGLDHPHALPGSRREAPKRGKAGPAMRQPGSGSSSPDSCPTGERSPRMEGACRPG 1122
DB 181 CCGLDHPHALPGSRREAPKRGKAGPAMRQPGSGSSSPDSCPTGERSPRMEGACRPG 1122
QY 1123 GALOGMSALFAOKLEIRKSPMFSAGKRPDLPCVYLPHAPGAGGSPAAASAMTVSR 1182
DB 241 GALOGMSALFAOKLEIRKSPMFSAGKRPDLPCVYLPHAPGAGGSPAAASAMTVSR 1182
QY 1183 VLVVALYPMHCLRTGLL PMLACGP 1207
DB 301 VLVVALYPMHCLRTGLL PMLACGP 1207

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```

RESULT 3
US-09-804-969-15
; Sequence 15, Application US/09804969
; Patent No. US20020081595A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Donoho, Gregory
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abuh, Alejandro
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides
; FILE REFERENCE: LEX-0148-USA
; CURRENT APPLICATION NUMBER: US/09/804,969
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,885
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 60/189,693
; PRIOR FILING DATE: 2000-03-15

```

NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 762
TYPE: PRT
ORGANISM: homo sapiens
US-09-804-969-15

Query Match 22.6%; Score 1441; DB 10; Length 762;
Best Local Similarity 36.3%; Pred. No. 3.2e-79;
Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;

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QY 45 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 102
DB 18 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 76
QY 103 VFORPDGSPDNCCFSYTHGSHRESLDVSTSEVARTVYTGRIYLMAGISDDSLARR 162
DB 77 LRLSLAEELPLRQGTTFYFHG--RNSNLDLMANSVEEADIMRGQLLDVLTSMD----H 131
QY 163 ORTRDOWLKOTFEADKNGDLSIGEVYLLHKLNLVNLPRQRYKMPREADTDDHOGTL 222
DB 132 QERLDOWLMDVFORDKNDGKMSQEVORLLHLMNVEMDEYAFSLQADT--SOGSTL 190
QY 223 GFEFCAFYKMMSTRDLYLLMLTYSNKHDLDAASLORFLQVQKAGVTLSCODITE 282
DB 191 EGEEFVQFKALTKRAVEOLFESFSADGOKLTLLFELDFLOEOKERDCTSELALELID 250
QY 283 QREPERENKSKGLGIDFTNTYTRPAGDINPREHNVHODMOTPLSHFTTSSHNTYLV 342
DB 251 RYPSDGSGLRHLVLSMDGFLSTLCKDIDTFNPACLPYIDMOTPLNHTFICSSHNTYLV 310
QY 343 GDLMSQSRVDMYAVWYLAQRCVVDWCDGPDGPRIYHNGYTLTKLIFKDVLETINKY 402
DB 311 GDLQCGSSVEGYIRALKRGCCVEVDWDPGSGEPVYHGHITLSRILFKVAVATVAQY 370
QY 403 AFKNEYRPIVLSIENHCYIQQKMAQYLTDLGKLDLSVSSSDATTLSPOMLKAKI 462
DB 371 AFQTSQYPIVLSLETNHCSEWQOQTMAHILTEIGQLSTLTIDGVLPTOLPSPBELARRKI 430
QY 463 LVKGGKLPANISEDAEBSGVEDSDADEIDDDCKILNDGASTNRKRVENTAKRKLDLTK 522
DB 431 LVKGGKLP--TLREDL--EYEEBAPELELE-----SELA 461
QY 523 ESKIRDCEDPNFNSVSTLSPSGKLGKSKAEEDVESGEDAGASRRNGRLVVGFSFRKKK 582
DB 462 ESOFTFEPERPO-----EONLNKND-----KKKK 484
QY 583 GSKLKAASVEBDEGODSPGOSRGATROKTKMKLSRALSDLYVYTKSYA----THDIE 638
DB 485 SKRPI-----LCPALSSLVLYLTKSVSFRSFTH--S 511
QY 639 MEAASWQVSFSETKAHQILOQPAOYLRFNOOQLSRYPSSRYDSSNYNPQPFNNAG 698
DB 512 KEHYHFEIISSEBTAKRIKEAGNEFYOHNTWQLSRYRPSGLRTDSSNYNPQELMANN 571
QY 699 COMVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLRGOLKKOL 756
DB 572 COMVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLRGOLKKOL 629
QY 757 VLRITISQOOLPKRDSMLDGRGELIDPEFVETIIGLVDCSROTRVVDONGFNPTMEET 816
DB 630 LIOVITISQOOLPKRDKT---KEGSTVLDVLVAVOQLFGVALDTRARQETNVENNGNPNPTWGT 686
QY 817 LVFVAVHPEIALVFLVWDDPIGR--DFIGORTLAFSSMMKGYRHVYL--EG--MEAS 870
DB 687 LCFVFLVPELALMRFVYVMDYDKSRNDEIGQYTLPTCMQOQYRHHILLSKDISLAPAS 746
QY 871 IFVAVANSIDISGKAYKALGK 892
DB 747 IFVYICIOE-----GLEG 759
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RESULT 4
US-09-908-664-2
Sequence 2, Application US/0908664
Patent No. US20020115178A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Tsai, Fong Yin
TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
FILE REFERENCE: 38155-20022.00
CURRENT APPLICATION NUMBER: US/09/908,664
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/218,675
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 762
TYPE: PRT
ORGANISM: Homo sapiens
US-09-908-664-2

Query Match 22.6%; Score 1441; DB 10; Length 762;
Best Local Similarity 36.3%; Pred. No. 3.2e-79;
Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;

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QY 45 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 102
DB 18 MOEGMOMVRLKSGSKGLVFFYLLDHRSCIRW--RPSRKNKAKISIDISIOEVSEGR0SE 76
QY 103 VFORPDGSPDNCCFSYTHGSHRESLDVSTSEVARTVYTGRIYLMAGISDDSLARR 162
DB 77 LRLSLAEELPLRQGTTFYFHG--RNSNLDLMANSVEEADIMRGQLLDVLTSMD----H 131
QY 163 ORTRDOWLKOTFEADKNGDLSIGEVYLLHKLNLVNLPRQRYKMPREADTDDHOGTL 222
DB 251 RYPSDGSGLRHLVLSMDGFLSTLCKDIDTFNPACLPYIDMOTPLNHTFICSSHNTYLV 310
QY 343 GDLMSQSRVDMYAVWYLAQRCVVDWCDGPDGPRIYHNGYTLTKLIFKDVLETINKY 402
DB 311 GDLQCGSSVEGYIRALKRGCCVEVDWDPGSGEPVYHGHITLSRILFKVAVATVAQY 370
QY 403 AFKNEYRPIVLSIENHCYIQQKMAQYLTDLGKLDLSVSSSDATTLSPOMLKAKI 462
DB 371 AFQTSQYPIVLSLETNHCSEWQOQTMAHILTEIGQLSTLTIDGVLPTOLPSPBELARRKI 430
QY 463 LVKGGKLPANISEDAEBSGVEDSDADEIDDDCKILNDGASTNRKRVENTAKRKLDLTK 522
DB 431 LVKGGKLP--TLREDL--EYEEBAPELELE-----SELA 461
QY 523 ESKIRDCEDPNFNSVSTLSPSGKLGKSKAEEDVESGEDAGASRRNGRLVVGFSFRKKK 582
DB 462 ESOFTFEPERPO-----EONLNKND-----KKKK 484
QY 583 GSKLKAASVEBDEGODSPGOSRGATROKTKMKLSRALSDLYVYTKSYA----THDIE 638
DB 485 SKRPI-----LCPALSSLVLYLTKSVSFRSFTH--S 511
QY 639 MEAASWQVSFSETKAHQILOQPAOYLRFNOOQLSRYPSSRYDSSNYNPQPFNNAG 698
DB 512 KEHYHFEIISSEBTAKRIKEAGNEFYOHNTWQLSRYRPSGLRTDSSNYNPQELMANN 571
QY 699 COMVALNTOSEGRMLQLNRAKFSANGCGYVLKPGCM--CQGVFNPNSEDPLRGOLKKOL 756
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Db	572	COMVAMNOQTAGLEMDICDGHFRONGGGGYLKPFDRLDIQSSPHR--EXPISPFKQTL 629
Oy	757	VLRISGQGLKRPBMSLGDGELLIDPFVEKEIIGLEVDCSREOTRYVDNDGNGNPMWEET 816
Db	630	LIQVTSQGLKRPKVDKT--KEGSTVDPYLPKQVLEFVRLDTRARETNNVENNGNGNPMWQOT 686
Oy	817	LVFNVMHEIALVFLVMDHDHPICR-DFIGORTLAFSSAMPGRHYVL--EG--KEEAS 870
Db	687	LCFRLVDELMLRFFVWMDYDMKSRNDPIGYTLPLWCMQGGVRRHILHLSKDISLRPAS 746
Oy	871	IFVHVAVSDISGKVKQALGKIG 892
Db	747	IFVYICIE-----GLEG 759

RESULT 5
 US-10-096-961-4
 : Sequence 4, Application US/10096961
 : Patient No. US2002015572A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: GUEGLER, Karl et al.
 : TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
 : TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 : TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 : FILE REFERENCE: C1000849DIV
 : CURRENT APPLICATION NUMBER: US/10/096,961
 : CURRENT FILING DATE: 2002-03-14
 : PRIOR APPLICATION NUMBER: 60/232,632
 : PRIOR FILING DATE: 2000-09-14
 : PRIOR APPLICATION NUMBER: 09/738,884
 : PRIOR FILING DATE: 2000-12-18
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 4
 : LENGTH: 744
 :
 : TYPE: PRT
 : ORGANISM: Cricetus griseus
 : US-10-096-961-4

	Query Match	20.1%	Score 1281;	DB 9;	Length 744;
	Best Local Similarity	35.7%;	Pred No. 1.4e-69;		
	Matches 306;	Conservative 128;	Mismatches 276;	Indels 144;	Gaps 16.
QY	44 AMOEGMOMVATLNGSGKGLVFYYLDENHRSCLIMWRPSRK---- <td>99</td> <td></td> <td></td> <td></td>	99			
Dd	10 :	10			
QY	100 GSEFVORYPDGSFDDNCSSSIYHSHRESDLVYSSSEFAKWTVGTGLRTLMAGISDESL	159			
Dd	69 RREGLEEKRA-RIPEDRCSTIYFKQQRNTLTDLAASSADAOHWVGOLRI---IHHSGM	124			
QY	160 ARROTRDQMVLKOTPEADKNKGDSLSTGEVYLQLHLKLVNLP--PROVKOMFEAD---TD	216			
Dd	125 DOROQLQ-HWISCLRKAADKNDKNMFNFELKDPLKEINIQVDYSGARIRFECHSQTD	183			
QY	217 DHOGFLGEEFCACAFKMSTSRDYLILMLITSNHHDDLDAASLORFLOYEQCMAGVTLES	276			
Dd	184 -----SLEBEIEFTPKMLQORAEIDRVRAEAAGSAETLSVEKTLTFVLFIHQOEENAGPAL	239			
QY	277 CODITEOFEPCEPNKSKGLIGDTFNTRYTRSPAGIFENPHEHNHYQMDTOPRSHYFTSS	336			
Dd	240 ALSTIEREPESETAKAQOMTKDDFLMYLLLSADGSAFSIAHRRYVQDMDOPLSHLYVSS	299			
QY	337 HNTYVYGSQLMSOSNVDMAYAVLQAGCCVCVEDCDHGDEGPYAHNGYTLLTSKLIFKOYT	396			
Dd	300 HNTYILEPOLLGPSSTEVATRALCKGCSCLELDCDGDGNQEBEITYIHGYTFSTKSIFYVYL	359			
QY	397 ETINKAPAIKKNEYPIVISIENHCASYILOOKMAQYFTLDIGKLDLSSSVSSEDATPTLSPQ	456			
Dd	360 RAIRDYAFKASPYPVILISTENHWCSTLEGOQVVARHKLAILGPM-LDQGLDVGYMSLSPQE	418			
QY	457 MLKKILLVKGKK-----LPANISEABEVEVSDSDADEIDDDCKLLINGDASTNNRRVENT	512			

[illegible]

```

RESULT 6
US-09-800-971-2
; Sequence 2, Application us/09800971
; Patent No. US20020098577A1
; GENERAL INFORMATION:
; APPLICANT: Rachel A. Meyers
; TITLE OF INVENTION: 16833, A NOVEL HUMAN PHOSPHOLIPASE C
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-023001
; CURRENT APPLICATION NUMBER: us/09/800, 971
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,453
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/188,032
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapiens
; IS-09-800-971-2

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[illegible]

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Db 185 LEG-AEIEFLRLRLKRPLEIEIFHOYSGEDRVLSAPELLEFE--DGEEGATLARAQOL 242
QY 281 IEQEPCEPNKSKGLIGDFTNTRSPAGDIFNPEHHVHODMTOPLSHTFTSSHTY 340
Db 243 IOTVELNETAKOHEIMTLDGFMWYLLSPEGALDNTHTCVQDMQOPLAHYFISSSHNTY 302
QY 341 LVGDOLMSGRVDMYAWYLQAGRCVEYDCWDGPDGEPIVHGHVTLTSKILFKDYIETIN 400
Db 303 LQDSQIGGSSSTEAYVRAFAQCRVELDCWEGPGEPIYHGHVTLTSKILFKDYIETIN 362
QY 401 KYAFIKNEYPVLLSIENHCSYVIOQRMAQYLLDGLKDLSSVSSEDAATLPSQMLKG 460
Db 363 DIAFTLSPYVLLSIENHCSYVIOQRMAQYLLDGLKDLSSVSSEDAATLPSQMLKG 422
QY 461 KILVGGKRLPANISDA-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 520
Db 423 RVLVGGKRLPANISDA-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 484
QY 521 IKRSKIRDCEDPNFVSSTLSPSGKLGKRSKAEDEYSEGEDAGASRRNGRLVYGSFRRK 580
Db 455 -----EVEEVE-----AAQORRLAK----- 469
QY 581 KKGSKLKAASVEEGDEGODSPGCGSRGATROKTKMLSRALSDLYKTKSVATHDIE-- 638
Db 470 -----QISPELSALAVYCHARTRLRTLHPA 493
QY 639 MEAASMOYSSPSETKAHOILOQKPAQYLRFNQOOLSRIPSSYRDSNTNYPQPMNAG 698
Db 494 PNPAPCOVSSLSERAKKILIRAGNSFVRHNAKQILTRYPLGLRNNANSANYSPQEMNNG 553
QY 699 COMVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGVTPNPSE--DP-LPGOLKOL 756
Db 554 COLVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGVTPNPSE--DP-LPGOLKOL 609
QY 757 VLAIISSGQLP-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 811
Db 610 STVDPLVRIEIHGVPAQCAKQETDYVLLNNGFND 661
QY 812 TWBETLVFWHMEPIALVRLVMDHPIG--RDFIGORTLAFSSMMPGYRHVYL-----EG 865
Db 662 RMGOTLOFOLRAPELALVRYVEDYDATSNDVGGFTLPLSLKQGYRIHILSLDGAS 721
QY 866 MEASIFVHAV 877
Db 722 LSPATLFIQIRI 733

RESULT 7
US-10-096-961-2
; Sequence 2, Application US/10096961
; Patent No. US2002015572A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NOCTEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CL000849DIV
; CURRENT APPLICATION NUMBER: US/10/096,961
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/232,632
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/738,884
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-961-2

Query Match 20.0%; Score 1278.5; DB 9; Length 736;
Best Local Similarity 34.6%; Pred. No. 2e-69;

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Matches 297; Conservative 129; Mismatches 273; Indels 159; Gaps 18;
QY 44 AMQGMQVRLRGSSKGLVRYVLDHRSCLR---PPSRKNEKAKISIDISQEVSEGRQ 100
Db 11 AMLGSRKLRKTRSTWKEKRLYLOEDGLSV--WQORIPAPASQHIFFVGHIEAVRGHQ 69
QY 101 SEVFORPDGSPDNCFESIYHSHRESLDSVTSSEVARTWTGLRYLMAGISDEDSLA 160
Db 70 SEGRLRF--GGAFAFARCLTIAFKGRKRLDLAAPTAEAOVRWVGLTKLRARL---DAMS 125
QY 161 RQRTROMLKQTDDEADKNGDGLSISGEVQLLKLNVMLPRQVAKQREADTDHOG 220
Db 126 QRERL--DWIMHSYLHRAISNDQSKSFKEIKSLIRVNVDMNDYAYALLRECHDSNDR 184
QY 221 TLGFEFCAFYKMMSTRDLYLMLTYSNHRDHLDAISLQRELOVEQKMAVTLESQDI 280
Db 185 LEG-AEIEFLRLRLKRPLEIEIFHOYSGEDRVLSAPELLEFE--DGEEGATLARAQOL 242
QY 281 IEQEPCEPNKSKGLIGDFTNTRSPAGDIFNPEHHVHODMTOPLSHTFTSSHTY 340
Db 243 IOTVELNETAKOHEIMTLDGFMWYLLSPEGALDNTHTCVQDMQOPLAHYFISSSHNTY 302
QY 341 LVGDOLMSGRVDMYAWYLQAGRCVEYDCWDGPDGEPIVHGHVTLTSKILFKDYIETIN 400
Db 303 LQDSQIGGSSSTEAYVRAFAQCRVELDCWEGPGEPIYHGHVTLTSKILFKDYIETIN 362
QY 401 KYAFIKNEYPVLLSIENHCSYVIOQRMAQYLLDGLKDLSSVSSEDAATLPSQMLKG 460
Db 363 DIAFTLSPYVLLSIENHCSYVIOQRMAQYLLDGLKDLSSVSSEDAATLPSQMLKG 422
QY 461 KILVGGKRLPANISDA-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 520
Db 423 RVLVGGKRLPANISDA-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 484
QY 521 IKRSKIRDCEDPNFVSSTLSPSGKLGKRSKAEDEYSEGEDAGASRRNGRLVYGSFRRK 580
Db 455 -----EVEEVE-----AAQORRLAK----- 469
QY 581 KKGSKLKAASVEEGDEGODSPGCGSRGATROKTKMLSRALSDLYKTKSVATHDIE-- 638
Db 470 -----QISPELSALAVYCHARTRLRTLHPA 493
QY 639 MEAASMOYSSPSETKAHOILOQKPAQYLRFNQOOLSRIPSSYRDSNTNYPQPMNAG 698
Db 494 PNPAPCOVSSLSERAKKILIRAGNSFVRHNAKQILTRYPLGLRNNANSANYSPQEMNNG 553
QY 699 COMVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGVTPNPSE--DP-LPGOLKOL 756
Db 554 COLVALNTOSEGHMLQJLNRAKFSANGCGYVLPKPGCMCGVTPNPSE--DP-LPGOLKOL 609
QY 757 VLAIISSGQLP-----KPRDSMLGDEIIPVEVEIIGLPGDCRQETRYVDGFPN 811
Db 610 STVDPLVRIEIHGVPAQCAKQETDYVLLNNGFND 661
QY 812 TWBETLVFWHMEPIALVRLVMDHPIG--RDFIGORTLAFSSMMPGYRHVYL-----EG 865
Db 662 RMGOTLOFOLRAPELALVRYVEDYDATSNDVGGFTLPLSLKQGYRIHILSLDGAS 721
QY 866 MEASIFVHAV 877
Db 722 LSPATLFIQIRI 733

RESULT 8
US-10-096-961-5
; Sequence 5, Application US/10096961
; Patent No. US2002015572A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NOCTEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CL000849DIV

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CURRENT APPLICATION NUMBER: US/10/096,961
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: 60/232,632
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 09/738,884
 PRIOR FILING DATE: 2000-12-18
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 744
 TYPE: PR
 ORGANISM: Mus musculus
 US-10-096-961-5

Query Match 19.8%; Score 1262; DB 9; Length 744;
 Best Local Similarity 35.9%; Pred. No. 2e-68;
 Matches 308; Conservative 188; Mismatches 274; Indels 148; Gaps 19;

44 ANOEGMOMVLRGSGKGLVFFYLLDEHRSCTMRPSRK---NEKAKISDSIOEVSFGR 99
 10 ALKGSQGLKVKSSWRREFYKLOEDCKTI-WQESRKVWSPESQLFSTIEDIQEVRMGH 68
 100 QSEVFORPDGSPDPCSFYHSHRESLDTSTSEVAFRTWYGLRIAGISDESL 159
 69 RTGGLKFA-RDIPEDRCSTYFKDQNTLDLAPSPADVQHWVGLRKI---IDRSGSM 124
 160 ARQRTDQMLKQTFDEADKNGDGLSIGEVLLHKLNVNLPQRVQKMFREAD---TD 216
 125 DQROKIQ-HVHISCLRKADKNKKNKMFKEVDLKLAVQVDDSAKRIFFEDHSQTD 183
 217 DHQGTGFEEFCAYKMKSTRDLVLLMLTYSNKHDLDAALQRFLOVEOK-MAGVTL 274
 184 ----SLEDEITETFMVLTQRAEDRAFAEAGSAGTSLSEKLVYFLQHQREEGAPAL 239
 275 ESCQDIIIEFEPCEPNKSKGLIGDFTVTYTRSPADIDFPENHNHODMOPLSHYFT 334
 240 --ALSTIEREPESETAKQROMTKOGLMYLISADGNAPSLAHKRYVODMOPLSHYVS 297
 335 SSNNTLVADQMLSSQSDVMTAVTQAGRCYEVDCWDGPDPEPIVHNGYTLTKILFKD 394
 298 SSNNTLVADQMLSSQSDVMTAVTQAGRCYEVDCWDGPDPEPIVHNGYTLTKILFKD 357
 395 VLETTIKYAFINKEPVILSIENHCSVLDQKMAQYLDIDDKLDSVSESDTTPS 454
 358 VLRATRDVAFKSPYVILSIENHCSVLDQKMAQYLDIDDKLDSVSESDTTPS 416
 455 PMLKGLILVGRK---LPANISDAEVEGVSDESDADEIDDDCKLNGASTNRKKE 510
 417 PMLKGLILVGRK---LPANISDAEVEGVSDESDADEIDDDCKLNGASTNRKKE 467
 511 NPAKRLDLISKIRIROPEDNPNFVSYTLSPGSKLGRKKAEEVSEGEDAGASRRNGR 570
 468 H-----RPKED----- 473
 571 LVVGSFRRKKKSKLKAASVEEGDQDPSGQSRGATROKTKMLSRALSDLVYTK 630
 474 -----KTKVPELSDVYTK 489
 631 SVATHDIMEAAS---WQVSFSETKAHQLIQKPAQYLFNFNOOLSRIPSSRYVDS 687
 490 SVHFGFSPTSGQAFYEMASFSERLRLQESGNSFVHNHNGHLSRIYPAQRDSS 549
 668 NYNPOFPNAGCOMVALYVSEGRMLQANRAKFAANGCGVYLPKGCN--CQGYFNPSE 745
 550 NISPEVEMNGGQVALVNFQTPGEMDVYLCGCFDNGCGVYLPKALRDPDTFNSRAL 609
 746 DPLQGLKQVLRLIISGOQLPKPRDSMLGDRGELIDPEFVEVEIIGLYVDSRQOTVVD 805
 610 TGGPMARKKLRLVMIISGOQLPKYK---NKNSIVDPKVLVEIHGQDQVASTAVIT 665
 806 DNGFPTVEETLVMTMPEQALVFLVWDHPGR-DEIGQRTIARSSWMPGRHYYLE 864
 666 NNGFPRMDTEFEVAVVAPDLALVRFVMEVDYSSKNDFTIGQSTIIPNNSLKQGRHHL 725

QY 865 GME-----EASIFVHAV 877
 DB 726 SKNGDLHPSATLEFKISI 743

RESULT 9
 US-09-908-664-5
 Sequence 5, Application US/09908664
 Patent No. US20020115178A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Meyers, Rachel
 APPLICANT: Rudolph-Owen, Laura
 APPLICANT: Tsai, Fong Yin
 TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
 TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
 FILE REFERENCE: 38155-20022.00
 CURRENT APPLICATION NUMBER: US/09/908,664
 PRIOR APPLICATION NUMBER: 2001-07-17
 PRIOR FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 608
 TYPE: PR
 ORGANISM: Homo sapiens
 US-09-908-664-5

Query Match 17.0%; Score 1085.5; DB 10; Length 608;
 Best Local Similarity 36.1%; Pred. No. 6.9e-58;
 Matches 257; Conservative 114; Mismatches 198; Indels 143; Gaps 15;

183 GSLSIGEVLLHKLNVNLPQRVQKMFREADTDHOGTGFEEFCAYKMKSTRDLV 242
 17 GKINLEKFORLLEKLDRCSTYHVKQIFKQNDRLKGRITIEFRAIYVILTHREITE 75
 243 LMLTYSNKHDLDAALQRFLOVEOKMAGYTLSECDIIIEFEPCEPNKSKGLIGDFT 302
 76 IFNTYSENKRLILASNAQFLTQDYAEMSKAIAFEIIOKYPRIEVRKAHOMSELEFT 135
 303 NYTRSPADIDFPENHNHODMOPLSHYFTSSNNTLVADQMLSSQSDVMTAVTQAG 362
 136 RYMDSRCLLFKNCRKRYVQDMTHPLNDYFISSNNTLVADQMLSSQSDVMTAVTQAG 195
 363 CRCEVDCWDGPDPEPIVHNGYTLTKILFKDYIETINKYATKNEYPVILSIENHCSV 422
 196 CRCEVDCWDGPDPEPIVHNGYTLTKILFKDYIETINKYATKNEYPVILSIENHCSV 255
 423 QOKMAQYLDIDDKLDSVSESDTTPSPOMLKGKLVGRKLPANISDAEVEG 482
 256 QOEVMDNLQATGESL-LSDMDLDPDTLPSPALKKFLVANKKI 301
 483 SDESDADEIDDDCKLNGASTNRKRYENTAKRLDLISKIRIROPEDNPNFVSYTLSP 542
 302 -----GLKTEHERKGD----- 314
 543 SGKLGKSKAEEDVEGEDAGASRRNGRLVYGSFRRKKKSKLKAASVEEGDQDPS 602
 315 -----KHDNDKEGV-----KRLPVYMLKPKKTKRL----- 343
 603 GQSGRGATROKTKMLSRALSDLVYTKSVATHDIMEAASNOVS-----SPSE 652
 344 -----KALALSDLVYTKA-----EFKSFQSRRLYQOFNENNSIGE 381
 653 TKAHQLIQKPAQYLFNFNOOLSRIPSSRYVDSNYNPOFPNAGCOMVALYVSEGRM 712
 382 TQARKLSKLRLVHFIPTKRLITRIYPAQRDSSNPNQEFEMNGGQVALVNFQTPGLP 441
 713 LQANRAKFAANGCGVYLPKGCN--CQGYFNP-NSDPLPGLKQVLRLIISGOQLPKP 769
 442 MDLQNGKFLDNGSGVILKPHFLRESKSYFNPSNIRKGM-----ITLTRLISGIQLPLT 497

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Oy      770  RDSMLSGRGEIIDFVEVEIEIIGLIVDSCRSBOTRVVDNGFNPTEETLTFVMPVHPDETALV  829
Db      498  HSS--SNKG---DSLVIEVFGVNDQKQOTRIKKNAPSPPRNEFFTLIHPELALH  552

Oy      830  RELVWDHNPt-GRDFtGORTLAFSSMMGCRHRYVL-----EGMEASIFVHV  875
Db      553  REVVEGQGLLIGNEFLGQYTLPLLCIMNKGVRRIPLFSRMGESLEPASFVYV  604

RESULT 10
US-09-835-996A-8
Sequence 8, Application US/09835996A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Montgomey, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyang
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Duntui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US/09/835, 996A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 567
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-8

Query Match      15.7%; Score 1002; DB 10; Length 567;
Best Local Similarity 36.1%; Pred. No.76-53;
Matches 227; Conservative 106; Mismatches 201; Indels 112; Gaps 13

Oy      45  MDSGMQVRLRGSGSKGLVRFYVLDHRSCLRW-RRSRRKNEKKISIDSIOEVSSEGRSE  102
Db      18  MDSMPMRKRYRSKSMKKLRFRLQNDQMTV-WARQARSGSAKFSISDVETIRKNDHSE  76

Oy      103  VFGCPYPGSGSDPNMCSEFSIYHSHRESIDLIVSTSEVARTVWTGLRYLMAGISDEDSLARR  162
Db      77  LIRSLABELPLDEGFTLVPHG-RRSNLDIMANVSVEAQIMRGILQLLVDLVTSMD-----H  131

Oy      163  QRTRDQWLKOTFDEADKNGSGSLSTGEVLDLLKRLNNPLPRQVKKQKMFRRADDHDDHGT  222
Db      132  QERLDQMLSMWFQGRGNDQCKMSFOVORLLIMNVEMOEYAFSLFOADT-RSOGTL  190

Oy      223  GFEFCAFYKMSSTRBLYLMLTVYNSHKHIDLAASIQRLQYEOKMGAGVTLSECODIE  282
Db      191  EGFEFVQFYKMLTKRAVYQELFEFSADGQKLTLEFLDFLOEQRKRDCTSELALELID  250

Oy      283  QEPCEPENKSGKLIGDQFTNTYTSRPGADIPNPEHHVYHODMOPRLSHYFTTSHNTYV  342
Db      283  QEPCEPENKSGKLIGDQFTNTYTSRPGADIPNPEHHVYHODMOPRLSHYFTTSHNTYV  342

```

[illegible]

US-09-822-635-2	RESULT 11	
/ Sequence 2, Application US/09822635		
/ Patent No. US20010039331A1		
GENERAL INFORMATION:		
APPLICANT: Hunter, John J.		
APPLICANT: Meyers, Rachel A.		
TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND		
TITLE OF INVENTION: USES THEREOF		
FILE REFERENCE: 10448-035001		
CURRENT APPLICATION NUMBER: US/09/822,635		
CURRENT FILING DATE: 2001-03-30		
PRIOR APPLICATION NUMBER: US 60/193,921		
PRIOR FILING DATE: 2000-03-31		
NUMBER OF SEQ ID NOS: 9		
SOFTWARE: FastSeq for Windows Version 4.0		
SEQ ID NO 2		
LENGTH: 1809		
TYPE: prt		
ORGANISM: Homo sapiens		
US-09-822-635-2		
Query Match	13.2%;	Score 840.5; DB 10; Length 1809;
Best Local Similarity	27.4%;	Pred No. 1.8e-42;
Matches 268; Conservative 139; Mismatches 315; Indels 257; Gaps		33
QY	2	APTAGPLPPALPPEDP-----GPDPESHWLFLSANILPYVERCMGAMOEQMVKLNG 56
DB	664	SPMLAGTSPRPVPSSPVLSSNKSPPSSAMSSSSNH-----GRING 705
QY	57	GSGLVRFYLLDEHRSICIRNP-----SRKREKAKISIDSIQEVSEGRSEVFORPY 108
DB	706	GMGQFOSFVMSDSNMSVFEVVELFKFSVRSKRDLQDPVYAVPCNRSG--SESAPLYT 763
QY	109	DGSPDPCFCFSIVGHSHRESLIDVSTSEVARTWVYGLRYIMAGISDEDSLARROPTQD 168
DB	764	NLTIDET-----SDIQPDLDLITRN-----VSDLGLE--IKSKQQLSDNQRQISD 807
QY	169	WLKQTFDEADKNGDCGSLIC---EVIQLHLKLNVLPRORVKOMPREADTDDHOGTIGF 224
DB	808	ALMAASIVTNGTGTEISTSLGIFGVGIQ--LNDLVYNC-----QG----- 845
QY	225	EEPCAFKMMSTRDYLMLMLTYSNKHODHDAASLQFLQEOGMAGVTLSECODITIEPF 284
DB	846	EHCITYDEILS-----IIQKF 860

QY 285 EPCPEKSKGLIGDFTNTYRSPAGDIF--NPEHHVHODMTOPLSHYFTTSSHTNYLVG 343
 DB 861 EPTSMCHQGLMSEFGARFLMDKENFANKNDESEQENIKELQPLSTYITFESSHNTYLTG 920
 QY 344 DOLMSORVMYAWYLQAGRCVYDCWDGPDGEPIYHNGYITLSTKLFKDYETITNKYA 403
 DB 921 HOLGESSVELYSOVLLQGRSVELDCWDGDPDIYHGHITLTKTPKEVEYEAIDRSA 980
 QY 404 FKNNEYVLIISNHCNCSVIOQKKAQYLTDILGDKL--DLSSVSSDATTLPSPOMKG 460
 DB 981 FINSDELIIISNHCNCSVIOQKKAQYLTDILGDKL--DLSSVSSDATTLPSPOMKG 1040
 QY 461 KILYKGGKLL-----PANTISEDAEVEGED- 486
 DB 1041 KVLKNNKLLAHOTPYDILKOKAHOLASMOYQAYNGNANPRANNNEEDEDDEYDIY 1100
 QY 487 ---SADEIDDD---C-KL---LNGDASTRKREVENTAKK-----LDS 519
 DB 1101 ESLSDNIILEDREPKNSCNDKLOFETNEETPKRIKADNSACKKGVYDMELCEEFYLDQ 1160
 QY 520 LIESK-----TRCEDPNNFSVSTLSPSG-KLGKRSKAEDVESEGDAGARRNG 569
 DB 1161 NKESRQIAPELSDIYCOAVKFGPLSTLNASGSSRGKERSKSI-----FGNPG 1213
 QY 570 RLVVG---SPSRKKKSKLKAASVEEDGEGDPSGSGRATROKKTMLSRALSDLY 626
 DB 1214 RMPSPGETASNNKTSKSS---CEGIRQTWESESSP-----LNPYTSLSAII 1256
 QY 627 KYTKSVATHDIEMEAASQVSSFSETKAHQILOOKPAQYLRFNOQOISRTYSSRYVS 686
 DB 1257 RFPK-----CYHISLSLNNAKKRLCRYSOKLTOHTACQLTKRTYPAATRIDIS 1303
 QY 687 SANNPQPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLR-----GCMCOGVF 740
 DB 1304 SNNPQPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLR-----GCMCOGVF 1363
 QY 741 NPNSEDPPLGOLKQVLRIISGOOLPKPRDSMLDGRGELIDPEVEEIIIGLPVCCSRQ 800
 DB 1364 SPLERO-LDSMPAYSLITVSGQV--CPSSNM-----GSPCEVYVLGMPDLSCHFR 1414
 QY 801 TRVVDNGENPFWETLVFMVHPELALVRLVMDHPDGRDIFGORTLAFSSMMPGYRH 860
 DB 1415 TRVVDNGENPFWETLVFMVHPELALVRLVMDHPDGRDIFGORTLAFSSMMPGYRH 1472
 QY 861 VYL-----EGMEASIFVH 874
 DB 1473 LQRLNLAHEVLEISSLFTN 1491

RESULT 12
 US-09-828-447-11
 : Sequence 11, Application US/09828447
 : Patent No. US20020069432A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSMALDO DA
 : APPLICANT: BOHNETT, HANS J.
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 : TITLE OF INVENTION: OF USE IN PLANTS
 : FILE REFERENCE: 16313-0037
 : CURRENT APPLICATION NUMBER: US/09/828,447
 : CURRENT FILING DATE: 2001-08-20
 : PRIOR APPLICATION NUMBER: 60/196,001
 : PRIOR FILING DATE: 2000-04-07
 : NUMBER OF SEQ ID NOS: 41
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 11
 : LENGTH: 1054
 : TYPE: PRT
 : ORGANISM: Physcomitrella patens
 : US-09-828-447-11

Query Match 11.3%, Score 723.5; DB 10; Length 1054;
 Best Local similarity 31.6%; Pred. No. 1e-35;
 Matches 218; Conservative 103; Mismatches 273; Indels 95; Gaps 21;
 QY 230 FYKMMSTRDLYLML-----TYSNKHCHLDAASIQRFLOYEQKAGYTLSECDIIEOF 284
 DB 426 FPKRSKKGDLAODLIGVFSYSEN--GKLDAGELIKELQTEGGGSSLDADAKHVELI 484
 QY 285 EPCPEKSK-----GLIGDFTNTYRSPAGDIFNPEHHVHODMTOPLSHYFTTSSH 337
 DB 485 RN-ERHKSQFPFIYSSDLSKGFKNYLSR--DLNGVLESTYHODMTOPLSHYFTTGH 541
 QY 338 NTYLVGDOLMSORVMTAWYLQAGRCVYDCWDGPDGEPIYHNGYITLSTKLFKDYIE 397
 DB 542 NSYLTGNOLSSDSDYPTAALQGRVYELDLPDOKGKIYHNGYITLSTKLFKDYIE 601
 QY 398 TINKYAFIKNEYPVLIISNHCNCSVIOQKKAQYLTDILGDKLDSVSSDATTLPSPOM 457
 DB 602 AIKANAFYSKTPVYITLEDHLSPLQALAEITLNLIGEDL--YPPSSDGFKELPSPES 660
 QY 458 LKGLILVKGKLPANISED--AEGEVSEDESADEIDDDCKLNGDASTRKREVENTAKR 515
 DB 661 LKGLILSTKP--PREYLEAAVAQKALKDE-----KILNEFKADKLDQOSTAP- 708
 QY 516 KLDLSIKRSKTRDCEDPNNFSVSTLSPSGIKRK---SKAEDEVESEGDAGARRNGRLV 572
 DB 709 ---VSPVEKKIAPVSEKTKSISEKDLSEKVGMLRVDSSEGSADPAPASPDG--- 760
 QY 573 VGSFSRRKSKSKLKAASVEEDGEGDPSGSGRATROKKTMLSRALS--DLVYTKS 631
 DB 761 ---KKNITLADSESDDD-----NKNPEIARLTIHQSPSKG 796
 QY 632 VATDIEEMEAASQVSSFSETKAHQILOOKPAQYLRFNOQOISRTYSSRYVS 691
 DB 797 TVVED-RKVEGVYVRLSTSETKLEKTEEFPELVYFTQRLNIRVYPAQNRVNSNYP 855
 QY 692 QPFNNAGCOMALYQSEGRMLQUNRAKFSANGCGYVLRPGCMCGV-----FNNSEDP 746
 DB 856 TAAMIHQAQVAMQMOGYGKELMOAHGKFRNGCGYVLRPKYLLDLPNGKRFNPSA-- 913
 QY 747 PLGOLKQVLRIISGOOLPKPRDSMLDGRGELIDPEVEEIIIGLPVCCSRQ 806
 DB 914 --PQDTKMLIKVMTMGWDKAFPKYHFDLSPDPFTRLTATGYRADYAKKTSYIID 971
 QY 807 NGEPFWETLVFMVHPELALVRLVMDHPDGRDIFGORTLAFSSMMPGYRHYLEG 865
 DB 972 -VWEPHNNEDHEFYLCPELALRIEVRDHDSEODEFEOACLPNHEITKDGRCYQM-- 1028
 QY 866 MEASIFVHVAVSDISQVKAOLGLGLF 894
 DB 1029 -----YDKKGSYLR--GVKMLF 1043

RESULT 13
 US-09-828-447-12
 : Sequence 12, Application US/09828447
 : Patent No. US20020069432A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSMALDO DA
 : APPLICANT: BOHNETT, HANS J.
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 : TITLE OF INVENTION: OF USE IN PLANTS
 : FILE REFERENCE: 16313-0037
 : CURRENT APPLICATION NUMBER: US/09/828,447
 : CURRENT FILING DATE: 2001-08-20
 : PRIOR APPLICATION NUMBER: 60/196,001
 : PRIOR FILING DATE: 2000-04-07
 : NUMBER OF SEQ ID NOS: 41
 : SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 12
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-447-12

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Query Match      10.7%; Score 685.5; DB 10; Length 628;
Best Local Similarity 30.9%; Pred. No. 1e-33; Indels 97; Gaps 20;
Matches 200; Conservative 104; Mismatches 246;

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QY 238 RDLYLMLTYSHNHKDLDAASQIFLOVEOKMAGVLESQDIIIOFEPCEPKSGLLG 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 QDLVGVFTIYSENERMSBGLKFLHTHEGGVDFPTLDAQIMIRIR-DWKKSGFLAS 76
QY 298 I-----DGFYTRSPAGDITNPEHHVHODMOTPLSHYFTTSSHNTYLVDOQMSOR 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 INSDLSKEAFRRYLMNP--DLNGVJLHNVHODMOTPMSHYFTTGHNSYLTGNLSQSS 134
QY 352 VDMYAVNLQAGRCVVDCCPDGEPYVHGVYTLTKILFKDVIETIKYAFINREYV 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 135 DFPFALALRGYAVVELDLPDPDKGKMYTHGNTLTNPSPKCYATIKNNAFSTSEYV 194
QY 412 ILSIENHCSTVIOCKMAQYLTDLGDKIDLSSVSESDATLTPSPOMLKGKILVKGKLLPA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 195 CVTIEDHLTSELQGHAAEILFQILDAL-YPPPTDALVEFSPESLKRKIIISTK---- 249
QY 472 NISEDAEEGEVDESDADEIDDDCKLLNGDASTNRKRVENTAKRKLDLSIKESKIDCED 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 -----PKEYLEAG-----STOKLAMEN--RNIVEELEKEDKLEQ--- 282
QY 532 PNFPSVTLSPSGKLGKRSKAEDVESGEDAGASRRNGRLVVGSPSRRK-----KK 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 -----TTFAP-----LEENHLIGENTPELRKE-----VEVLSQKEMSTPAELNSRS 323
QY 583 GSKLTKAASY--BEGDEGODSPGOSRGATROKTKMLKLSRLS-DLVKTKSAV-THDIE 638
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 324 PSDLGESTSTRYSKSGNDGNP-----KHKRYALTLITRLAKHAKGTSMERHQ 372
QY 639 MEAASSQVVSFSETKHAQILOOKPAOYLFRNQOOLSRTPSSRYDSSNYNPQPFMNG 698
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 VD--ESVKRISLSESKLEKYEKPELALVFKIKNILRYPAANRVSSNFCPTLAMNG 430
QY 699 QCNVALNYQSEGRMLQINRAKFSANGCGGYLKPCCMCQGV-----FNPNSEDPRLGQLK 753
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 AQVVAQNMVGKELMGAQFKFGNGCGGYLKPQYLLLEMLPGSVNPPTS---PRNTT 486
QY 754 KQVLKRTISQQLPKPRDSMLGREGELIDPEVEVEIIGLVDCSRQGTRYVDDNGFPTW 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 487 LILIKIKVTTGLGMDKAFSKRHFDLESPDPFTRYIVGVPADEAKKKTSTV-DNSNAPHW 545
QY 814 EETLVFWHPEIALVRELVWDHPIDGRD-FIGORTLAFSSMMFGYR 859
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 NEDHEFPLKCEPLALLRIEVRDHDHDSKDEFEQGTCLPIHEVRDGYR 592

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RESULT 14
US-09-835-996A-19
; Sequence 19, Application US/09835996A
; Patent No. US20020142953A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing
; APPLICANT: Weinman, Tom
; APPLICANT: Drmenac, Radoje
; APPLICANT: Ren, Feiyen
; APPLICANT: Qian, Xiahong

```

```

; APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-19

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Query Match      8.2%; Score 522.5; DB 10; Length 340;
Best Local Similarity 37.1%; Pred. No. 3.2e-24; Indels 21; Gaps 6;
Matches 124; Conservative 53; Mismatches 136;

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QY 45 MOEGQMYKLRGSGKGLRFYULDEHRSICRW--RPSRKNKAKISIDSIOGVSEGRQSE 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18 MOEGMPKRVKRSKSKKRLRYFLQNDGMTV-WHAQANGSAKPSISIDVETIRGHQSE 76
QY 103 VFQRPDGSFDPNCFSTIYHGSHRSLDVLSTSSVATWTYGLRYLMAGISDSDSLAR 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 LIRSLAEELPLEQGTIYFHG--RNSNLDMANSVBEADIMWGLQLLDVLTSMQ---H 131
QY 163 QSTROWLQTFPDEADKNDGSLSGEVLQDLKTNVILPRQYVOMFREADTDHOGTL 222
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 QERLDQWLSDFQORQDKNDGKMSFOYORLLHLMNVEMDEYAFSLQOADT--SQSGTL 190
QY 223 GFEFCATKYMSTRDLYLMLTYSNKHDIIDAASLOFLOVEOKMAGVLESQDIIIE 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 EGEEFQFYKALTKRAVELFESPSADGQKLTLEFLDFLOEKEKEDCSEALLETID 250
QY 283 QEPCEPKNSKGLIGDGTNTYTRSPAGIDFNPENHNVHODMOTPLSHYFTTSSHNTYLV 342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 RYPSDSGKLRHVLSDGFLSTLCSKGDIFNPACLPIDQMTQPLNHFICSSHNTYLV 310
QY 343 GDOLMSQSRVDMYAVNLQAGRCVVDCCPDG 376
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 GDOLGQSSVEGY-----IRCSGGRBG 332

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RESULT 15
US-09-908-664-22
; Sequence 22, Application US/09908664
; Patent No. US20020115178A1

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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 191
; TYPE: PRT

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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-908-664-22

Query Match 8.1%; Score 515; DB 10; Length 191;
Best Local Similarity 53.4%; Pred. No. 4.3e-24;
Matches 101; Conservative 29; Mismatches 51; Indels 8; Gaps 4;

QY 307 SPAGDINPEHHVHODMTQPLSHYFTSSHNTYLVGDQIMS-OSRYDMYAWYLQAGCRC 365
Db 1 SPDCNVFDPPEHKQVHQDMNQPLSHYFINS SHNTYLVGNQLSGSSSEVEMTQALIKGCRC 60
QY 366 VEVDCMDGPDG--EPYVHGTYLTSLKFKDVIETINKYAFIKNEYPVILSTENHCSVI- 422
Db 61 IELDCMDGKGDDEPILTHGHTMTTELISFKDCLEAIKEHAFVTSYEVILSTENHCDSTP 120
QY 423 -QOKKMAQVLTDLIGDKL--DLSSVSESDATLPSPOMLKGIIVKGGKLLPANISEDAE 478
Db 121 QOQAKMAEYCKEYFGDMLFTEPLESPLEPGKELPSPEELKRLILINKKLEKSESEKES 180
QY 479 EGEYSDEDS 487
Db 181 EEKKTDEET 189

Search completed: March 28, 2003, 14:00:57
Job time : 46 secs

GenCore version 5.1.4-P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 13:48:00 ; Search time 31 Seconds
(without alignments)
1145.596 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379

Sequence: 1 MAPPTACPLPEPALPPEDPG.....ALPYHCLRGTLPLMLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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SUMMARIES

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1	1281	20.1	744	US-09-738-884-4	Sequence 4, App1
2	1278.5	20.0	736	US-09-738-884-2	Sequence 2, App1
3	1262	19.8	744	US-09-738-884-5	Sequence 5, App1
4	985	15.4	1290	US-08-138-641-2	Sequence 2, App1
5	985	15.4	1290	US-08-138-133-2	Sequence 2, App1
6	192	3.0	2972	US-09-579-181-2	Sequence 1, App1
7	192	3.0	3118	US-09-579-181-1	Sequence 2, App1
8	189	3.0	960	US-09-219-849-5	Sequence 5, App1
9	181	2.8	1064	US-08-642-255-62	Sequence 62, App1
10	180	2.8	1057	US-08-931-820-1	Sequence 1, App1
11	179	2.8	696	US-08-906-865-4	Sequence 4, App1
12	179	2.8	696	US-09-129-668-4	Sequence 4, App1
13	177.5	2.8	252	US-08-642-255-61	Sequence 61, App1
14	176	2.8	1057	US-08-931-820-4	Sequence 2, App1
15	175.5	2.8	529	US-09-247-806-2	Sequence 12, App1
16	175.5	2.8	1442	US-08-316-650-12	Sequence 12, App1
17	175.5	2.8	1442	PCT-US95-02251-12	Sequence 12, App1
18	175	2.7	1078	US-08-963-825-21	Sequence 21, App1
19	175	2.7	1078	US-09-500-811-21	Sequence 21, App1
20	175	2.7	1078	US-09-570-573-21	Sequence 21, App1
21	175	2.7	1078	US-09-548-608-21	Sequence 21, App1
22	175	2.7	1336	US-08-231-193A-58	Sequence 58, App1
23	174	2.7	1336	US-08-486-273A-58	Sequence 58, App1
24	174	2.7	1336	US-08-940-086A-58	Sequence 58, App1
25	174	2.7	1336	US-08-940-035A-58	Sequence 58, App1
26	174	2.7	1336	US-08-935-105A-58	Sequence 58, App1
27	174	2.7	1336	US-09-648-797-58	Sequence 58, App1

28	172	2.7	595	4	US-09-219-849-48	Sequence 48, App1
29	172	2.7	595	4	US-09-219-849-50	Sequence 50, App1
30	172	2.7	822	4	US-09-219-849-49	Sequence 49, App1
31	172	2.7	1341	3	US-08-963-825-18	Sequence 18, App1
32	172	2.7	1341	4	US-09-500-811-18	Sequence 18, App1
33	172	2.7	1341	4	US-09-570-573-18	Sequence 18, App1
34	172	2.7	1341	4	US-09-548-608-18	Sequence 18, App1
35	172	2.7	1461	4	US-09-585-887-9	Sequence 9, App1
36	172	2.7	1461	4	US-09-289-578-9	Sequence 9, App1
37	170	2.7	1060	3	US-08-931-820-3	Sequence 3, App1
38	170	2.7	1418	3	US-08-963-825-20	Sequence 20, App1
39	170	2.7	1418	4	US-09-500-811-20	Sequence 20, App1
40	170	2.7	1418	4	US-09-570-573-20	Sequence 20, App1
41	170	2.7	1418	4	US-09-548-608-20	Sequence 20, App1
42	169.5	2.7	1418	4	US-09-548-608-20	Sequence 20, App1
43	169	2.6	633	1	US-08-642-255-73	Sequence 73, App1
44	168	2.6	493	4	US-08-556-978B-59	Sequence 59, App1
45	168	2.6	595	1	US-08-425-069-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-738-884-4
Sequence 4, Application US/09738884
Patent No. 6391606
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000849
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 744
TYPE: PRT
ORGANISM: Cricetus griseus
US-09-738-884-4

Query Match 20.1%; Score 1281; DB 4; Length 744;
Best Local Similarity 35.7%; Pred. No. 2.4e-90;
Matches 306; Conservative 128; Mismatches 278; Indels 144; Gaps 16;

44 AMOEGQMYKLRGSGKLVRYFYLDHRSICIRWRSR-----NEKAKISIDSIQEVSEGR 99
10 ALLKSGQLKLVKSSMRRERFYKLDCKTI-WQSRKVMRSPESQLFIEDIQVRMGH 68
100 QSEVFQRYPDGSPDNCFSIYHSHRESLDVSTSEFAKRWVGLRTLMAGIDEDSL 159
69 RTGLKKFA-RDIPEDRCFSIYFKDQDRLDLIAPSSAQHMQVQLRKT---IHHSQM 124
160 ARRORTDQMLKQTFEADKNGDGLSIEGVLQILKLVNVPKQVKQMFREAD---TD 216
125 DQKQKLD-KHHSCLKADKKNKKNFKELDLKELNIOYDVSARIRPDCDSQND 183
217 DHOGTIGFEFCFAFYKMSSTRDLYLIMLTYSNKHDLDAISQRLQYQKMAQTLES 276
184 ----SLEDEIEFYFKMLQRAIEDIVFAEASATLISVEKLVYFLQHQOREAAGPAL 239
277 CQDILDFEFCFPKNSKGLIGIDFTNTPSPAGDIFNEHHVHODMOPSHYFTSS 336
240 ALSLIEREYSEFAKQKQRTKQDGLMTLISADGSAFSLAHRVYQDMQPLSHYVSS 299
337 HNTYLVQDLMSQSRVDMAMVLAQGRCEVDCMDGPDGEPIVHGYLTSLFKDYI 396
300 HNTYLVQDLMSQSRVDMAMVLAQGRCEVDCMDGPDGEPIVHGYLTSLFKDYI 359
397 ETIKVAFINNEPVILISINHSVIOQKMAQYLDIIGDKDLSSVSSEDAITLPSPO 456

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Db 360 RAIDYAFKASPYVYLLSLENHCSLEQOQVMAHKLALILGPMI-IDPILDVITSLPSPE 418
QY 457 MLKGIILVKGK---LPANISEDAEEGEVSEDESADEIDDDCKLNGDASTNRKRENT 512
Db 419 QLKGIILVKGKFGGLLPAGEENGPEITDVSDDEAAEMDE----- 460
QY 513 AKRDLILKESKIRDCEDENRNFVSSTLSPSGKLGKRSKAEDVESGEDAGASRRNGRLV 572
Db 461 -----A 461
QY 573 VGSFRRKKKSKLKAASVEEGDEGDSPGGSRGATRQKTKMLSRALSDLVYTKTSV 632
Db 462 VRSVOQKSKEDKLNVAPE-----LSDVYVICKSV 491
QY 633 ATIDIEEAAS---WVSSFSETHAKHOLLQOKPAQYLRPNQOLSRIPSSRYVDSNV 689
Db 492 HEGGFSPNSTSGAFAFEMASFSERNRRLRLOESGNFNHNSHLSTRIPAGRTDSSNV 551
QY 690 NPOFVNAGCOMVALNYVOSGSRMLDLNRAKFSANGGCGVYLKPGCM--COGVFNPSDEP 747
Db 552 SPVEMNNGGOIYALNFOTPGPMDVYLGPFODNGACGVYLPAPLRDPTAFNPRALNQ 611
QY 748 LRGOLKOLVRLIISGOQLPKPRDSMLGDRGELIDFVEVEIIGLPVDCSRQOTRYVDN 807
Db 612 GPMMAOKRLRVRVYISGOQLPKVKS---KNSLVDPKVYVEHGVQDYASQOTAVITNN 667
QY 808 GPNPTEETLVPMVMPETALVRLVMDHPIGR-DFIGORTLAFSSMMPGYRHVYL-- 863
Db 668 GPNPMDTEEEVAVPDLALVFEVEDYDASSKNDFTIGOSTIIPNNSLKOGYRHVHLLSK 727
QY 864 --EGMEASIFVHVAV 877
Db 728 NGDQHPSATLFFKISL 743

RESULT 2
US-09-738-884-2
; Sequence 2, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human
US-09-738-884-2

Query Match 20.0%; Score 1278.5; DB 4; Length 736;
Best Local Similarity 34.6%; Pred. No. 3.7e-90;
Matches 297; Conservative 129; Mismatches 273; Indels 159; Gaps 18;

QY 44 AMOEGMOMVTLRGSGSKGLVRFYLLDEHRSCTRW---RPSKNEKAKISIDSIOEVSEGRQ 100
Db 11 AMLRGSRLKIRKIRTKHKEKRLYRLOEDGLSV-WFORIRIPAPSOHIFVYOHIAVREGHQ 69
QY 101 SEVFORYPDGSFPNCFSTYHSGSHRESLDLVGSSSEVARTWTGLRYLMAGISDEDSLA 160
Db 70 SEGILRRF-GGAFAPARCLTIAFGGRKNEDLAPTAPEAORWRVGLKTLARL---DAMS 125
QY 161 RROKTRQMLKQTFDEADKNGDGLSIEGVLLHLKLVNLPRQRYKOMFEADITDHOQ 220
Db 126 QREBL-DHWTHSYLHRDSSMODSKMSFKIKSLIRVNVDMNDMYVLLFKEDDHNNR 184
QY 221 TLFEFECAFYKMMSTRDLYLMLTYSNKIKDLDAASIQRFYQVAKAGVTLSECODI 280

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Db 185 LRG-AEIEEFLRLKRPLEEIFHOYSGEDRVLSAPLEEFLE-DQEGEGATLARAQOL 242
QY 281 IBOFPCPEPNKSKGLIGDFTNTRYSPAGDLFNFENHHVHODMOPRASHFTISSNHTY 340
Db 243 IQTYELNETAKOHEMLMTLDGFMVYLLSPBGRALDNTHTVCVODMNOPLAHYFISSNHTY 302
QY 341 LVGDOLMSQSRDYMAYLQAGRCVEVDCWDGPDGDEIVHGYTLTKILFKDIETIN 400
Db 303 LTRDSQIGPSSTEAVVRAFAAGRCRCVELDCWEGPGGEPVYHGHITLSKILFRVQAQAVR 362
QY 401 KYAFITKNEYPVLLSIENHCSTYLOOKMAOYLJDLILGDKLDSVSSSEBATTLPSPOMLG 460
Db 363 DHAFTLSPYVILLSENNCGLEQOANAKRHCTTLDGMLTYQALDSPPELPSPEDQK 422
QY 461 KILVKGKLPANISDA-----EEGEVSDSDADEIDDDCKLNGDASTNRKRENTAK 514
Db 423 RVLVYKGLLPARSDEGDRALSDREGEDDEEBEE-----VEAAQ 464
QY 515 RLKDLISKESKIRDCEDENRNFVSSTLSPSGKLGKRSKAEDVESGEDAGASRRNGRLV 574
Db 465 RRL----- 467
QY 575 SFSRRKKKSKLKAASVEEGDEGDSPGGSRGATRQKTKMLSRALSDLVYTKTSVAT 634
Db 468 -----AKOISPELSALAVYCHATRL 487
QY 635 HDIE--MEASSWQVSSEFSETHAKHOLLQOKPAQYLRPNQOLSRIPSSRYVDSNVNPQ 692
Db 488 RTLHPAPNAQPCQVSSLSERKAKKILREAGNSFVRHNAHQLRVYPLGRMNSANVSQ 547
QY 693 PFVNAGCOMVALNYVOSGSRMLDLNRAKFSANGGCGVYLKPGCMCOGVFNPSDEP-DP-LRG 750
Db 548 EMNNSGGOIYALNFOTPGYEMDLNAGFVLNGCGGVYLPACLRQ---PDSTFDEYRG 603
QY 751 QLKQVLRLIISGOQLP---KPRDSMLGDRGELIDFVEVEIIGLPVDCSRQOTRYVD 805
Db 604 PPRITLSIOVTLAQOLPKLNAEKPH-----SYDPLRIEIHGVADCARQETIDYL 655
QY 806 DNGFNPTEETLVPMVMPETALVRLVMDHPIGR-RDIGORTLAFSSMMPGYRHVYL- 863
Db 656 NNGFNPRTKGTLOPLARAPALVRFVVEDYDATSPNDEGVQFTPLSLKOGYRHVHLL 715
QY 864 ----EGMEASIFVHVAV 877
Db 716 SKDGASIPATLFIQIRI 733

RESULT 3
US-09-738-884-5
; Sequence 5, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-738-884-5

Query Match 19.8%; Score 1262; DB 4; Length 744;
Best Local Similarity 35.9%; Pred. No. 7.1e-89;
Matches 308; Conservative 128; Mismatches 274; Indels 148; Gaps 19;

QY 44 AMOEGMOMVTLRGSGSKGLVRFYLLDEHRSCTRWPRSK---NEKAKISIDSIOEVSEGR 99

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Db 10 ALTKSQLLKVVSSSMRRERFKLQEDCKTI--WQSRKVMRSPESQFSLIEDIOEVRMGH 68
QY 100 OSEVFORYPDGSFDPNCPSTIYHSHRSIDLVTSSSEVARTWYGLYIMAGISDESL 159
Db 69 RREGLEKFA-RDIPEDRCFSIVFKDQRTNLDLAPSPADVOHMYOGLKRI---IDRSGSM 124
QY 160 ARQRTRQOMLQOTDEADKNGDGLSIGEVQLLHKLNVLPRQRYKMPREAD---TD 216
Db 125 DQRQKIQ--HWISCLRKADKKNKMKREYDFLKLNVQVDSYAKRIPECHQSOTD 183
QY 217 DHQGTGFEFECFAFKMSTRDLYLLMLTVSNHKLDAASLQRFLOVEOK--MAGVTL 274
Db 184 ----SLEDEIEFTRFMTLQRAIEDRAFAEAGSAETLSVEKLYTFLQHQEEEGPAL 239
QY 275 ESCQDIIIEFPCPEKSKGLGIDGFTYTTSPAGDIFNPNHHVHODMOPLSHYFT 334
Db 240 --ALSLIEREPESETAKAQRMTKQGFMTYLLSADGNASLHRRRYODMNPPLSHYLV 297
QY 335 SSHNTLVGDQMLMSGRVYMWVLQAGRCVEVDCMDPDEPIVHHGYTLTSKILEFD 394
Db 298 SSNTYLLLEDQLTGSPSTATYIRALCKGRCLEDCMDSPNEPIIYHGYTTSKILFCD 357
QY 395 VIETINKYAFIKNEYVYLLSIENHGSVIOQKMAQYLDLIDDKDLSSVSEDAITLPS 454
Db 358 VLRARIDYAFKASPYVILLSENHCSLEEQRYAHHLRAILPML-LDQPLDGYTSLPS 416
QY 455 PQMLKGTILYKGGK---IPANISEDAEVEGDESDADEIDDDCKLNGASTNKRKY 510
Db 417 PEOLKEKILKKGKLLGCLLPAGEGNEPEATVDSDEBAEMEDYAV-----RSQVQ 467
QY 511 NTAKRKILSLIKESKIRDCEDPNPFVSSTLSPSGILGRKSKAEDEYSEGEDAGASRRNG 570
Db 468 H-----KPKED----- 473
QY 571 LVVGSFSRRKKKSKLKAASVEGBQDQSPGQSGRATROKTKMLSLRAISDLVYKTK 630
Db 474 -----KTLPELSDMVYICK 489
QY 631 SVATHDIEMBAASS---WQVSFSETKAHQILQKPAQYLRFNQOOLSRIYSSVYVDS 687
Db 490 SVHGGGSSSTSGOAFYEMASFSERLRLDDESGNPFHNVGHLSRIYPAQWMTDSS 549
QY 688 NYNPFPMNAGCMVALNYGSEGRMLQLNPAKFSANCGCYVLKPCM--CQGVFNPSE 745
Db 550 NYSPEVMNCGCQVALNFOTPGRPEMDVYLGCFODNMGCGCYVLKPAFLRDPDTFNSRAL 609
QY 746 DPLRQALKQVLRKLTISGQOLPRRDSMLGDRBEIIDPEFEVEVILGLPVNCSREQTRVVD 805
Db 610 TQGWMAAPKRLRWIISGQOLPKVKN---NKSIVDPKYVIEIHGVGDVYASRQTAVIT 665
QY 806 DNGFNPTMEETLVFMVHAPETALVRLVMDHPICR--DFTGQRTLAESSMMPGRHYVLE 864
Db 666 NNGNPNMDREFEVVAVPLDALVRFVWEYDSSSKNDFIGOSTIIPWNSLKQGRVHVL 725
QY 865 GME-----EASIVYHVAV 877
Db 726 SKNGDLHPSATLFFVKISI 743

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RESULT 4
US-08-138-641-2
Sequence 2, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:
APPLICANT: Koblman, Kenneth S.
TITLE OF INVENTION: Assay to determine inhibitors of
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Mulhard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway

```

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STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulhard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-138-641-2

Query Match 15.4%, Score 985; DB 1; Length 1290;
Best Local Similarity 25.6%; Pred. No. 4e-67;
Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;

QY 74 IWRDSRKNKAKISID--SIQVSEGRQSEVFORYP--PDGSP--DPNCPSTIYGS--HR 126
Db 60 ITW--SRGADKLEGSIDIREIKERPKTSRDFRYQEDPAFRPDQSHCFVILYGMERL 117
QY 127 ESDLVSTSSSEFARTWYGLYIMAGISDESL--ARQRTRQOMLQOTDEADKNGDGL 185
Db 118 KRLSLQATSESDVNMWITGLTWLM---EDTLQATPLQIETMLRKQFYSYDRKREIRI 172
QY 186 STGEVQLLHLKLNVLPRQRYKMPREADTDDHQ--GTIGFEFECFAFK--NMSTRDLY 241
Db 173 SAKDLKNMLSQYNYRPNKR--FLERLTDFEGRSGDITYGQFQVLSRLYSAQKTM 229
QY 242 LML-----TYSNHKDLDAASLQRF-----LOVQKAGVTLSECOI 281
Db 230 LPLETNTLKTGERPELCQVSLSEFOQLLEYQGLMAVDRQVQDFMLSLRDLREIE 289
QY 282 EQFEPEPKSKGLGIDGFTYTRSPAGDIFNPNHHV--HODMOTPLSHYFTSSHTY 340
Db 290 EPI-----FLDELVTFLFSKENSVMNSQLDAVCPETMNPPLSHYISSHNTY 338
QY 341 LVGDQMLMSGRVYMWVLQAGRCVEVDCMDPDEPIVHHGYTLTSKILFKDYIETIN 400
Db 339 LTGDQFSSSSLEAVARCLRMGRCIEIDCMPDPMPIYIGHLTLTIKFSDVLTITK 398
QY 401 KYAFIKNEYPVYLLSIENHGSVIOQKMAQYLDLIDDKDLSSVSEDAITLPSOMLKG 460
Db 399 EHAFFVASEYPVYLLSIDHCSIAQQRMAOHFRKVLGDTL-LTRPYDIAADGLPSNOLKR 457
QY 461 KILVKGKLLPA-----NISDAEES----- 480
Db 458 KILIKHKKLAEGSAVEYPTSVMYSENDISNISKNIILVLEDPVNHVPHYVLTSSKI 517
QY 481 ---EVSDESDADEIDDKLLNGDASTNKRKY-----EPTAKRKIDS----- 519
Db 518 YSEETSSDQGNDEDEPKASGSTELHSEKWFHGLGAGRGRIARLLETICYETG 577
QY 520 ---LIKES-----KIRDC----- 529
Db 578 APDQSLVRESEFVGDYTLTFWRKNGVQVQCRHSHQDAGTPKFFLTDLNLYPDSLYDLT 637
QY 530 -----E 530

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Db 638 HYQVPLRCNEFEMRLSEPVQTNHESKEWYHASLTRAQAEHMLMVRPDGAFIVKRN 697
 QY 531 DPNNFSVSTLSPGK-----LGRKSK-----551
 Db 698 EPNSTALS-FAEGKIKKCHVQOEGQVLMGNSEFSLVDLISYEKHPILKRMKLRYPI 756
 QY 552 -----AED-----VESG-----559
 Db 757 NEALEKIGTAEPDYGALYEGRNPFYVEANPMTFKCAVKALFDYKAQREDELFTTSA 816
 QY 560 -----EDAGASR-----566
 Db 817 IIVNVEKODGWMRGDYGKKQLMFPSSNYVEEMINPAILEPERHDENSPLGDLRGVL 876
 QY 567 -----RNGRLVYGSFSSRRKKSGSKLTKAASVEE-----GDEGDSFGG 604
 Db 877 DVPAQAIAREPCKNNRLVFSISMPSVAQMSLDVYAADSELDQWYKALREVAQIADAR 936
 QY 605 QSRGATQKTKMLKSLDLVYTKVATHD--TEMEAASSWQVSSFSFETKAQIILQO- 661
 Db 937 LTBGKMMERR-KKIALSELVYVCRVPDEEKIGTERACYRDMSSFPETKAEKYNKA 995
 QY 662 KPAQYLFNQQOOLSRIPSSYRVDSNYNPQPMNAGCOMVALINQSEGMLQINAKES 721
 Db 996 KKKFQIYNLQLSRITPKQORLDSNYDPLPMWICSGQLVNLFPQDPKPMQMOALPM 1055
 QY 722 ANGCGYVYKPGCMQGVNPNSEDLPGQLKQVLRILISGOOLPKPRDSMLGDEGII 781
 Db 1056 AGGCGYVYLOPSTMIRDAEPFDPKSSIRGLPCVICIEVLGARHLK-----NGRG-IV 1108
 QY 782 DPEVEEIIIGLVDCSEORRVYDNDGNFTW--EFTLVPRVNHPELALVFLVMDHPDG 840
 Db 1109 CPVEIEVACAEYDSTKQKEEYVYDNGNLNFWPAKPFHFOISNDEPAFLRFVYEDMES 1168
 QY 841 -RDFIGQRLAFSSMMPGYRHV-----YLEGMEASIFVHAV 877
 Db 1169 DONFLAOFPPVYKLGKTYRAVPLKNNYSDELASLLIKIDI 1211
 RESULT 5
 US-08-138-133-2
 Sequence 2, Application US/08138133
 Patent No. 5519163
 GENERAL INFORMATION:
 APPLICANT: GIBBS, JACKSON B.
 APPLICANT: KOBIAN, KENNETH S.
 APPLICANT: MACLEOD, ANGUS M.
 APPLICANT: MERCHANT, KEVIN J.
 TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID A. MUTHARD
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: U.S.A.
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,133
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MUTHARD, DAVID A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 18938
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3903
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1290 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-138-133-2

Query Match 15.4%; Score 985; DB 1; Length 1290;
 Best local similarity 25.6%; Pred No. 4e-67;
 Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;
 QY 74 IMRPSRKNKAKISID--SIGEVSEGRSEVFORV-PDGSF--DPNCCFSYHGS--HR 126
 Db 60 ITW--SRGADKIEGSDIRKEIRKPKTSRDFRYQEDPAFRPDQSCFVILKMERL 117
 QY 127 ESIDLVTSSSEVARTWYGLRLMAGISDEDSL-ARRORTDQWLKQTFEADKNGDGL 185
 Db 118 KTLISLQATISEDEVNMMIGLWLM-----EDTLQATPLQIERMLRKQFYSVDRNREDRI 172
 QY 186 SIGEVLQILHLKLVNLPRQRYKMFREADTDHQ--GTIGFEERCAFYK--MSTRRLY 241
 Db 173 SAKDLKNNLSQVNYRVPMNR--FLRERLTDFEQRSGDITYGQALQSLSLMSAQATMD 229
 QY 242 LLM-----TYSNKKHDLDAISLQF-----LOVEOKNAGVTLSECODII 281
 Db 230 LPFLETNLRIGTERDELQVSSSEFOPLFLYOGELMAVDRLQOEFMLSLRPLNEIE 289
 QY 282 EQFEPCKENKSGLLIGDGFINTYRSPAGDLEFNEBHNV--HODMTOPLSHFTTSSNTY 340
 Db 290 EBY-----PFLDELVTFLFSKENSVMNSQLDVCETNNPNSHWTSSSHNTY 338
 QY 341 LVGDQMSQSRVDMYAWYLAQRCRCVEYDCWDGPEYVHGTYLTKLFEKVIETIN 400
 Db 339 LTGDQFSSESLAVARCLRMGCRCIELDCWDGPDGMPIYIHGHTLTTKIKFSVLTITK 398
 QY 401 KYAFIKNEYPYLSTENKCSYIOOKKAAOYITDLGKRLDSSVSDATFLSPOMLKG 460
 Db 399 EHAFAVASEYPIYLSTIEDCSIAQORNNAAOHRKYLIGTL-LTKPVYDIAADGLSPNOLKR 457
 QY 461 KILVGGKKLPA-----NISDAEAG-----480
 Db 458 KILKHKKLAGSAYEEVPTSVMSSENDISNGLIYLEDYNNHMYHYVYVLTSSKI 517
 QY 481 ---EVSDESDADEIDDOCKLNGDASTNRRV-----ENTAKRKLDS-----519
 Db 518 YSSETSSDOQNEDEEPKASGSTELHSEKWFHCKLAGAGRDGRHIAERLLTEYCIENG 577
 QY 520 -----LIKES-----KIRDC-----529
 Db 578 APDGSFLVRESEYFVGDTYLSFWRNGKVQCHRSKODAGTPKFFLTNDLVFDSLVDLT 637
 QY 530 -----530
 Db 638 HYQVPLRCNEFEMRLSEPVQTNHESKEWYHASLTRAQAEHMLMVRPDGAFIVKRN 697
 QY 531 DPNNFSVSTLSPGK-----LGRKSK-----551
 Db 698 EPNSTALS-FAEGKIKKCHVQOEGQVLMGNSEFSLVDLISYEKHPILKRMKLRYPI 756
 QY 552 -----AED-----VESG-----559
 Db 757 NEALEKIGTAEPDYGALYEGRNPFYVEANPMTFKCAVKALFDYKAQREDELFTTSA 816
 QY 560 -----EDAGASR-----566
 Db 817 IIVNVEKODGWMRGDYGKKQLMFPSSNYVEEMINPAILEPERHDENSPLGDLRGVL 876
 QY 567 -----RNGRLVYGSFSSRRKKSGSKLTKAASVEE-----GDEGDSFGG 604

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Db 877 DVPACQIAIRPGKNNRLFEVSIKMPVSAQMSLDVAADSOEELQDPWKIREVAQTADAR 936
Qy 605 QSRGATROKTKMKSRLSALSDLYTKKSAVTHD--IEMPAASWOVSSESEKKAHIILOO- 661
Db 937 ILEGKMMERR-KKIALSELVLYCRPVPEDEKIGTRACRYRDMSSPETKAETYNKA 995
Qy 662 KRAOVLRFMOOOLSHYSSYRVDSNNYPOPFNAGCOMVALANTQSGRMLOLRAAFS 721
Db 996 KKKKFLQIKRLOLSRTIKRGQRLDSSNTDPLPMTCGSQVALANTQTDKPMQMOALFM 1055
Qy 722 ANGCGGYLKPCCMCOGVFNPNSEDLPGQLKQOLVLRILISGOOLPKPRDSMLGDRGELI 781
Db 1056 AGHGCGYVLPSTMDPADPDKSSRLGELPCVICIEVLGARHLPK-----NGRG-IV 1108
Qy 782 DPEVEYIIGLVYDCSREOTRYVDNGNFPWT-EETIVFMVMPETALVRELWMDHPIG 840
Db 1109 CPEVELEVAGAEYDSTKQCTEYVDNGLNVPAPKPFHQQISNPERALFREVYEDMFS 1168
Qy 841 -RDEIGORTLAFFSSMMPGYRHV-----YLEGMEASIFVHVAV 877
Db 1169 DQNFIAQATFPYKGLKTYRAVPLKNNYSDELIALSLIKID 1211

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RESULT 6
US-09-579-181-2
Sequence 2, Application US/09579181
Patent No. 6365372
GENERAL INFORMATION:
APPLICANT: Chivlia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2972
TYPE: PRT
ORGANISM: Human
US-09-579-181-2

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Query Match 3.0%; Score 192; DB 4; Length 2972;
Best Local Similarity 19.6%; Pred. No. 2, 4e-05;
Matches 187; Conservative 121; Mismatches 326; Indels 318; Gaps 42;

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Qy 406 KNEYPVILSIENHCYSVIOQKMAQYLTDLIGKLDLSSVSED-ATTLPSPOMLKGIIV 464
Db 173 EEPPOVLEIKPPSAVTOQNKQPMHDEDEDEFTANEAEDEEDTIAAEQLEGEV-- 230
Qy 465 KKKLPLNISDEDAEEGVSS-----DEDSADEIDDDCKLLNGDA 502
Db 231 ---DHAMELSLAREGELSMBELLOQYAGAYAPGSGSSEDEDEDEVANSDEE-PEGV 266
Qy 503 STNRKRVNTAKRLDLSILKESKIRDCEDPNNTSVSTLSPGKIGRKAEDVESGEDA 562
Db 287 EAEPPEQEDSSQS-DEY--EDRSEDEDEHSEBEETSASASESESESEDAOSQSA 343
Qy 563 GASRRNGRLVYGSFSRKKKSKIKKAASVEGEGODSPGQSGRG----- 608
Db 344 DEEBDDDFGEVYLLARDEQSE-----ADAGSGPTPEPTLLGPKKETITDIAAAS 396
Qy 609 -----ATROKKT-----MKLSRALSLDLVYTKKSVAT 634
Db 337 LQPKGYTLATYQVTPFPLLRGLQREYOHIGDMVIMYMKKLLNGILADEMGKTIQT 456
Qy 635 HDI-----EKEA-----ASSWOVSF-----SETKA----- 655
Db 457 ISLHLACEKGNMGPHLIIVTSYMLNMWELKRMCPFSKILTYGAQKERRKILKRGWT 516
Qy 656 -----HQLLOQKPAOYLRFNQOQLSRITPSSRVDSNYNQ----- 692

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Db 517 KPAHFVICTSYKLVLDHDAFRKKMRYLLIDBAQIKNKFSQRMOSILNFNSORLL 576
Qy 693 ---PFNAGCOMVALANTQSGRMLOLRAKFSANGCGGYLVKPGCMCOGVFNNSDEPLP 749
Db 577 TGTPLQSLMELMSLMFLMPLHYQSHRE-----FKMFSNPLT 615
Qy 750 GOLKQOLVLRILISGOOLPKPRDSMLGDRGELIDF---VEVEL-IGLP-----VDC-- 796
Db 616 G-----MIEGSO--EYNEGLYKRHLKHLRFLLRVAVYERKMPKRYEHVIRCL 664
Qy 797 SREOTRYVDNGNFPWTETLVFMVMPETALVREL-----YMDHDIIGRDFIGORT 848
Db 665 SKRQCLYDDMAQTTKETLATGFHMSVINITLMQKRCVNHNPMLDPRVTSPTI-TPG 723
Qy 849 LAFSSMMPGYRHVYLEGMEASIFVHVAVSDISGVKQALGLKGLFGRKPGSLDSHAA 908
Db 724 ICFSTASLVLRATDVHPLQRIDM-----GRF-DLIGLBERVSRYEADFLPRHRL 772
Qy 909 GR-----PPRPS-VSQRLKRTASAPTKSQPKGR-----GFPELVIGTRDTGS 952
Db 773 SRRVLEVAATAPDPPPRPKPKMKVNRMLQPV---KQEGRTVVVVNPRAPLGP----- 824
Qy 953 KGVADVVPFGPGAPAPAPAGEPG-----SGSPRGKAPAAVAEKSPVRRVP 1000
Db 825 -----VPVRPPEBELSAOPTPEYPOVYLPASLMSASASAG-PPLIPASRPFGVLLP 876
Qy 1001 RYLDGPGPAGMAATCMKCVSGCAGVNTGQLRERPPSPGASRQALRQOPRARADSLG 1060
Db 877 PLQPPSG-----SLPOVLPSPGLVLSG---TSNPPTP-----TLSLKPFPAPVRLSP 921
Qy 1061 APCCG---LDPHALPGSRREAPKPGKPMRQPGSGSGMSDSSPSDPIGPEKSP----- 1112
Db 922 APPGSSSLKPLVTP-----PG-YTFPPAAATTTSTTAAVATTAVAPAPAPQR 971
Qy 1113 -----RMPEGACRQPGALQGEMSAFPQKLEIRSKSPMFSAG--KPL 1153
Db 972 LILSPDMQARLPSCGEVYSIGQL-----ASLQR-----PVANAGSKRL 1010

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RESULT 7
US-09-579-181-1
Sequence 1, Application US/09579181
Patent No. 6365372
GENERAL INFORMATION:
APPLICANT: Chivlia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3118
TYPE: PRT
ORGANISM: Human
US-09-579-181-1

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Query Match 3.0%; Score 192; DB 4; Length 3118;
Best Local Similarity 19.6%; Pred. No. 2, 6e-05;
Matches 187; Conservative 121; Mismatches 326; Indels 318; Gaps 42;

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Qy 406 KNEYPVILSIENHCYSVIOQKMAQYLTDLIGKLDLSSVSED-ATTLPSPOMLKGIIV 464
Db 319 EEPPOVLEIKPPSAVTOQNKQPMHDEDEDEFTANEAEDEEDTIAAEQLEGEV-- 376
Qy 465 KKKLPLNISDEDAEEGVSS-----DEDSADEIDDDCKLLNGDA 502
Db 377 ---DHAMELSLAREGELSMBELLOQYAGAYAPGSGSSEDEDEDEVANSDEE-PEGV 432

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? FILE REFERENCE: 2728-2
? CURRENT APPLICATION NUMBER: US/09/219,849
? CURRENT FILING DATE: 1998-12-23
? NUMBER OF SEQ. ID NOS: 50
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 5
? LENGTH: 960
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Illustrative
US-09-219-849-5

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Query Match	3.0%;	Score 189;	DB 4;	Length 960;
Best Local Similarity	30.4%;	Pred. No. 7.3e-06;		
Matches 90;	Conservative 7;	Mismatches 93;	Indels 106;	Gaps 19;

RESULT 9

Sequences², Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertam I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR

```

US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Assay for collagen degradation
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96202596.1
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-1

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1      RESULT 11
2      US-08-906-865-4
3      ; Sequence 4, Application US/08906865
4      ; Patent No. 6040168
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Greengard, Paul
9      ; APPLICANT: Porton, Barbara
10     ; APPLICANT: Kao, Hung-Teh
11     ; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
12     ; TITLE OF INVENTION: AND USES THEREOF
13     ; NUMBER OF SEQUENCES: 4
14     ;
15     ; CORRESPONDENCE ADDRESS:
16     ;
17     ; ADDRESSEE: David A. Jackson, Esq.
18     ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
19     ; STREET: Floor
20     ; CITY: Hackensack
21     ; STATE: New Jersey
22     ; COUNTRY: USA
23     ;
24     ; ZIP: 07601
25     ;
26     ; COMPUTER READABLE FORM:
27     ;
28     ; MEDIUM TYPE: Floppy disk
29     ; COMPUTER: IBM PC compatible
30     ; OPERATING SYSTEM: PC-DOS/MS-DOS
31     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
32     ;
33     ; CURRENT APPLICATION DATA:
34     ;
35     ; APPLICATION NUMBER: US/08/906,865
36     ;
37     ; FILING DATE:
38     ;
39     ; CLASSIFICATION: 536
40     ;
41     ; ATTORNEY/AGENT INFORMATION:
42     ;
43     ; NAME: Jackson Esq., David A.
44     ; REGISTRATION NUMBER: 26,742
45     ;
46     ; REFERENCE/DOCKET NUMBER: 600-1-202
47     ;
48     ; TELECOMMUNICATION INFORMATION:
49     ;
50     ; TELEPHONE: 201-487-5800
51     ; TELEFAX: 201-343-1684
52     ;
53     ; INFORMATION FOR SEO ID NO: 4:
54     ;
55     ; SEQUENCE CHARACTERISTICS:
56     ;
57     ; LENGTH: 696 amino acids
58     ;
59     ; TYPE: amino acid
60     ;
61     ; STRANDEDNESS: single
62     ;
63     ; TOPOLOGY: linear
64     ;
65     ; MOLECULE TYPE: protein
66     ;
67     ; DESCRIPTION: /desc = "synapsin Ia"
68     ;
69     ; HYPOTHETICAL: NO
70     ;
71     ; ORIGINAL SOURCE:

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ORGANISM: Homo sapiens
US-09-906-865-4

Query Match 2.8%; Score 179; DB 3; Length 696;
Best Local Similarity 21.7%; Pred. No. 2.7e-05;
Matches 152; Conservative 74; Mismatches 266; Indels 210; Gaps 36;

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QY 574 GSEFRKKKSKLKAASVEEGDEGDDSPGGOSRGATROKTKMLSRALSDLYKTSVA 633
DB 75 GFFSSLSNAVKQTTAAATAATFEQVGGSGGAGGGAASRLVLVDEPHDMAKYFKGK 134
QY 634 TH--DIEMEAASSMOWSSSETK--AH-----QIIQKPAOYLRFNQ 672
DB 135 IHGEIDIKVEQA-----EESDLNLVAHANGGSVDMEVLNKGKVKVRSLLKPDVLLR 188
QY 673 QLSRIYPSYR-----VDS--SNYN--PQPMNAGCOMVALNYSSEGRML 713
DB 189 AFSMARNGDYRSVLVIGLYAGIPSVNSLSHYNFCDKPWVF--AQWVRLH-----K 237
QY 714 QLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKQVLRILISGQQLPKPRDSM 773
DB 238 KLGTDEFP-----LIDQTFYPNHKEMLSSTTYVYVKKMGHAGSKGKVDN 284
QY 774 LGDRGEI-----IDPVE-----VEIIGLPVDCSRBQTRVYVDNGFNPTWEE 815
DB 285 QHDFODIASVVALKTYATAPEFLDAKYDVYVKIG-----QNYKAYMRTSVSGNW-K 336
QY 816 TLVFNVAHPEIALV-RLVWD-----HPIGRDFIGQRTLAFFSMMP 856
DB 337 TINTGSAMLEQIAMSDDRYKLTWDTCEIFGLDICAVALHKGKGRHIIIE---VGGSSMP 393
QY 857 GYRHVYLEG---MEASIFVNAVSDISGKYQALGLKGLFLRGPKGSDSHAAGRPA 913
DB 394 -----LIGHQDHDQKOLIVELVYN-----KMAQALPRQORNDASGR- GSHGQTPSPG 440
QY 914 RPSVSORILKRTASAPTKSQKPGRRGFPPELVLTGRDTGS-----KGV---A 956
DB 441 ALPLIGROTSSQAPAPPAQOEPPPGGPPGQGRGPPLOQRPPGQOHLSTGLGPPA 500
QY 957 DDVVP---PGGPAPAPPAQOE---PGSGSPRGKAPAAVAEKSPVRYRPPVLDGPGPAGM 1011
DB 501 GSPILPRLPSPTSAPOQPAQOAPPTQGGQGRSPVAGGAPAPPARPA---SPSPQRO 557
QY 1012 A---ATCMKCYVG---SCAGVNTGLOREPPS--PGPA--SKQAA-----I 1048
DB 558 AGPPQATROTSTVSGAPAPKASGAPPGQOQROGPPQKPPGAPPTROASOAGVPRTGPPT 617
QY 1049 ROQPARARADS-LGAPCCGLDPHAIPIGRSREAPKPGAMRQGGSGSSSDSSPDSPGI 1107
DB 618 TQQPRPSGPGPAGAP---KPOLAKRPSQDVPPPPATAAAGP-----PHQQLFNL 663
QY 1108 PERSPRWPEGACROPGALOGEMSALFAQKLEIRSKSPMESA 1149
DB 664 PEPAP-----PPPSLSODEV-----KAETIRSLRKSFPAS 692

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RESULT 12
US-09-129-668-4
Sequence 4, Application US/09129668B
Patent No. 6429010

GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: US/09/129, 668B
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906, 865
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4
LENGTH: 696
TYPE: PRT
ORGANISM: Homo sapiens
US-09-129-668-4

Query Match 2.8%; Score 179; DB 4; Length 696;
Best Local Similarity 21.7%; Pred. No. 2.7e-05;
Matches 152; Conservative 74; Mismatches 266; Indels 210; Gaps 36;

```

QY 574 GSEFRKKKSKLKAASVEEGDEGDDSPGGOSRGATROKTKMLSRALSDLYKTSVA 633
DB 75 GFFSSLSNAVKQTTAAATAATFEQVGGSGGAGGGAASRLVLVDEPHDMAKYFKGK 134
QY 634 TH--DIEMEAASSMOWSSSETK--AH-----QIIQKPAOYLRFNQ 672
DB 135 IHGEIDIKVEQA-----EESDLNLVAHANGGSVDMEVLNKGKVKVRSLLKPDVLLR 188
QY 673 QLSRIYPSYR-----VDS--SNYN--PQPMNAGCOMVALNYSSEGRML 713
DB 189 AFSMARNGDYRSVLVIGLYAGIPSVNSLSHYNFCDKPWVF--AQWVRLH-----K 237
QY 714 QLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKQVLRILISGQQLPKPRDSM 773
DB 238 KLGTDEFP-----LIDQTFYPNHKEMLSSTTYVYVKKMGHAGSKGKVDN 284
QY 774 LGDRGEI-----IDPVE-----VEIIGLPVDCSRBQTRVYVDNGFNPTWEE 815
DB 285 QHDFODIASVVALKTYATAPEFLDAKYDVYVKIG-----QNYKAYMRTSVSGNW-K 336
QY 816 TLVFNVAHPEIALV-RLVWD-----HPIGRDFIGQRTLAFFSMMP 856
DB 337 TINTGSAMLEQIAMSDDRYKLTWDTCEIFGLDICAVALHKGKGRHIIIE---VGGSSMP 393
QY 857 GYRHVYLEG---MEASIFVNAVSDISGKYQALGLKGLFLRGPKGSDSHAAGRPA 913
DB 394 -----LIGHQDHDQKOLIVELVYN-----KMAQALPRQORNDASGR- GSHGQTPSPG 440
QY 914 RPSVSORILKRTASAPTKSQKPGRRGFPPELVLTGRDTGS-----KGV---A 956
DB 441 ALPLIGROTSSQAPAPPAQOEPPPGGPPGQGRGPPLOQRPPGQOHLSTGLGPPA 500
QY 957 DDVVP---PGGPAPAPPAQOE---PGSGSPRGKAPAAVAEKSPVRYRPPVLDGPGPAGM 1011
DB 501 GSPILPRLPSPTSAPOQPAQOAPPTQGGQGRSPVAGGAPAPPARPA---SPSPQRO 557
QY 1012 A---ATCMKCYVG---SCAGVNTGLOREPPS--PGPA--SKQAA-----I 1048
DB 558 AGPPQATROTSTVSGAPAPKASGAPPGQOQROGPPQKPPGAPPTROASOAGVPRTGPPT 617
QY 1049 ROQPARARADS-LGAPCCGLDPHAIPIGRSREAPKPGAMRQGGSGSSSDSSPDSPGI 1107
DB 618 TQQPRPSGPGPAGAP---KPOLAKRPSQDVPPPPATAAAGP-----PHQQLFNL 663
QY 1108 PERSPRWPEGACROPGALOGEMSALFAQKLEIRSKSPMESA 1149
DB 664 PEPAP-----PPPSLSODEV-----KAETIRSLRKSFPAS 692

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RESULT 13
US-08-642-255-61
Sequence 61, Application US/08642255
Patent No. 5773249

GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertam I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-255-61

Query Match 2.8%; Score 177.5; DB 1; Length 252;
Best Local Similarity 30.3%; Pred. No. 7.4e-06;
Matches 90; Conservative 6; Mismatches 108; Indels 93; Gaps 19;

QY 897 GPK--GSLDSHAAGPPAPSVSQRILRRTASAPKSKQKPGRGPPPELVLRDTSKSG 954
DB 16 GPGABE-----PAGPPGSKGDC-----PPGAPPPAGPPGSKG-----DGGPPG 55
QY 955 VADVVPPG-----PGAPPAEPAQEG--PGS---GSPRGKAPAAVAEKSPVRRPPVLDG 1005
DB 56 APGAPGPGSGRDPG--PGAPGAPGPPGSGDGGPPGAPGAPG-----PPGSRGD 104
QY 1006 PGRAGMAATCMKCVSCAGVNTGGLOREPPFPSPGASRAALRQPPRAAD--SLGAPC 1063
DB 105 PGPGGAPG-----AGPPGSRDPPGPPGAPGAPG-----PPGSGDPPGAPG 147
QY 1064 CGLDPPHAIPGRREAPKPGFAMWPGPGSGMSDSSPSPGIPERSPPWPGACROPG 1123
DB 148 ---GPGAPPG--SKGDPGPPGA--PGPAGPPGSGDPPGPPGAPG-----PAGPPGSGDPPG 196
QY 1124 ALQEMSALEFAOKLEIRSKSPMFSAGKPLLPVCVLPHPAGMAGP---GSPAAASH 1176
DB 197 PPGAPGPA-----GPPGSRDPPG-----GPPGAPGAPGPPGSGDPPGPPGA 236

RESULT 14
US-08-931-820-4
Sequence 4, Application US/08931820
Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1

FILING DATE:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type III
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1055
OTHER INFORMATION: /label= Modified
OTHER INFORMATION: /note= "Ala may be Pro"

US-08-931-820-4

Query Match 2.8%; Score 176; DB 3; Length 1057;
Best Local Similarity 26.5%; Pred. No. 8.5e-05;
Matches 95; Conservative 22; Mismatches 121; Indels 120; Gaps 20;

QY 887 ALGLGLRGRKPGSLDSHAAGRP---PARPSVSORIL--RRTASAPKSKQKGRRGF 940
DB 681 APGEKG---EGGPPG-----VAGPPGSGGAPGPPGQGVKEKSPGGPGAPGAPGARGL 732
QY 941 PELVLTGTRDTGSGVADVVPPG-----DGPAPPAEPAQEGSGSPGKAPAAVA 990
DB 733 P-----GPPGSGNGRPPGPPGSGSPGKDGPPGAPGAPGAPGAPGAPGAPGAPGAPG 783
QY 991 EKSPVRRPPVRLDPPGAPMAATCMKCVSCAGVNTGGLOREPP-----SPGPAS 1043
DB 784 KSPGAPGPP--GAPGGLGI-----AGI--TGAGLAPGPPGPPGPPGPPGPPGPPGPPG 825
QY 1044 RQAAIRQPPRARADSLGAPCCGLDPPHAIPGRREAPK-----GPGAP---WRQG--PGSSG 1093
DB 826 -GVGGESEKPPANGLSGERPPGPGGLAGTAGFERGRCNPSDDLPPGRDSSPGKSG 884
QY 1094 SMSDSSSPDPPGIP-----ERSPPWPGACROPAL----- 1125
DB 885 D--RGENGSPGAPGAPGHPGPPGPPGAPGSGDGGSGPAGAPGAPGAPGAPGAPGAPGAPG 943
QY 1126 ---QGEMSALEFAOKLEIRSKSPMFSAGKPLLPVCVLPHPAGMAGP-----GSPAAA 1174
DB 944 GPKGTEGGERGAAGIGHRG---FPGN-----PGAPGSPGAPGAPGAPGAPGAPGAPGAPG 988

RESULT 15
US-09-247-806-2
Sequence 2, Application US/09247806
Patent No. 6280747
GENERAL INFORMATION:
APPLICANT: PHILIPPE, Michel
APPLICANT: GABSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2
LENGTH: 529
TYPE: PRT
ORGANISM: Nephila clavipes
US-09-247-806-2

Query Match 2.8%; Score 175.5; DB 4; Length 529;

Best Local Similarity 25.68; Pred. No. 3.3e-05;
Matches 85; Conservative 30; Mismatches 132; Indels 85; Gaps 13;

[illegible]

Search completed: March 28, 2003, 13:53:14
Job time : 43 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:45:25 ; Search time 113 seconds
(without alignments)
2200.875 Million cell updates/sec

Title: US-09-927-112-2
6379

Sequence: 1 MAPPPAGLPPEPALPPEDPG.....ALYPMHCLRTLLPWLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3450	54.1	656	4	08TEH5 homo sapien
2	2343	36.7	787	4	09UPR3 mus musculu
3	1587.5	24.9	1128	11	090UG1 mus musculu
4	1583.5	24.8	716	4	08WUS6 homo sapien
5	1578	23.9	1154	4	09UPR0 homo sapien
6	1524.5	23.9	997	4	015111 homo sapien
7	1517	23.8	1096	11	062688 rattus norv
8	1463	22.9	772	6	08SPR7 sus scrofa
9	1441	22.6	762	4	09BRC7 homo sapien
10	1315.5	20.6	772	11	062711 rattus norv
11	1297	20.3	895	5	017232 caenorhabd
12	1294	20.3	771	11	063693 rattus norv
13	1289	20.2	789	4	08TEC1 homo sapien
14	1287	20.2	745	11	060450 cricetus
15	1281	20.1	757	4	08TF37 homo sapien
16	1271	19.9	745	6	029517 oryctolagus

17	1268	19.9	756	11	0921B4	0921B4 mus musculu
18	1266	19.8	756	11	08R3B1	08R3B1 mus musculu
19	1256.5	19.7	466	4	09H9U2	09H9U2 homo sapien
20	1158.5	18.2	502	4	096FL6	096FL6 homo sapien
21	1107	17.4	502	13	091423	091423 catfish, ph
22	1106	17.3	677	4	09H8U0	09H8U0 homo sapien
23	1096	17.2	641	6	095J51	095J51 macaca fasc
24	1091.5	17.1	640	6	095J50	095J50 macaca fasc
25	1075.5	16.9	738	5	097037	097037 hydra magni
26	1000.5	15.7	1175	11	091U21	091U21 mus musculu
27	992.5	15.6	1283	5	097034	097034 ephydatia f
28	990	15.5	1236	5	09VXH3	09VXH3 drosophila
29	986	15.5	1230	5	024284	024284 drosophila
30	965	15.1	504	4	096J70	096J70 homo sapien
31	956.5	15.0	1265	4	096975	096975 homo sapien
32	947	14.8	537	11	09D9N4	09D9N4 mus musculu
33	942	14.8	1173	11	0920E5	0920E5 mus musculu
34	942	14.8	1216	11	0921B3	0921B3 mus musculu
35	940	14.7	1012	5	097035	097035 hydra magni
36	939	14.7	751	5	021734	021734 caenorhabd
37	935	14.7	1311	5	0961D5	0961D5 drosophila
38	928.5	14.6	1418	5	0906B9	0906B9 caenorhabd
39	925	14.5	1419	5	095X30	095X30 caenorhabd
40	925	14.5	1431	5	095X29	095X29 caenorhabd
41	920	14.4	1095	5	0944G4	0944G4 drosophila
42	915.5	14.4	1210	13	092137	092137 xenopus lae
43	886	13.9	1183	11	089040	089040 rattus norv
44	881.5	13.8	1211	13	091086	091086 melagris g
45	880	13.8	1299	5	022070	022070 caenorhabd

ALIGNMENTS

RESULT 1

ID	ORTEH5	PRELIMINARY;	PRT;	656 AA.
AC	08TEH5	01-JUN-2002 (TREMBlrel. 21, Created)		
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	FLJ00222 protein (Fragment).			
GN	FLJ00222.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=SPLEEN;			
RA	Ukuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;			
RT	"The nucleotide sequence of a long cDNA clone isolated from human spleen."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AK074149; BAB84975.1; -			
PT	NON-TER			
SO	SEQUENCE	656 AA;	70138 MW;	1E65D386AB07FIDA CRC64;

QY	552	AEDVESGEGDASRRNRLVVGSPFRKRGKSKIKRAAAYEGDEGQDSPGQSRGATR	611
QY	1	AEEMESGEDAGASRRNRLVVGSPFRKRGKSKIKRAAAYEGDEGQDSPGQSRGATR	60
QY	612	OKTKKLSRALSDLVKTKSVATHDIEMEAASMQVSSFTKAHQILOQPAQYLFNQ	671
QY	61	OKTKKLSRALSDLVKTKSVATHDIEMEAASMQVSSFTKAHQILOQPAQYLFNQ	120
QY	672	QOLSTRIPSYVDSSNTNPPQFMAAGVAINVQSGRLQINRAKFSANGCGVLEK	731
QY	121	QOLSTRIPSYVDSSNTNPPQFMAAGVAINVQSGRLQINRAKFSANGCGVLEK	100


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QY 732 PGCMCGYFNNSDPLPGQLKQLVIRIISGQLPRPRDMLDREIIDEVEVEITG 791
DB 181 PGCMCGYFNNSDPLPGQLKQLVIRIISGQLPRPRDMLDREIIDEVEVEITG 240
QY 792 LPVDCSREOFYVNDNGFNPMWETLVFVNHMPETALVRLVMDHDPDIGNDFIGQRTIAF 851
DB 241 LPVDCSREOFYVNDNGFNPMWETLVFVNHMPETALVRLVMDHDPDIGNDFIGQRTIAF 300
QY 852 SSMPGGRHYVLEGMEEASIFVHVAVSDISGKVAQALGLGLRGRKPGSLDASHAGRP 911
DB 301 SSMPGGRHYVLEGMEEASIFVHVAVSDISGKVAQALGLGLRGRKPGSLDASHAGRP 360
QY 912 PARVSQRLIRRTASAPRTSQKPRGRGPELVLTGRTDTSKGVADVVPGRGPAPEAR 971
DB 361 PARVSQRLIRRTASAPRTSQKPRGRGPELVLTGRTDTSKGVADVVPGRGPAPEAR 420
QY 972 AOEGRPGSGRGAAPAAVAKSPVPRVPLVPGPAGAAATCMKCVGSCAGVTGGL 1031
DB 421 AOEGRPGSGRGAAPAAVAKSPVPRVPLVPGPAGAAATCMKCVGSCAGVTGGL 480
QY 1032 QERPRSPGASROAAIROQPARADSLGAPCCGLDPHAIIPGRSRAPKPGAMROGPGG 1091
DB 481 QERPRSPGASROAAIROQPARADSLGAPCCGLDPHAIIPGRSRAPKPGAMROGPGG 540
QY 1092 SGMSDSSDSSPSPGIPERSPRMPEGACRQPGALOGEMSAITRAQKLEIRSKSPMFSACK 1151
DB 541 SGMSDSSDSSPSPGIPERSPRMPEGACRQPGALOGEMSAITRAQKLEIRSKSPMFSACK 600
QY 1152 PLIPCVYLPHAPMAGPGSPAAASAMTVSPRYLVALVPMHCLRGTLTLPWLACGP 1207
DB 601 PLIPCVYLPHAPMAGPGSPAAASAMTVSPRYLVALVPMHCLRGTLTLPWLACGP 656

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RESULT 2
090PT3 PRELIMINARY: PRT: 787 AA.

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AC 090PT3:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE KIA1069 protein (Fragment).
GN KIA1069.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE=99397452; PubMed=10470851;
RA Kiluno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.
RL DNA Res. 6:187-203(1999).
DR HSP; AB028992; BAA83021.1; -.
DR HSP; P10688; IDJH.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PL_PLC-X; 1.
DR Pfam; PF00387; PL_PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PPHILIPASEC.
DR Prodom; PD001202; PL_PLC_Y; 1.
DR SMART; SM00339; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PSS0004; C2_DOMAIN_2; 1.

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DR PROSITE: PSS0007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PSS0008; PIPLC_Y_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 787 AA; 89169 MW; 2EFC0355E4C0FC8D CRC64;

Query Match 36.7%; Score 2343; DB 4; Length 787;
Best Local Similarity 61.4%; Fred. No. 1.2e-139;
Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;

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QY 239 DLYLMLTYSNHKLDAASLORFLOEOKMAGVLESCODIIRFOECPENKSKGLIGI 298
DB 1 DLYLMLTYSCKKDLHYELAEAFKAYOKANNVTYDCLDIKKEFEVEENKKNVYGI 60
QY 299 DGFYVTSPPAGDIPNPHHHVHODMTPLSHYFTSSSHNTYLVGDQLMSQRYDAMV 358
DB 61 EGFYVTSPPAGDIPNPHHHVHODMTPLSHYFTSSSHNTYLVGDQLMSQRYDAMV 120
QY 359 IQAGRCVEVDCMDGDEPIVHGGYTLTKLTKRDVETINAKAFIKNEYVILSTENH 418
DB 121 IQAGRCVEVDCMDGDEPIVHGGYTLTKLTKRDVETINAKAFIKNEYVILSTENH 180
QY 419 CSYIOQKMAOYLNDILGDKLIDLSVSEDAATLPSQMLKGLTVGKILPANISHDAE 478
DB 181 CSYIOQKMAOYLNDILGDKLIDLSVSEDAATLPSQMLKGLTVGKILPANISHDAE 240
QY 479 EGEVSEDESADEIDDDCKL-LNGDASTNRKRYENTATRKLDLSIKESKINDCEDPNFVS 537
DB 241 EGEVSEDESADEIDDECFKLIHNSGTEHQVESFIRKLESLIKESQIDKDEDPDSFTV 300
QY 538 STLSPSGRLGRKS--KAEDY-ESGEDAGASRRGRGLVVSFSRRKKSKLTKKASVEE 594
DB 301 RALLKATHEGLNAHLKOSPDYKESG-----KSHGRSLMTNFGKHKTTSRKSSTYSTD 355
QY 595 GDEGODS---PGGSRATROKTMKLSRLSDLVYTKSVATHDIEMAASSMOVSSFS 651
DB 356 EEDTQOSTGKEGGQLYRLGRRRKTMKLCRELSDLVYVTSVAADI-VDDGTGNVLSFS 414
QY 652 ETKAHLIQOKPAQYLRFNOQLSRIPSSRYVDSYNNQPPMNMAGQVAMANTYSEGR 711
DB 415 ETKAHLIQOKPAQYLRFNOQLSRIPSSRYVDSYNNQPPMNMAGQVAMANTYSEGR 474
QY 712 MLOLNRAKFSANGCGYVLPKGCOCGVFNPNSEDLPGQLKQLVIRIISGQLPKPRD 771
DB 475 MLOLNRAKFSANGCGYVLPKGCOCGVFNPNSEDLPGQLKQLVIRIISGQLPKPRD 534
QY 772 SMLDGRGEIIDPVEVEIIGLPVDCSREOTRYVDNGFNPMWETLVFVNHMPETALVRF 831
DB 535 SMLDGRGEIIDPVEVEIIGLPVDCSREOTRYVDNGFNPMWETLVFVNHMPETALVRF 594
QY 832 LVMDHDPDIGNDFIGQRTIAFSSMPGGRHYVLEGMEEASIFVHVAVSDISG----- 882
DB 595 LVMDHDPDIGNDFIGQRTIAFSSMPGGRHYVLEGMEEASIFVHVAVSDISG----- 654
QY 883 -----KYKALIGLGLRGRKPGSLDASHAGRPAPRVSQRLIRRTASAPRT 931
DB 655 STYILFLFGLATKRNQLOGLGKFNKNPRHSSSENN--HYVKKRSIGRILIRRTASAPAK 712
QY 932 SQKPRGGRPELVLTGRTDTSKGVADVVPGRGPAPEAR 957
DB 713 GRKSKGQFQEMV-EIKDSVSEATRD 737

```

RESULT 3
090YGI PRELIMINARY: PRT: 1128 AA.
AC 090YGI:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase C-12.
GN PLC12 OR PLC2 OR PLC-L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20050058; PubMed=10581172;
 RA Otsuki M., Fukami K., Kohno T., Yokota J., Takenawa T.;
 "Identification and characterization of a new phospholipase C-like
 RT protein, PLC-L2."
 RL Biochem. Biophys. Res. Commun. 266:97-103(1999).
 DR EMBL: AB03615; BAA89457.1; .
 DR HSSP: P10688; 10AS.
 DR MGD: MGI:1352756; PLC12.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 1128 AA; 125763 MW; 8598CC59D89ADC65 CRC64;

Query Match 24.98; Score 1587.5; DB 11; Length 1128;
 Best Local Similarity 36.58; Pred. No. 1.1e-91;
 Matches 352; Conservative 168; Mismatches 280; Indels 165; Gaps 21;

OY 4 PTAGPLPGLPAPLP-----EDPGDPSPSRMLFLSANILPYVER-----CMGAMQEG 48
 DB 88 PAAGPVRDSKPGGLPRRSSTINDQTKQKREKKTVSFSSMPFEKKTSSASDCIHSVVEG 147
 OY 49 MOWKVLKSGSKGLVRYFYLDENHSCITWRPSRK-NEAKAISIDSIOVSESGROSEVQRX 107
 DB 148 SELKKVNSRIRYHRYFLDLADQSLRMEPSKDKSEKAKIDIKSIKVRKGNKIDIFR-- 205
 OY 108 PDG---SFDPRCCSIYHSGHRESLDVSTSSSEVARTWVGLRYTMA-GISDEDSLARQ 163
 DB 206 SNGISEQISEQCAFSAVYIGENYESLDLVANSADVANIWVGLRLISYCKHTLDMLESSQ 265
 OY 164 -RTRDQWLKQTFDEADKNGDLSLSIGEVQLLHLKLVNLPQRYVQKQFREA-DTDDHOGT 221
 DB 266 DNMRTSWISQMFSEIDVDGLCHITLCHAVOCIRMLNPGIKTSKIELFKELHKSCKDAGT 325
 OY 222 -LGFEEFCATFKMMSTRDLYLLMLITYSNHNDHLDASLOFLOVEKMACVTLESODI 280
 DB 326 EITKEEFLEVEHRELTREITFELLVOFSNKEFDTKDLMFLEEGVAINESISLEI 385
 OY 281 IEQFEPCEPKSKGLIGIDGFTNTYRSPAGDIFNPEHHHVDMTQPLSHYFTSSNNTY 340
 DB 386 IHKYPSEKGEQKGLSDGFTNYLMSDVCYIPDEHKHVKQODMKOPLSHFINSNTY 445
 OY 341 LVGDQMSOSRVDYAMVLOAGRCVENDCDPGEDEIVHAGTLYTSKILFKVNIENY 400
 DB 446 LTEDDFRGSDITGYIRALKMKGRSVELDVMDPNEPVYVYGTMTSQTIVFRSYDILIN 505
 OY 401 KYAFIKNEPVLTISIEHNSVLTQKKMAQYLTDILGDKLIDLSVSESDATTLPSPMOLG 460
 DB 506 KAFPAFSEFPLTCLNHSIKQKQVWQHMKKILGDKLYTSPMWEB-SYLPSPDVLKG 564
 OY 461 KILVKGKILPANI SEDAEGEVSDSDADEIDDCIKLLNGASTNRKRYENTAKKLDL 520
 DB 565 KILIKAKKILSSNCS--GVGADVTDDEGAEM-----SORMKRENV----- 602

OY 521 IKESKIRDCEDPNPNFSVSTLSPSGIKGRSKAEDEVEDSGDAGASRRNGLVYGSFSRRK 580
 DB 603 -----EQPNHVPV----- 610
 OY 581 KKSGLKKAASVEGDEGDSGGSGSRGATROKTKMTLSRALSDLYTKTSVATHD--IE 638
 DB 611 -----KRFOLCKELSELVSTIGCSVQFKERQVS 637
 OY 639 MEAASMOVSSFSETKAHQILQOKPAQYLRPNQOOLSRITPSSRYDSSNYPNPQPEWNA 698
 DB 638 FQVQKTYEVCNFENYLAASKYANENPGDVNNKRFELARVPSPARIDSSNMNPQDFKCG 697
 OY 699 COMVALNTQSEGRMLQINRAKFSANGCGGYLAKGCMQGY--FNPSSEPLPQOLKOL 756
 DB 698 CQIVAMNFOTGLMMDLNVGWFNRQNGCYLRPAIMKEEVSFSPSATKDSVPSQDL 757
 OY 757 VLRITSGOULKRPBSMLGDRGEIIPDVEEIIIGLPVDCSREOTRVYDNGFNPTEET 816
 DB 758 HIKIISQNFPPKPGS--GANGDVVDVYVEIHGIPADCAADRKTIVNONGDAPRIFDES 815
 OY 817 LVFVHMPLEIALVRLVMDHPDPIGRDFIGORTLAFSSMMPGYRHYLT----EGMEEAS 871
 DB 816 FEFQINPELANVRVYVDDVDYIGDEFIQYTIPECIQTGYRHHVPLQSLTGEVLAHSL 875
 OY 872 EVHVAVSDISG-----KYQALGLKGLFLRQPKGSLDS-HAAGPPAPR 915
 DB 876 FVHVATITNRGGGKPKHKKRLSVKGGKREYASLFTLWIK-----TVDEFKRNAPPIRD 930
 OY 916 SVSOR 920
 DB 931 ATDLR 935

RESULT 4
 O8WUS6 PRELIMINARY; PRT: 716 AA.
 ID O8WUS6;
 AC O8WUS6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Hypothetical 75.7 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Stransberg R.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC019679; AAH19679.1; .
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KW Hypothetical protein.
 FT NON-TER 1
 SQ SEQUENCE 716 AA; 75724 MW; 148244B142852AB0 CRC64;

Query Match 24.88; Score 1583.5; DB 4; Length 716;
 Best Local Similarity 61.58; Pred. No. 1e-91;
 Matches 350; Conservative 19; Mismatches 101; Indels 99; Gaps 14;

OY 697 AGCOMVALNTQSEGRMLQINRAKFSANGCGGYLAKPCMCQGYFNPNSDEPLPQOLKOL 756
 DB 1 AGCOMVALNTQSEGRMLQINRAKFSANGCGGYLAKPCMCQGYFNPNSDEPLPQOLKOL 60
 OY 757 VLRITSGOULKRPBSMLGDRGEIIPDVEEIIIGLPVDCSREOTRVYDNGFNPTEET 816

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Db 61 VLRISGQQLPKPRDSMLDGRGELIDFEVEIIGLPLVDCSREGTRVVDNGFPTDEET 120
QY 817 LVFWVHMEILVRLVWDHDPICRDTLGGOTLAFSSMMEGYRIYVLEGMEASIFVHVA 876
Db 121 LVFWVHMEILVRLVWDHDPICRDTLGGOTLAFSSMMEGYRIYVLEGMEASIFVHVA 180
QY 877 VSDISGRVKALGLKGLRGPCKGSLDSHAAGRPAPSVSQRILKRTASAPTKSKPG 936
Db 181 VSDISGRVKALGLKGLRGPCKGSLDSHAAGRPAPSVSQRILKRTASAPTKSKPG 240
QY 937 RRGPELVIGTRDGSAGVADVVPPGPPAPAPAOEGSGSSPRKAPAAVAEKSPVR 996
Db 241 RRGPELVIGTRDGSAGVADVVPPGPPAPAPAOEGSGSSPRKAPAAVAEKSPVR 295
QY 997 VRPP-----RVLDGPPAGMAATCMKCVSGAGVGTGLOLHRRPSR--GPASRQA 1046
Db 296 PLPLCLSLLETIAEPAPAGPPPPPPA-----VFTSSQ--GRPYPTGPGANVA 342
QY 1047 AIKQAPARADSLGAPCCG-----LDPAHAPGRSR-----EAPK 1080
Db 343 SPLDEEPEPDSRPRPCNEGAGAYERAPGSGTDRSOPRTLGLPYLRVASEGQVPT 402
QY 1081 GP-GAWR-----QGPGSGSSSDSSSPSPGIPERS--PR 1113
Db 403 EPIGGRPLAAPPAPAVYSDATGSDPLMORLEPCGRHDSVSSSSSSSDTYIDLSTPS 462
QY 1114 WPGACRO--PGALGEMSALEPAQKLEIRSKSPMFSACKPLPLPCVYLPHA--PGMAGPS 1170
Db 463 LGLGRRENLAGAHMGRLP-----PRHSASAPRPLPYTKSKSPNPLRATQO 511
QY 1171 -----PAASAMVYSPRYLVALLVLPWHL 1195
Db 512 RPIPELQPRSLAPMAGLPPRPWGCL 540

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RESULT 5
Q9UPRO
ID Q9UPRO PRELIMINARY; PRT: 1154 AA.
AC Q9UPRO:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE KIA1092 protein (Fragment).
CN KIA1092.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. XIV.
RT The completion of the coding sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.*.
RL DNA Res. 6:197-205(1999).
DR EMBL: AB029015; BAA83044.1; -
DR HSSP: P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001192; PL_PLC.
DR InterPro: IPR000909; PL_PLC_Xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00388; PL_PLC-X; 1.
DR Pfam: PF00387; PL_PLC-Y; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00390; PHPLIPASEC.
DR ProDom: PD001202; PL_PLC_Y; 1.

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DR SMART: SM00239; C2; 1.  
DR SMART: SM00233; PH; 1.  
DR SMART: SM00148; PLCYC; 1.  
DR SMART: SM00149; PLCYC; 1.  
DR PROSITE: PS50004; C2_DOMAIN_2; 1.  
DR PROSITE: PS50003; PH_DOMAIN; 1.  
DR PROSITE: PS50007; PL_PLC_X_DOMAIN; 1.  
DR PROSITE: PS50008; PL_PLC_Y_DOMAIN; 1.  
FT NON_TER 1  
SEQUENCE 1154 AA; 128371 MW; 848B2744ADE5A334 CRC64;

```

Query Match 24.7%; Score 1578; DB 4; Length 1154;
Best Local Similarity 36.4%; Pred. No. 4,6e-91;

Matches 357; Conservative 166; Mismatches 279; Indels 180; Gaps 24;

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QY 2 APPTAGP-----LPGPA-----LPPED--PGDP-----ESRWLFSLANILPV 37
Db 97 ASPTGPGVALAPRPSAVVCTLPRESKPGGLPRSSITIKGTOKERKKTVSFSSMPT 156
QY 38 VER-----CMGAMQGMVYKLGSKGLVRYLDEHRSICIRMPSPRK--NEKAKTID 90
Db 157 EKKISSASDCINSWEGSELKRVNSRIYHRYFLDLADMSLWEPDSKDESEKADIK 216
QY 91 STOEYSEGRSEVFRYRDSFED---PNCPSIYHSHRESLDLVSTSEVARTWTGLR 147
Db 217 SIKEVTRKNTDIR--SNGISDQISEDCAFSVIYGENYESLDLVANSADVANIWTGLR 274
QY 148 YLMA-GISDEDLSLARO--RTRDOWLKOTFEADKNGDSLGSIGVQLLKLNVNIPROR 205
Db 275 YLISYGHKHTLMLLESSODNMRTSWVQSEIDVDNGLHTLCAVOCINLNLPGKLTSK 334
QY 206 VKOMEREA-DTDDHOGT--LGEERCAFYKMASTRDILYLMITYSNKHDLAASLQRF 263
Db 335 IELFKELHKSCKDAQTEVTEKEFEVFEHLCYRPEYFLLYVQSSNKEFLDKDLMFL 394
QY 264 QVEQKMAVTLDESCODITIEQFEPCKENSKGLLIGIDFTYNTSPAGDIPNPHHHVOD 323
Db 395 EAEQVHAINHEISLEIHHKYEPSKEQEGKWLSDIGFTYMLSPDCTYFDPKHKVYCD 454
QY 324 MTOPLSHYFTTSHNTYLVGDQLMSOSRVDMYAVYLQACRCVEVDMGDPDEPTVHG 383
Db 455 MKQPLSHYFTTSHNTYLVGDQLMSOSRVDMYAVYLQACRCVEVDMGDPDEPTVHG 514
QY 384 YTLTSKILFDVLETTINKYAFIKNEYPVILSTINHSVIOOKMAQYLLDIDGKLDSS 443
Db 515 HTMSQVFRSVYDIINKYAFASBPFLILCLNHSISIKQKVMYVHMKLLGDKLYTTS 574
QY 444 VSSEDAITLPSQMLGKTIYVGRKLPANTISEDAGEVSEDESDAEDIDCKILNGAS 503
Db 575 PNVEE--SYLSPDVLKGLIKILKAKKLSNCS--GYEGDVTDEDEGAEV----- 619
QY 504 TNKRREYNTAKRKLDSLKESKIRDEDPNNSVSTLSFGKLGKRSKAEDEVESEGDAG 563
Db 620 SQMKGEN-----MEQPNVY----- 636
QY 564 ASRRNGRLVYGSFRRKKKSKLKAASVEEGDEGDSGSGRGATROKTKMTKLSRALS 623
Db 637 ----- 646
QY 624 DLYKTKSAVATHD--TEMAASSWOVSSEFKAHQIILQKPAQYLRNQOOLSRITPSS 681
Db 647 ELVYSICKSVQFEFOVSFQVORYWEVCSFNEVLASKYAEENGDVYNNKRLRALVFPSP 706
QY 682 YRVDSNYPNPPFWNAGCOMVALNTOSSEGRMLQLNRAFPANAGCGGYLAKGCMQGY-- 739
Db 707 MRIDSSNMNPQDFWKGCGOIVAMNFOTPLMDLNLIGFVRONGCGYLRALNKEEVSF 766
QY 740 FNPSEDLPLGOLKQVLRILISGQQLPKPRDSMLDGRGELIDFEVEIIGLPLVDCSRE 799
Db 767 FSANTKSVYGPVSPOLHNLKTIISQGNPKPKGS--GAGGVADVPPVYVYHIGITADCAEQ 824
QY 800 QTRVVDNNGFNPTWEETLVFWVHMEILVRLVWDHDPICRDTLGGOTLAFSSMMEGYR 859

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Db 825 RTKTVHONGDAPITFDESEFQINLPELMAWRFVYVDDDYIGDEFIQYTIPEFCLDTGYR 884
 QY 860 HAYL-----EGMEASIFVHVAVSISG-----KYQALGLKGLFTRGPKR 899
 Db 885 HVPLOSLTGVLAHSLFVAITNRGGGPKHKGISYKKGKSRSEYASLRTLMWK--- 941
 QY 900 PGSLIDS-HAAGRPAPPSVSQR 920
 Db 942 --TVDEVEFKNAOPPIRDATDLR 961

RESULT 6

Q15111 PRELIMINARY; PRT; 997 AA.
 AC 015111;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Phospholipase C
 GN PLC-L (PLC-EPSILON)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9535973; PubMed=7633416;
 RA Kohno T., Otsuka T., Takano H., Yamamoto T., Hamaguchi M., Terada M.,
 RA Yokota J.;
 RT "Identification of a novel phospholipase C family gene at chromosome
 RT 2q33 that is homozygously deleted in human small cell lung
 RT carcinoma."
 RL Hum. Mol. Genet. 4:667-674(1995).
 DR EMBL; D42108; BA07688.1; -
 DR HSSP; P10688; IQAS.
 DR Interpro: IPR000008; C2.
 DR Interpro: IPR001849; PH.
 DR Interpro: IPR001192; PL_PLC.
 DR Interpro: IPR000909; PL_PLC_Xdom.
 DR Interpro: IPR001711; PL_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00380; PHPLIPASEC.
 DR ProDom; PD001202; PL_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCY; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 997 AA; 112955 MW; 08D3CEC28AD652B7 CRC64;

Query Match

23.9% Score 1524.5; DB 4; Length 997;

Best Local Similarity 36.2%; Pred. No. 9e-88;
 Matches 348; Conservative 158; Mismatches 279; Indels 177; Gaps 20;

QY 41 CMGAMQGMQVRLRGSGKLVFYLDEHRSCTIRNRPSPRN-EKAKISIDISIOEVSQR 99
 Db 13 CIFMQAGELKAKVRNRSRYNRFILDPDIALRWEPSSKDEKAKLIDSAIKETRLGK 72
 QY 100 QSEVFORIPPGSPD---PNCCEFIYSGHRESIDLYSTSEVNRWVGTGLRYIMACISDE 156
 Db 73 NTEIFTN--NGLADQICECPAFSILGENTESLDVANSADVANINWVSGRLIVSSKOP 130
 QY 157 -DSLARQRT-RDQWLKOTFDEADKNGDSLSIGEVYQLLHLKLVNLPROVRQMRREAD 214
 Db 131 LDFMEGNQNTPRFWMLKTVFEADVDVONGIMLIDTSEVLKQLNPLTKLKAIRLKRFEIQ 190

QY 215 TDDHOGT--LGFEEPCAFKYMNMSTRDLYLMLTYSNKHDLDAASLQRLQVEQKACV 272
 Db 191 KSKKELITTRVTEEEFCEAFCELCSTRPEYVLLVQISKNNKEYLDANDLMLFLEAGGYTHI 250
 QY 273 TIESCODITDEPPEPCENKSKGLIDGTNTYTRPADIDFNRPHNHOMTOPLSHYF 332
 Db 251 TEDIICIDITIRRYLESEEGKQGFALIDFTQYLLSSECDIDPEEOKKAAQDPTOLSHY 310
 QY 333 ITSSHTYLVGDSQSVDMYAWYLQAGRCVENDCDGPDGPPIVHGYTLTKILF 392
 Db 311 INASHNTYLIEDQFRPADINGIYIRALKMGCSVELDSDGSDNEPILCNRRNMTTHVSE 370
 QY 393 KDVTETINKYAPLKNEYPIVLSIENHGSYIQKKAQYVITLIDGLKDLSSVSSDATT 452
 Db 371 RSVIEYINKFAFVASEYPLILGHNCSLPQOKVAAQOKKFKYGNKL-YTEAPLSESLV 429
 QY 453 PSMQMLKGLIVYKGLPLNPISDAEEGVSDESDADEIDDDCKLLNGDASTNRKREVT 512
 Db 430 PSEKLRMIVYKGLPLPSD--PDVLEGEVYDSD----- 461
 QY 513 AKRKLDSLIKESKIRDCEDPNNFSVSTLSPSGKLGKRAEDVESGEDAGASRRNGRLV 572
 Db 462 -----EQAQMSRR----- 469
 QY 573 VGSFSSRRKKKSKLKAASYEGDEGODSPGCGSRGATQKTKMLSLDLYKTKSV 632
 Db 470 -----MSVDYNGE-----QKQIRCRELSDLVSTICKSV 497
 QY 633 ATHDIE--MEASMSOVSSEFETKAHQLQKPAQYLFENQOLSRITYSSRYVDSNNY 690
 Db 498 QYRDFELSMKSONYEMCSSETEBASIAHVEDEYVNNKRLTIYSAMHDSNNL 557
 QY 691 POPFWNAGCQVVALNTYSEGRMLQLNPAKFSANGCGGYLKPCKMCGV--FNPNSDEL 748
 Db 558 PODEFWNCGCQIVAMNFQTPGPMMDLHTGWFLOMGCGGYVLRPSIMDEVSYSFANTKGL 617
 QY 749 PGOLKQVLRLITSGOGLPKPRDMLGDRGEITIDPEVEIILGLPYDCSEGRVAVDDNG 808
 Db 618 PGVSPPLHLIKITISGQNFPPKGA--KGDVDPYICITIHGIPADCSQKRTKYQNS 675
 QY 809 FNPMEETLVFMVAMPPIALVFLWMDHPIDGRFIGNRTIAPSSMMPGGRHYVLEGG--- 865
 Db 676 DNPLFDEFEEFQVNLPELAMIRFVYVDDDYIGDEFIQYTIPEFCLDPGYRHVPLRSFVG 735
 QY 866 --MEASIFVHVAVSISG-----KYQALGLKGLFTR-----GP 898
 Db 736 DIMEHVTLEFVAITNRSGGKAKQKRSLSYMGKRVETMLRNIGLTKTIDTIFKIAVHP 795
 QY 899 KPGSID-----SHAAGRPAPPSVSQRLRRASAPTKSQKPG-----RRGFP 941
 Db 796 LREALDMERNQNAIVSITKELGILPPI-ASLAKQCLLITLSLITSDMTSPSVLMKDSFP 854
 QY 942 EL 943
 Db 855 YL 856

RESULT 7

Q62688 PRELIMINARY; PRT; 1096 AA.
 AC 062688;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 130kDa-Ins(1,4,5)P3 binding protein.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MISTAR; TISSUE=BRAIN; MEDLINE=96132642; PubMed=8546702;

QY	41	CMOMEGOMVYLRGSGSGLYFRYYLUDBNHSCIRMPRSKN--BKAKTISIDISOEVS	EGR 99
Db	112	CISFMQGCBLKRVAPNSRIYVNFETTLTDLOALMEPSCXKDEKALISAKIETRG	171
QY	100	QSEVFORYPDGSF--PNCFSIYHSGHSRLDLVTSFSEVARTVYTGRIYMAGISD	156
Db	172	NTEFTFN--NGLADQICEDCAFSILGHENYSIDLVDANSADYANIVYSGIRIYVSSK	229
QY	157	-DELARORT-RDOMLKOTFDEADKNGSGSISTEVIQLHLKLVNLPRORYOMFREAD	214
Db	230	LDMENQNTPPRMVTKTYFEALADVDGIMLEDTSVELIKOLNPLTKESKIKLFEKIQ	289
QY	215	TDDHQT--LGEFECARVKKMSTREDDLYLMLTYSHNKHOLAASQRLYOEOMAY	272
Db	290	KSEKELTYRTEEECECAFCELTCPREYVYLLVQISKNKEYDANDMLFLEEGQVTHV	349
QY	273	TEESODDIEQEPCEPKSKGGLGIDGFTVYTRSPAGDIFNEHHVHODMTOPLSHYF	332
Db	350	TEDMCDDIRRELSSEDRQRGLADGFTQYLLSPEDCIFDEQKKVADOMTOLPSHY	409
QY	333	ITSNHTYLVGDOLMSOSRVDYAMVLOAGRCVYOCMCPGCEFTVHHGTYLISKILF	392
Db	410	INASHNTYLIEDQFGRPADINGYRALAKMCRSTELDVSDGPNEBTLCNRNMMLTSF	469
QY	393	KVIETINKYAFIKNEYVYLITFNHCSVTIQKRMAYLLDILGDYKILDS--VSESDAT	451
Db	470	KSVLELVINKFAFVASEPYLLICLGNHCSLPQORVMYQOMKRYGKNLYTEAPLSE--SY	527
QY	452	LPSPOLMKGILVYVGLKLPANISDEDAEEGVSDESDADELDDCKILNGDASTNKRVEN	511
Db	528	LPSPEKLKHMIIYVGGKLP--ESDLLEGVTEED-----	560
QY	512	TAKRRKLDSLKESKIRDCEDPNNVSVYTLSPSGLGRKKAEDYVESGEGDAGASRRGL	571
Db	561	-----EEABMSRR-----	568
QY	572	VYGSRSRRKKKGSYLKAAVYEBGDGQDSPGQSGKATRQKTKMLSRALSDLYVTKTS	631
Db	569	VSGDIN-----GECKHWLCRELSIDVSLICKS	595
QY	632	VATHDIE--MEAASSMQVSSFSFETKAHQILOQPAQYLRFNNOQLSRITYPSSYRVDSNY	689

DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Phospholipase C delta 4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith T.P.L.;
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF988759; AAM1812.1; -
 SQ SEQUENCE 772 AA; 88075 MW; 8655706A4247548 CRC64;

Query Match	22.9%	Score 1463	DB 6	Length 772
Best Local Similarity	38.9%	Pred. No. 4,8e-84		
Matches 339	Conservative 140	Mismatches 264	Indels 128	Gaps 21
Qy	35	LPVVERCMAMOGMOMVLTIRGSGGLVFRFYLLDEHNSCIWRRPSRNEKAK--ISIDSI	92	
Db	16	LPINOLL-LIMKGIMLRVVRKSKWKRLRYRLDDGMTV- <u>W</u> HARQAGRAKPSFSISDY	73	
Qy	93	QEVSEERSEVEFORYPDGSFDPNCESFYHSHSIEDLYVSSEVARTWYGLRTIMAG	152	
Db	74	EYVRGHESELRLNLA-E-FPLDGFTLVFRGRSNDLVANSVEEAQVMQGLDILVPT	132	
Qy	153	ISDESLARQRTDQWIKOTFDEADKNDGSLSIGEVLQILHLNVLNPRQVKRMERE	212	
Db	133	VINMD---QQRILQWISDMFQRDKKQDQRMSEFGEVQYKILHNVENDQEHAFQLFPT	188	
Qy	213	AQTDHQGLGFEEBCAFYKKMSTRRDLIYLLMTLYSNHKDHLDAASTLQRFLEQKMAVY	272	
Db	189	AQT-SQSGTLEEFEVEFYKSLTKRAEYQELFENFSSDQKLILLEFVDFLEQKEGR	247	
Qy	273	TLESQDILIEQEPREPKSKGLGIDGFTNYTRSPAGDIFENHHNVHODTQPLSHYF	332	
Db	248	ASDLAEILDRHEPDSGKLRHNVLSITGLSYLCSKDGIFLPTFCRIYDQMTQPLNHFF	307	
Qy	333	IRSSHNTLVAGDOLMSQSRVDMYMWVLQAGRCVENDCMQDPRGGEYVHNGTTLISKILF	392	

Db 308 INSSNHTYLVGDLQCGSSVEGYIRALAKGRCVENDIWDGPNRGPVYVYHGTILSRIF 367
 Qy 393 KVIETINKYAFIKNEYPYLILSIENHCYSIQKKAQYLTDLGDKLDSVSSSEDTAT 452
 Db 368 KDVVAIAAQYAFQTSYDYPVILSIENHCSEWQEMAHNLTLEIGDLSTLDGOLPTOL 427
 Qy 453 PPSQMLKGLKYLKGLKPLANISDAEGVSDSDSDELDIDDOCKTLNGASVNRKRVEMT 512
 Db 428 PSEPELRKRLVKGKTL-RTLEEDLEEEDEPESE-----LEG-----EDE 468
 Qy 513 AKRKLDSLIKESKIRDCEDPNNFSVTLSPSGKLGRRKKAEDVESGEDAGASRRNGRLV 572
 Db 469 AELELEAGEF-----SEPOE-----LSPRSK----- 489
 Qy 573 VGSFSRRKKSKRLKKAASVEEGDEGDSFGGSGRATROKTKMTKLSRLSDLVYTKTSY 632
 Db 490 -----DKKKVKAT-----LCPLALSALVYLVKAV 513
 Qy 633 ATHDI--EMEAASMOVSSPSETKAHQILOQKPAQYLRFNQOOLSRIPSSYRVDSNTN 690
 Db 514 SFSFASRHRHYRFEYLSISSESEAKASLIKESGNEFYQHNTQOLSKRYTPOGLTDSNTN 573
 Qy 691 POPFNAGCOMVALNTOSEGRMLQLNRAKESANGGCGYVLKPGCM--CQGVNPNSEDEL 748
 Db 574 POEFMAGCOMVAMNMQTAGLEMDLDCGLFRONAGCGYVLKPDPLRDAQGSFHP--ERP 631
 Qy 749 PGOLKQOLVRIISGOOLPRPDSMLGRBEIIPFVEVEIIGLPVDCSEEGTORYVDNG 808
 Db 632 SPKSAQTLTLOVTSGGOLPRVDS--KESTYDPLVRLVEIFGVPRPTAOGSTIYVNNG 688
 Qy 809 FNPWEETLVFVMPHMEIATLVRLVMDHPDIPGR--DFIGQRTLAFFSSMMPGRHYVL--E 864
 Db 689 FNPWGTQICRVLVPELALLRFVYKDYDMKSRNDFGQYTLTPWNCMOGVRHILHLSKD 748
 Qy 865 G--MEASIVFVAVSDISGKVKQALGKL 893
 Db 749 GISLHPASIFVHICIRE-----GIEGV 770

RESULT 9
 Q9BRCT PRELIMINARY; PRT; 762 AA.
 ID Q9BRCT
 AC 09BRCT
 DT 01-JUN-2001 (Tremblere, 17, Created)
 DT 01-JUN-2001 (Tremblere, 17, Last sequence update)
 DT 01-JUN-2002 (Tremblere, 21, Last annotation update)
 DE Hypothetical 87.6 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006355; AA06355.1;
 DR HSSP: P10688; IQAS.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PL-PLC.
 DR InterPro: IPR000909; PL-PLC_Xdom.
 DR InterPro: IPR001711; PL-PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00388; PL-PLC-X; 1.
 DR Pfam: PF00387; PL-PLC-Y; 1.
 DR PRINTS: PR00390; PHPLIPASSEC.
 DR ProDom: PD001202; PL-PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00554; EFh; 3.

DR SMART: SM00239; PH; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; EF_HAND; UNKNOWN_2.
 DR PROSITE: PS50018; PH_DOMAIN; 1.
 DR PROSITE: PS50003; PL-PLC_X; 1.
 DR PROSITE: PS50007; PL-PLC_Y; 1.
 DR PROSITE: PS50008; PL-PLC_Y; 1.
 DR Hypothetical protein.
 KW SEQUENCE 762 AA; 87585 MW; 544BE5CE2AE3EF CRC64;
 Query Match 22.6%; Score 1441; DB 4; Length 762;
 Best Local Similarity 38.3%; Pred. No. 1,2e-82;
 Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;
 Qy 45 MEGEQMYVLRGSGVLFYLLDEHRCIRW--RPSRKNKAKISIDISQIEVSGROSE 102
 Db 18 MEGEQMYVLRGSGVLFYLLDEHRCIRW--RPSRKNKAKISIDISQIEVSGROSE 76
 Qy 103 VFORYPDGSFDPNCFSTIYHSHRESLIVSTSEVARTWTGLRYLMAGISDESLARR 162
 Db 77 LRLSLAEELPLEOGFTYVHG--RRSLDLMANSVEAOITMNGDLQLDVLYTSM--H 131
 Qy 163 QRTROQWLKOTDEADKNKGDSLSIGEVLLHKLINVLPRGRVKNFPEADPTDHOGLT 222
 Db 132 QERTLDQWLSDFQGRGNKODGKMSFOEYORLHLMVENDQYAFSLQADPT--SOSGTL 190
 Qy 223 GFEFCFAFYKMMSTRDYLMLTYSNHRDHLDAASLQRFLOEQKMAGVTLSCODITE 282
 Db 191 EGSEFYQFQKALTKRAVQELFESFADQKLTLEFLDPLQBEQKERTSELMLELD 250
 Qy 283 QEPCEPCKNSKGLIGDFTNTRSPAGDIFENHHHVDMDTOPRSHFITSNHTYLV 342
 Db 251 RYEPSDQKRLHVLSDMGDTLYSCSKDGFENACLPITQDMTOPRSHFITSNHTYLV 310
 Qy 343 GDOLMSQRYDAMVYLQAGRCVEYVDCWDGPDGEPVHNGYVLSKILFKDVIETINKY 402
 Db 311 GDOLCGOSSVEGIRALAKRCRCVEYVDMGPGEGEVYVYHGTILSRIFKDVAVTAQY 370
 Qy 403 AFIKNEYPVILSIENHCYSIQKKAQYLTDLGDKLDSVSSSEDTATLPSPQMLKGL 462
 Db 371 AFQTSYDYPVILSIENHCSEWQEMAHNLTLEIGDLSTLDGOLPTOLPSEPELRKRL 430
 Qy 463 LVYKGLKPLANISDAEGVSDSDSDELDIDDOCKTLNGASTNRKRVEMTAKRKLDSLK 522
 Db 431 LVYKGLK--TLEEDL--EYEEBAEPELE-----SELM 461
 Qy 523 ESKIRDCEDPNNFSVTLSPSGKLGRRKKAEDVESGEDAGASRRNGRLVYGSFRKKK 582
 Db 462 ESKIRDCEDPNNFSVTLSPSGKLGRRKKAEDVESGEDAGASRRNGRLVYGSFRKKK 484
 Qy 583 GSKLKAASVEEGDEGDSFGGSGRATROKTKMTKLSRLSDLVYTKTSYV--THDIE 638
 Db 485 SKPI-----LCPLALSALVYLVKAV--S 511
 Qy 639 MEAASMOVSSPSETKAHQILOQKPAQYLRFNQOOLSRIPSSYRVDSNTNPOPFMAG 698
 Db 512 KEHHEFYISFSETKAKRLKEAGNEFYQHNTQOLSKRYTPOGLTDSNTN 571
 Qy 699 COMVALNTOSEGRMLQLNRAKESANGGCGYVLKPGCM--CQGVNPNSEDELPGOLKOL 756
 Db 572 COMVAMNMQTAGLEMDLDCGHFRONGCGYVLKPDPLRDAQGSFHP--ERP 631
 Qy 757 VLRITSGOOLKPRPDSMLGRBEIIPFVEVEIIGLPVDCSEEGTORYVDNGFNPTEET 816
 Db 630 LIOVTSGGOLPRVDS--KESTYDPLVRLVEIFGVPRPTAOGSTIYVNNG 688
 Qy 817 LVFVHMEIATLVRLVMDHPDIPGR--DFIGQRTLAFFSSMMPGRHYVL--EG--MEAS 870
 Db 689 LCFRLVPELALMRLRVYVDMKSRNDFIGQYTLPTCMOQGYRHILHLSKDGISLRPAS 746
 Qy 871 IFVHVAVSDISGKVKQALGKL 892

QY	45	MOEGHONAKKJGGSGILGRFYU--DENHSCILMRPSKRNEAKTISIDISIDVSEGRQSEV	103
Dd	18	MOGPMKMKVKTQKSMKIKRATRYRLODDGWTWNGHLESISKPTYSIDVETKRGQOSEL	77
QY	104	FORYPDSEDDNCCSESTYHNGHRESLDYVTSSEVARTWTGLRYLMAGISDESDIAR-	162
Dd	78	L-RYLYEERFLEGGFTYFENRRRLDVAANSVEAOTWNGQOLV-----DLYARMN	130
QY	163	-ORTRDOWLKQTFREBADRKNGDGSISIGEVLOLKLIVNLRPROUKOMFREAPTDHOQT	221
Dd	131	YQBDOLDKLRWFQOABRNDOSRMSFREAROLLLIMVNEDEVAEFGSLFEADLV--SQSNT	189
QY	222	LGFEEFCAYUKMSTRDYLMLLTUYNNHNDHDAASIGFLOVQORMAQVLTSECODIT	281
Dd	190	LDSEEFVQVYATLKRTIEIELEFENFSSDKOQLTLLEFVDFLEBQKESHSDSLAKYL	249
QY	282	BOFESEVENKSKGLGIDGFNTNRYSPAGIINFENHNHYNODTQORPLSHFTTSSNHTY	341

RESULT 11			
ID	017232	PRELIMINARY;	PRT; 895 AA.
AC	017232;		
DT	01-JAN-1998 (T-EMBLrel. 05, Created)		
DT	01-JAN-1998 (T-EMBLrel. 05, Last sequence update)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)		
DE	hypothetical I01.3 kDa protein.		
GN	K10F12.3.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea		
OC	Rhabditidae; Palodoridae; Caenorhabditis.		
NCBI_TaxID=6239;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		
RX	MEDLINE-99069613; PubMed-9851916;		
RA	None;		
RT	"Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium.,"		
RL	Science 282:2012-2018(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		
RA	Wohlmann P., Beck C.;		
RT	"The sequence of C. elegans cosmid K10F12.,"		
RT	submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		

Waterston R:
 RT "Direct Submission."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF025462; AAB71005.1;
 DR HSSP: P10688; 1DJH.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00233; C2; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCYC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PSS0004; C2_DOMAIN_2; 1.
 DR PROSITE: PSS0007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PSS0008; PIPLC_Y_DOMAIN; 1.
 DR Hypothetical protein.
 SO SEQUENCE 895 AA; 101303 MW; 424D2443D400655D CRC64;

Query Match 20.3%; Score 1297; DB 5; Length 895;
 Best Local Similarity 35.0%; Pred. No. 1.8e-73;
 Matches 310; Conservative 136; Mismatches 266; Indels 172; Gaps 23;

38 VERGCMAGQMGQVYKLGSGKGLVRYLYDEHRSCLRMWP-SRKNKAKISDSIOEVS 96
 46 VSDCMNMTQSDSDVYKLGTRKQPRRFFSLDADSLYIRWPTNKKPKHARIAIDREIR 105
 97 EGROSEVQRPDGSF---DPCNCFSTYHSHRESLDLVSSSEVATWTGLYLMAGI 153
 106 LGKNTLL-RSSDEVFDDLOECLEFSLIYGNYFTLLDIASSGDANVLMALYLNK 164
 154 SD-EDSLARORTDQMLKOTFEADKNGDGLSIGEVYQLHLNLVLPQRYKQMFRE 212
 165 YECKSSSQPTLKRWTLESFDEDTYKKNHDEQTFKALIHNSISHHRLTNLKE 224
 213 ADTDDHOGTLGFE-----FCAFYKMSSTRDLYLMLTYSNHKLDAASLQRF 262
 225 V-----TIGAESEERGIKESHVVDLYKIGTRPEVYFLMVRAN-KDYLSCODLTLF 276
 263 LOVEQKAGVYLESQDIIIOEPERPEKSKGLGIDGETVYTSPPADINPEHHVHQ 322
 277 LETEGMVGVTDTNCELTLEDEPESERENMLMTVDGFTSLFSPDCGVFDPNHRYVTM 336
 323 DMTOPLSHFITSNHTYLVGDQLMSQSRVDMYAVYLQAGRCVYVDCMD---GPDGP 378
 337 DKMOPFSRFTISSRSKSLVLEQDLPSSSSDGSFALKRNCRFLEFDLWDPREADGTEP 395
 379 IYHGGYTLTKLFRVDIETINKYFIKNEYVYLIENHGSVIOQKKAQYLTIDDK 438
 396 MYQNGOTATSKITISSARIIREFAFERSRYPLLKVSFHCSTDMOKVAAMLITVHLTR 455
 439 LCL-----SSVSEDAATLPSQMLKGLIYKGLKLPANISEDAEEGEVSEADEIDDC 495
 456 LVLKPNKPINWDEKKNCFPPQNRILYLGKLD---NPDDSEVSESD--DSL----- 506
 496 KLINGDASTNRKRVENTAKRLDSLKESKIDCED-----PNNFSVSTLSPSGKLGRKS 550
 507 -----ASTTR-----KSKRIOLCKELSLDLVVFVFNKTLN----- 537
 551 KAEVDES-----GEDAGASRRNGRLVYGSFRRKKKSKLKAASVGEQDPOGQGR 607
 538 -----DLSTAPGSTTMSKRN----- 554
 608 GATROKTKMLSLALSDLVYTKSVATHDIEMEAASSWQVSSFSSETKAHQIIOQKPAQYL 667
 555 -----LASVTESTCLRLMHTVATEFG 575

668 RFNOOOLSRITPSSYRVDSNYPQPFNNACQOMVALNYOEGRMLOLNRAKFSANGCG 727
 576 GATIRNYCYRVFPNPNBRVDSNLSNPQEFNNNGVQWCLNYQTPGLMMDLOEGKFSNGCG 635
 728 YVLKPGCMCOGVFNNSDEPLDGLQKLOLYRIISGOOLPRPROSMGLDREIIDPFV 787
 636 YVLKPGVMDKMFVPSDRVPSPI--LHLRLISGOOLPPRGS--NAKDSADPFV 690
 788 ETLGLPVDCSRQTRVDDNGFNPTMEETLYPMVAPETALVREFLYMDHDPGRDIFGR 847
 691 EYFGLPGDCAERTKTRVNDSTNPSFDSFQVSVPELALVRFVYDDDIYIGDIFIGQ 750
 848 TLFSSMPGYRRHYL---EG--MEEASTFVAVSDI--SGKVQ 886
 751 TIFECIAPGYRHLYLLNNEGDPLEHATLFVHATIRNGGKAKK 796

RESULT 12
 063693 PRELIMINARY; PRT; 771 AA.
 AC 063693;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Phospholipase C delta4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DONRU;
 RX MEDLINE=96132927; PubMed=8550586;
 RA Liu N., Fukami K., Yu H., Takenawa T.;
 RT "A new phospholipase C delta 4 is induced at s-phase of the cell cycle
 and appears in the nucleus";
 RL J. Biol. Chem. 271:355-360(1996).
 DR EMBL: D50455; BAA09046.1; -;
 DR HSSP: P10688; IQAS.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00387; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00054; Eph; 2.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCYC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PSS0004; C2_DOMAIN_2; 1.
 DR PROSITE: PSS0018; EF_HAND; UNKNOWN_1.
 DR PROSITE: PSS0003; PH_DOMAIN; 1.
 DR PROSITE: PSS0007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PSS0008; PIPLC_Y_DOMAIN; 1.
 SO SEQUENCE 771 AA; 88862 MW; PBFBD64A8B86E4F CRC64;

Query Match 20.3%; Score 1294; DB 11; Length 771;
 Best Local Similarity 36.8%; Pred. No. 2.3e-73;
 Matches 314; Conservative 134; Mismatches 280; Indels 126; Gaps 21;

45 MOEGMAYKLGSGKGLVRYLYL-DEHRSCLRMWRPRSRKNEKAKISDSIOEVSSEGRQSEV 103
 18 MOKGTMRKRVRTKSWKRLRYFLDDGMTVHGRHLESISKPTISISDIYERIKRGDQSEL 77


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QY 104 FORPDGSGFDPNCCFSIYHGSHRESLDLSTSEVARTWGLTYMAGISDEDSLAR- 162
DB 78 L-RYLVEEPLLEGFTIYFNRRRLDLYANVSBAQWMAQGLDLY-----DLVAMN 130
QY 163 -QRTDQOLKQTFDEADKNGSGSISGEVTLKHLKLVNLPKRVKQWFRADTDHOGT 221
DB 131 YOBOLDQMLREMFQOQADNODSRMSFRQORLLLMVEMEEYAFSLFQADY-SQSN 189
QY 222 LGFEFCAFYKMSRDLTYLMLTYSNHRKDLAASLQRLVQKAKGATLESODIT 281
DB 190 LDSEFVQFYALKRLREIEELFENFSDOKLTLLEFVDPDLREKQESHSDIALKLI 249
QY 282 EGFEPKPMNSKGLIGDFTNTRSPAGDIFENPEHHVHODMTPLSHYFTSSHTYL 341
DB 250 DRYEPSENGRLRLVLSKDGFLSYLCSADGNIFNPDCLPIYQDMQPLSHYINSHTYL 309
QY 342 VGDOLMSQSRDMYAWLQAGRCVCEWCDMPDGERIVHNGITLPSKILPKDIETINK 401
DB 310 LGDPPCOSSVEGITRALKRCRCVCEWCDMPDGERIVHNGITLPSKILPKDIETINK 369
QY 402 YAFIKNEYPVLSIENHCYVIOQKM-AQYLTDLIGDKLSSVSSSEADATLPSQMLKG 460
DB 370 YAFQSDYPLISLNDNCTWQCKTMAHLIALIGBOL-LSTLLEQIDIMSPSPE-LRG 427
QY 461 KILYKGGKL-PANISEAEGEVSDSDADEIDDDCKLNGASTNRKRVENAKRKIDS 519
DB 428 KILYKGGKLTIYEVESDEKEELEKDEGSDLD-----PASAELO- 467
QY 520 LINESKIRDCEDPNFVSFLSPSGKLGKRSKAEDVEGSEDAGASRRNKLTVGSPSR 579
DB 468 -----WQSPESQEOAS-----GKSKRN 485
QY 580 KKKGSKLKAASVEBDEGODSPGSGRGATRKQKTKMLSRALSDLYKTKSYA---TH 635
DB 486 KKK-----FLQSSFTIILCPDLASALVYLKRAPECSFTH 519
QY 636 DIMEAASSWQVSSFSEKHAQILOOKPAQYLFNQQOISRIYPSRYRDDSSYNNQPPW 695
DB 520 --SKENYHIYDISFSESRAKNIIRFANGNEFVONAKROCRYPGSLRDSSTYNNQPEHM 577
QY 696 MAGCOVALNYOSEGRMLDINRAKFSANGCGVYLKPGCM--COGFVFNSEDPPLPGOLK 753
DB 578 NNGCOVANNMOTAGSAMIDICDLFRQNGSGGYLKPFLRDTQGSFNMK-----PVSLY 633
QY 754 KO--LYLRIISGQOLKPPRDSMLGDEGLIDPVEVEITGLVYDCSRQDTRVYDNGFNP 811
DB 634 KQOILVVOYISGORLKPVDKT---KETTIVDPLVRELYGVBEDTKQOETSYVENNGINP 690
QY 812 TWEEFLVFNHPELALVFLVWDHPDPIGR-DFIGORTLAFSSMMPGVRHYVL-----EG 865
DB 691 YNGEFTFYQIOVPELAMLRFYVKDYSRTRSNNFICQYITLPLWTCMKHGRHVSLSKDGT 750
QY 866 MEASIFVAVASD 879
DB 751 LHPASHFYVTCMOE 764

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RESULT 13

OBTECT

ID OBTECT1 PRELIMINARY; PRT: 789 AA.

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AC 08TEC1;
DB 01-JUN-2002 (TREMBLrel. 21, Created)
DB 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ23660 fis, clone HEP00931.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiyi T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

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RA Okitani R., Ota T., Suzuki Y., Oabayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEBO human cDNA sequencing project."
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK074240; BAB85029.1;
SQ SEQUENCE 789 AA; 89258 MW; C6901404D2C9D070 CRC64;

Query Match
Best Local Similarity 20.2%; Score 1289; DB 4; Length 789;
Matches 309; Conservative 136; Mismatches 290; Indels 168; Gaps 22;

QY 1 MAPRTGRLPGALPPEDGPPRPSNMLPLSANILPVERCKG-----AMQGMQV 52
DB 26 VAPAPVA--LPSPTSDGCKRPGRLAL-----KKMGLDEDDVAMLRGSLR 72
QY 53 KLGSGSKGLVREYUUDENHRCIRW--RPSRKNEKAKISIDIOEVSGROSEVQRPD 109
DB 73 KIRSRTHKERLYRLQEDGLSV-WFORRIPRAPSQHIFVCHTEVAVRGHQSEGLRRP-G 130
QY 110 GSPDPNCCSIYHGSHRESLDLSTSEVARTWGLTYMAGISDEDSLARQRTPDQW 169
DB 131 GAFAPARCLTTFKGRKKRLDLAAPTAEAOQWVGLTKRLRL--DAMQGREL-DHW 186
QY 170 LKQTFDEADKNGDGLSISGEVTLKHLKLVNLPKRVKQWFRADTDHOGTLCPEEPCA 229
DB 187 IHSYLHRADSNDSKMSKREKLSLRMYNVNDMDYALFLKECDHSNDRLEG-AETEE 245
QY 230 FYKMSSTRDLTYLMLTYSNHRKDLAASLQRLVQKAKGATLESODITFEPECPPE 289
DB 246 FLRLRLKRLPELEIFHQSGEDRVLSAPLELEPLE-DGEGGALTLARAQOLQYTELNET 304
QY 290 NKSGLIGDGFNTTRSPAGDIFENPEHHVHODMTPLSHYFTSSHTNYLVGDOLMSQ 349
DB 305 AKQHEMLTLDGFPMATLSPGALDNTHTCYFQOMNPPLATYFTSSHTNYLTSQIGCP 364
QY 365 SRVDMYANVLOAGRCVCEWCDMPDGERIVHNGITLPSKILPKDIETINKYAFIKNEY 409
DB 355 SSTEAVYRAFAQGCRCVCEWCDMPDGERIVHNGITLPSKILPKDIETINKYAFIKNEY 424
QY 410 PYLISIEHNCYVIOQKMAQYLTDLIGDKLSSVSSSEADATLPSQMLKGLIYKGRKL 469
DB 425 PYLISIEHNCYVIOQKMAQYLTDLIGDKLSSVSSSEADATLPSQMLKGLIYKGRKL 484
QY 470 PANISEAEGEVSDSDADEIDDDCKLNGASTNRKRVENAKRKRLDLSIESKIROC 529
DB 485 PAARSEDOGR--ALSDREEEEDDEE----- 507
QY 530 EDPNNFVSFLSPSGKLGKRSKAEDVEGSEDAGASRRNKLTVGSPSRKKKSKLKA 589
DB 508 -----EVEEVE--AAQGRRLAK----- 522
QY 590 ASVEEGDEGODSPGSGRGATRKQKTKMLSRALSDLYKTKSYAITHDIE--MEAASSMOV 647
DB 523 -----QISPESLALVYCHARTRLRLHPAPNAPQCV 555
QY 648 SFSSEKHAQILOOKPAQYLFNQQOISRIYPSRYRDDSSYNNQPPWMAQGMQV 707
DB 556 SLSSEKRAKLIBAGNSFYRNAARQITRYPLGLMANSNANYSPOEMNSGCOLVALNFO 615
QY 708 SEGKMLDINRAKFSANGCGVYLKPGCMCOGFVFNSE--DP-LPGOLKQVLYLRIISGOO 765
DB 616 TPGVEMDLNAGRLVNGOCGYLKPACLRQ---PDSTFDPPEYGPPTTLISIQVLTAAQ 671
QY 766 LP-----KPRDSMLGDEGLIDPVEVEITGLVYDCSRQDTRVYDNGFNPWEETLVFM 820
DB 672 LPLKNEKPH-----SLVDPVLIETIHGVPADARQETVYLVNNGPFWMGOTLQFO 723
QY 821 VNHPELALVFLVWDHPDPIGR-RDFIGORTLAFSSMMPGVRHYVL-----EGMEASIFVH 874
DB 724 LRAPELALVFLVVEYDASPNDVFGFTLPLSSLKQGRHRIHLSKQASLSPATLTIO 783
QY 875 VAV 877

```

DB 784 IRI 786

RESULT 14

060450 PRELIMINARY; PRT: 745 AA.

AC 060450: 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Phospholipase C-delta1 (Fragment).

OS Crictellus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Crictellus.

ON NCBI_Taxid=10029;

OX [1]

RP SEQUENCE FROM N.A.

RA Leonis M.A., Silbert D.F.;

RT "Organization of the Hamster Phospholipase C-delta1 Gene: Differential

RT Loss of Separate Alleles of the Phospholipase C-delta1 Gene in Two

RT Fibroblast Mutants Lacking Phospholipase C-delta1."

RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: U50566; AAA93481.1; JOINED.

DR EMBL: U50565; AAA93481.1; JOINED.

DR HSSP: P10688; IMA1.

DR InterPro: IPR000008; C2.

DR InterPro: IPR002048; EF-hand.

DR InterPro: IPR001849; PH.

DR InterPro: IPR001192; PL-PLC.

DR InterPro: IPR000909; PL-PLC_xdom.

DR Pfam: PF00168; C2; 1.

DR Pfam: PF00036; ehand; 2.

DR Pfam: PF00169; PH; 1.

DR Pfam: PF00386; PL-PLC-X; 1.

DR Pfam: PF00387; PL-PLC-Y; 1.

DR PRINTS: PR00360; C2DOMAIN.

DR PRINTS: PR00390; PHPLIPASEC.

DR Prodom: PD001202; PL-PLC_Y; 1.

DR SMART: SM00239; C2; 1.

DR SMART: SM00233; PH; 1.

DR SMART: SM00146; PLCX; 1.

DR SMART: SM00149; PLCY; 1.

DR PROSITE: PS00004; C2_DOMAIN_2; 1.

DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.

DR PROSITE: PS50003; PH_DOMAIN; 1.

DR PROSITE: PS50007; PLPLC_X_DOMAIN; 1.

DR PROSITE: PS50008; PLPLC_Y_DOMAIN; 1.

FT NON_TER 1

SQ SEQUENCE 745 AA; 84638 MW; BE13C729C41C705E CRC64;

Query Match 20.2%; Score 1287; DB 11; Length 745;

Best Local Similarity 35.8%; Pred. No. 6.1e-73;

Matches 307; Conservative 128; Mismatches 279; Indels 144; Gaps 16;

DB 44 AMOEGMOMKLGSGKGLVYLDHRSICRMPSRK---NEKAKISIDISIQVSEGR 99

DB 10 ALLGSQLKAVKSSWRREFFYKLOEDCKTI-WQSRKMRPESQLSIEDIOEVRRCH 68

QY 100 GSEVFORVYDGSFDPNCFSTIYHSHRESLDLVSTSEVARTWTVGLRYLMAGISDEDSL 159

DB 69 RREGLEKFA-RDIPEDRCSTIYFKDQRTNLDLAPSSADAQHWVGLRKT--IHHSQM 124

QY 160 ARRRRTDQWQKOTDEAKNGDGSIGEVQLLHKLNVNLPKRVKQMFREAD---TD 216

DB 125 DQKQKQ-QHWISCLKAKKKNKKNKNEKELDFKEINIOVDSDYARKIFRECHSDQTD 183

QY 217 DQKQ 276

DB 184 ----SLEDEIEITFYKMLQRAEIDRVFAAGSAETLSVEKLVYFLQHQGEAAGPAL 239

QY 277 CODIIEPEPCENKSKGLGIDGFTNTYSSPADIDNPENHHVQDMOTPLSHYFTSS 336

DB 240 ALSTIEREPESETAKAOROMTKDGLFMYLLSADGSASFSLAHRRYQDMOPLSHYLVSS 299

QY 337 HNTLVGDLMSOSRVMYAMVLAQGCRCVYDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQ 396

DB 300 HNTLVLEQDLGTPSTETVIRALCKGRCLDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQ 359

QY 397 ETINKVAFIKNEYVVIISIEHNCVIOQKKMAQYLTDLGDKLDSVSSSEDAATLPSQ 456

DB 360 RAIDYAFKASPYVILSLHNHCSLEBOQVYARILKAILPML-LDPLDGYMKSLSPE 418

QY 457 MKGKILYKGGK---LPANISDAEAGEVSDSDADEIDDCKLNGASTNKRREYNT 512

DB 419 QLKGIILKKGKFGGLLPAGENGPEFTTDVSDDEEAEMEDE----- 460

QY 513 AKRKLDLSIKESKIRDCEDDPNPFVSSTLSPGKIGRKSKEDEVEDGADAGARRRLV 572

DB 461 -----A 461

QY 573 VGSFRRKKKSKLKAAYEEDGQDPSGQSGATRQKTKLSRLSDLVKTKSV 632

DB 462 VRSQYQKSKEDKLNVAPE-----LSDMYIKSV 491

QY 633 ATHDIEEAASS---WOVSFSETKAHQIIOQFAQYLRFNQQLSHYSSSYRVDSSNY 689

DB 492 HEGGFSPNPTSGQAFYEASFSERNRRLILOESGNNFVRHVSLSRTYPAGRRDSSN 551

QY 690 NPQPFVNAQCMVALNOSSEBMLQINRAKFSANGGCVLKPCGM--CGVFPNSED 747

DB 552 SPVENMNGCQIYALNFOPTPEPENVYLGKQDAGAGYVLPKFLDPPTEAPRALQ 611

QY 748 LPQGLKQLYRIISGOOLPKPRDSMLGDRGEIIDPEVEEILIPDCSREQTRVVDN 807

DB 612 GPWMAQKRLRVRVSGOGLPKVNNK---KMSYDPAVYIEVHVGQDVASRQTAVTNN 667

QY 808 GPNPTEETLVFMYHMEPIALVFLVWDHDTGR-DPIQRTALFSSMPGQYRHYV--- 863

DB 668 GFNPMDTEFEFEVAVPDLVRFVEVDYDASSKNDIIGOSTIYWNLSIKQYRHVHLSK 727

QY 864 --EGMEASIFVHVAVSD 879

DB 728 NGDHPKATLVFKISLQD 745

RESULT 15

08TF37 PRELIMINARY; PRT: 757 AA.

AC 08TF37: 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE KIA1964 protein (Fragment).

CN KIA1964.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

ON NCBI_Taxid=9606;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=11853319;

RA Nagase T., Kikuno R., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XXII.

RT The complete sequences of 50 new cDNA clones which code for large

RT proteins."

RL DNA Res. 8:319-327(2001).

DR EMBL: AB075844; BAB85550.1; -.

FT NON_TER 1

SQ SEQUENCE 757 AA; 85776 MW; 1CA68FF03779055 CRC64;

Query Match 20.1%; Score 1281; DB 4; Length 757;

Best Local Similarity 34.1%; Pred. No. 1.5e-72;

Matches 305; Conservative 135; Mismatches 288; Indels 166; Gaps 21;

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QY 10 PGPALPPEDPPDPESRKLFLSANILPYVERCMG-----AMQEGMOMYKLRGSGKL 61
Db 1 PSPPPSDGGTKRPGRLAL-----KMGTEDEVDYAMLRGSRKIRSRTHWK 49
QY 62 VRFYYLDHHRSCIRW---RPSRKNKEKAKISIDISIOEVSEGRSEVFORYPDGSFPDNCCE 118
Db 50 ERLYRLQEDGSLV-WFORIRIPRASQHLFFVOHITAVREGHSEGLRRF-GGAFAPARCL 107
QY 119 SIYHSHRESIDLVTSSSEVARTWVTLGRYLMAGISDEDSLARQRTDQWLKQTFDEAD 178
Db 108 TIAFGRRKKNIDLAAPFAEEAQRWVRLTKLRARL--DAMQQRERL-DHWIHSYLHRAD 163
QY 179 KNGGGSISIGEVLOLHKLANVLPQRQYKQMFREADTDHOGTIGFEFCAFYKMASTRR 238
Db 164 SNQDSKMSFEKIKSILRNVNVMNDMAYLLFKEDHSNNDRLRG-AEIEFLRLRLKRP 222
QY 239 DLYLMLTYSNHKKDHIDAASLQRFLOVEQKMAVTLSECODIIEQFEPCKENKSKLLGI 298
Db 223 ELEELFHQYSGEDVLSAPLELLEFLF-DQGEAGTLARAQOLIQYELNETAKOHEIMTL 281
QY 239 DGFNTYTRSPAGDIFNPEHHVHODMTOPLSHYFTSSHNTYLVGDQUMSQRVDMYAV 358
Db 282 DGFMYTLLSPGALDMDTHTCVFQDMNQPLAHYFISSSHNTYLFDSQIGPSSTEAAYRA 341
QY 359 LQAGRCREVCNMGDPQSEPIVHHGYTLTSKLFKDVETETINKYAFINKREYVLLISTENH 418
Db 342 PAQGRCEVELDCWEGPGEPIYHGHITLSKILRQVAVRDHAFITLSPYVILLENH 401
QY 419 CSVIOQKKMAQYITNDILGDKLDLSSVSESDATTLPSQMLKGLIKGLIPANISEDAE 478
Db 402 CGLEQQAAMAHNLCTIIGDMLVTQALDSPNEELPSPEQLKGRVLYKCKLPAARSEDR 461
QY 479 EGEVSEDESDAIEDDCKLNGDASTNRKRVENTAKRKLDLIESKIRDCEDPNNESVS 538
Db 462 --ALSDREEEEDDE----- 475
QY 539 TLPSPGKLRKSAEEDVESGEDAGASRRNGRLVYGSFSRRKKSGSKLKAASVEEGDEG 598
Db 476 -----EEEVE---AAQRRLAK----- 490
QY 599 QDSPGQSRGATRQKTKMLKSRLSLDLVYTKSVATHDIE--MEAASSWQVSSFSSETRAH 656
Db 491 -----QISPELSALAVYCHATRRLTLHPAPNAPQPCQVSSLSERKAK 532
QY 657 QIILOQKPAQYIARFNOQOLSRIYPSYSYRVDSSNYPQPFWMNAGCOMVALNYOSEGRMLOLN 716
Db 533 KLIREAGNSFVRHNAQDLTRYPLGLLRMNSANYSPQEMWNSGCOLVALNFPOTPGYEMDLN 592
QY 717 RAKFSANGCGGYVLKPGCMCGVFNPNSE--DP-LPGOLKQVLVRIISGOQLP-----KP 769
Db 593 AGRFLVNGQCGGYVLKPAKLRQ---PDSTFPEYRPGPRTTLSIQVLTAAQLPKLNAEKP 648
QY 770 RDSMLGDRGELIIDFVEVELIIGLPVDCSREQTRVVDNGCFNPWEETLVFMVHMPETALV 829
Db 649 H-----SIVDELVRIEIHGVADACARQETDYLVNNGFNPRWGQTLQFOLRAPELALV 700
QY 830 RFLVMDHDPYG-RDFIGORTLAFSSMMPGYRHYL-----EGMEASIFVHYAV 877
Db 701 RFVVEDYDATSPNDFVGQFTLPLISLKGYRHHLLSKDGASISPAULFIQIRI 754
```

Search completed: March 28, 2003, 13:51:32
Job time : 122 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:39:49 ; Search time 29 Seconds
(without alignments)
1726.273 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPPTAGPLPGPALPEDPG.....ALYPMHCLRGTLPLWLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1738	27.2	Y450_HUMAN	O75038 homo sapien
2	1285	20.1	P1D1_HUMAN	P51178 homo sapien
3	1258	19.7	P1D1_RAT	P10688 rattus norv
4	1235.5	19.4	P1G1_BOVIN	P10895 bos taurus
5	1009	15.8	P1G1_BOVIN	P08487 bos taurus
6	999.5	15.7	P1B4_HUMAN	Q15147 homo sapien
7	997.5	15.6	P1G1_HUMAN	P19174 homo sapien
8	996.5	15.6	P1B4_RAT	Q96407 rattus norv
9	985	15.4	P1G1_RAT	P10686 rattus norv
10	968.5	15.2	P1G2_HUMAN	P24135 rattus norv
11	950.5	14.9	P1G2_HUMAN	P16885 homo sapien
12	945.5	14.8	P1G1_DROME	P25455 drosophila
13	945	14.8	P1B1_RAT	P10687 rattus norv
14	937.5	14.7	P1B4_BOVIN	Q07722 bos taurus
15	937	14.7	P1B1_HUMAN	Q96466 homo sapien
16	936	14.7	P1B1_BOVIN	P10894 bos taurus
17	925	14.5	P1PA_DICDI	Q02158 dictyosteli
18	920	14.4	P1PA_DROME	P13217 drosophila
19	908.5	14.2	P1B2_HUMAN	Q00722 homo sapien
20	900	14.1	P1P3_HUMAN	Q01970 homo sapien
21	865.5	13.6	P1C1_SCHPO	P40977 schizosacch
22	863	13.5	P1P3_MOUSE	P51432 mus musculu
23	682.5	10.7	P1C1_YEAST	P33383 saccharomyc
24	677	10.6	P1C1_CANAL	O13433 candida alb
25	225.5	3.5	P1G1_MOUSE	Q62077 mus musculu
26	202	3.2	P1F8_PRYKA	P33479 pseudorabie
27	201.5	3.0	P1F8_MOUSE	Q07092 homo sapien
28	194.5	3.0	P1F8_MOUSE	P03181 epstein-bar
29	185.5	2.9	P1F8_MOUSE	P17599 bos taurus
30	185.5	2.9	P1F8_MOUSE	P11675 pseudorabie
31	184.5	2.9	P1F8_MOUSE	P32521 saccharomyc
32	184.5	2.9	P1F8_MOUSE	P55787 oryctolagus
33	184.5	2.9	P1F8_MOUSE	P17600 homo sapien

34	184.5	2.9	1685	1	CA54_HUMAN	P29400 homo sapien
35	181.5	2.8	1163	1	Y222_HUMAN	Q22618 homo sapien
36	180	2.8	1464	1	CA11_HUMAN	P02452 homo sapien
37	179	2.8	1464	1	CA13_MOUSE	P08121 mus musculu
38	178.5	2.8	704	1	SYN1_RAT	P09951 rattus norv
39	178	2.8	625	1	DUS8_HUMAN	Q13202 homo sapien
40	177.5	2.8	2845	1	APC_MOUSE	Q61315 mus musculu
41	177.5	2.8	2944	1	CA17_HUMAN	Q02388 homo sapien
42	176.5	2.8	1388	1	CA1E_HUMAN	P39059 homo sapien
43	176.5	2.8	1453	1	CA11_CHICK	P02457 gallus gall
44	176	2.8	1466	1	CA12_HUMAN	P02461 homo sapien
45	175.5	2.8	1459	1	CA12_MOUSE	P28481 mus musculu

ALIGNMENTS

RESULT 1

ID Y450_HUMAN STANDARD; PRT; 425 AA.

AC 075038;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein KIAA0450.

GN KIAA0450.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98116662; PubMed=9455484;

RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,

RA Nakajima D., Nomura N., Ohara O.;

RT "Characterization of cDNA clones in size-fractionated cDNA libraries

from human brain.";

RL DNA Res. 4:345-349(1997).

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or send an email to license@sdb.ch).

CC EMBL: AB007919; BAA32295.1; -

KW Hypothetical protein.

SQ SEQUENCE 425 AA: 43842 MW: 2A6D733CA149E665 CRC64:

Query Match 27.2% Score 1738; DB 1; Length 425;

Best Local Similarity 99.7%; Pred. No. 7,5e-78;

Matches 324; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	883	KYKQALGKGLFLGPPGSLDSHAAGRPAPRSVSRITLRRTASAPTKQKGRGFP	942
DB	101	QYKQALGKGLFLGPPGSLDSHAAGRPAPRSVSRITLRRTASAPTKQKGRGFP	160
QY	943	LVLTGTRDGSAGVADVPVPGPGAPAPAPAOEGSGSPGKAPAAVAEKSPPVRRPV	1002
DB	161	LVLTGTRDGSAGVADVPVPGPGAPAPAPAOEGSGSPGKAPAAVAEKSPPVRRPV	220
QY	1003	LDGPGAPGMAATCKKCVVSCAGVNTGLOREPPSGFASROAIIQOPRAADSLGAP	1062
DB	221	LDGPGAPGMAATCKKCVVSCAGVNTGLOREPPSGFASROAIIQOPRAADSLGAP	280
QY	1063	CCGGLDPHAIIPRSREAPRGAPAROGSGSGMSDSSPSPCIPRSPRMPGACROP	1122
DB	281	CCGGLDPHAIIPRSREAPRGAPAROGSGSGMSDSSPSPCIPRSPRMPGACROP	340
QY	1123	GALGEGMSALPAOKLEIRSKSPMSAGKPLLPVVLPHAPGMAGPGSPAASAMTSPR	1182

DB 341 CALGEMSALEFRQKLEETRSSPMSACKPLPCVLPHPAGMAGPGSPAASAMTVSPR 400
 OY 1183 VLVALYPMWCHLRTGLLPWLAGCP 1207
 DB 401 VLVALYPMWCHLRTGLLPWLAGCP 425

RESULT 2
 ID PDI_HUMAN STANDARD; PRT: 756 AA.
 AC P51178;
 DT 01-OCT-1996 (Rel. 34, Last Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Aorta;
 RX MEDLINE=95197554; PubMed=7890667;
 RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
 RA Lomansney J.W., King K.;
 RT Cloning and identification of amino acid residues of human
 RT phospholipase C delta 1 essential for catalysis.";
 RL J. Biol. Chem. 270:5495-5505(1995).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U09117; AAA73567.1; -
 DR HSSP: P10688; IMA1.
 DR Genew; HGNC:9060; PLCD1.
 DR MIM: 602142; -
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; P1_PLC.
 DR InterPro: IPR000909; P1_PLC_Xdom.
 DR InterPro: IPR001711; P1_PLC_Y.
 DR Pfam: PF00036; ehand; 2.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00387; P1_PLC_Y; 1.
 DR Pfam: PF00388; P1_PLC_X; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; P1_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00233; PH; 1.

DR SMART: SM00148; PLCXG; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PSS00018; EF_HAND; 2.
 DR PROSITE: PSS0003; PH_DOMAIN; 1.
 DR PROSITE: PSS0004; C2_DOMAIN_2; 1.
 DR PROSITE: PSS0007; P1_PLC_X_DOMAIN; 1.
 DR PROSITE: PSS0008; P1_PLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Calcium-binding; Repeat.
 FT DOMAIN 21
 FT CA_BIND 153 164 PH.
 FT CA_BIND 189 200 EF_HAND 1 (POTENTIAL).
 FT DOMAIN 296 440 EF_HAND 2 (POTENTIAL).
 FT DOMAIN 492 609 DOMAIN X.
 FT DOMAIN 616 720 DOMAIN Y.
 FT ACT_SITE 311 311 C2 DOMAIN.
 FT ACT_SITE 356 356 BY SIMILARITY.
 FT ACT_SITE 356 356 BY SIMILARITY.
 SQ SEQUENCE 756 AA; 85763 MW; AD9A4251C5EBADEF CRC64;

Query Match 20.1%; Score 1285; DB 1; Length 756;
 Best Local Similarity 35.6%; Pred. No. 1.6e-55;
 Matches 308; Conservative 134; Mismatches 265; Indels 158; Gaps 19;

OY 44 AMQEGMAYKLGSGKGLVREYIDHNSCIRWPSRK-----NEKAKISDSIQEVSEGR 99
 DB 21 ALIKSGQLIKVKSRRERFYKIQEDCKTI-WQSRKVMTPPSQLEFIDQEVKRGH 79
 OY 100 OSEVORY-----PDSPFNCCFSTYHSHESLDVTSSEVARTVYGLRYLMAGISD 155
 DB 80 KTEGLEKFAADVPE-----DRCESTVFQDORNTDLIPSPADQHWYGLHKT----IHH 131
 OY 156 EDLSARRQRTDQWLKQTFDEADKNGDGLSIGEVYQLHLYNLVPRQVKNQFREAD- 214
 DB 132 SSGMQQRKLO-HWHSCLRADKKNKDKMFKELQNTLKLNTQVDSYARKFFRECDH 190
 OY 215 --TDHQTGTFEEECATYKMASTRDLYLMLTYSNKHDLDAASIQRLQVYQKMAVY 272
 DB 191 SQTD-----SLDEETLEARYKMLTORVELDRTFABAAGGFTLVSDQLVTFQHQOREEA 246
 OY 273 TLESCDIIQEFPEPEKSKGLIGIDFTNTYTSRPAQDIPNPHHVDQMTQPLSHYF 332
 DB 247 GPALALSLIENYEPSETTKAQRQTKGFLMYTLISADGSAFSLAHRVYDQMGQPLSHYL 306
 OY 333 ITSSNIVLVGDQQLMSQSDVDMYAVLQAGRCVEVDCMDGPDGEPIVHNGYTTSTKILF 392
 DB 307 VSSSNIVLVGDQQLMSQSDVDMYAVLQAGRCVEVDCMDGPDGEPIVHNGYTTSTKILF 366
 OY 393 KDVIETIKKVAFINNEYVYLSTENHCSYVQKMAQYLDIADKL---DLSVSEDA 449
 DB 367 CDVLRAIRDAIFAKSPYPIVILSTENHCTLRQVRMARHLAIGPMLNRPDGVN--- 423
 OY 450 TLPSPQMLKGLILYKGRKLPANISEDAEAGE-----VSDESDADEIDDCKLLNGASTN 505
 DB 424 -SLSPSPQMLKGLILYKGRKLPANISEDAEAGE-----VSDESDADEIDDCKLLNGASTN 473
 OY 506 RKREVENTAKRRLDLSLEKSTRDCEDPNPNSVSTLSPSGKLGKSKAAEDVESGEDAGAS 565
 DB 474 KSRVQHKP-----KEDKLR----- 487
 OY 566 RRNGRLVYGSFSSRRKKKSKLKKAASVEEGDEGDSPGSGSRGATQKTKMKSRLASDL 625
 DB 488 -----LAQELSDM 495
 OY 626 VKTKYSVAITHIEMEAA--SSMQVSSFSETKAHQILQOKPAQYLRFNQOQLSRIPSSY 682
 DB 496 VIYCKSVHFGFGFSPTGPGQAFYEMASFSENNRALLRLDSEGNFVAHNNGHLSRITPAW 555
 OY 683 RYDSNNYRQPFWNAGQWALNYQSBGRMLQLNRAKFSANGCGYVLPQGM--CQGVF 740
 DB 556 RTSSNFSVPEAMNNGGQVIALNFQTPGEMDYQRFQDNGACGVLKPAFLRDPNGTF 615
 OY 741 NPNSDEPLPGQLKKQVLRISQGLPKPRDSMLGREGELIDPEFVVEVETIGLPVYCSRQ 800
 DB 616 NPRLAAGPMMARKRLINIRIVISGQQLPKYK-----NKNSTVDKVTVEITHGVSRDVASRQ 671

QY 801 TRAYDDGNDPMPTEETLVEFVWDEPITALVEFLVWHDHPGR-DEFGQPTLAFSSXMPGXR 855
 Db 672 TAVTINNGFNWMDTEPAFEVYVVDLALFLVEDYEDTADSSKNDFFIGQSTIPLNSLKQGR 731
 QY 860 HVYL-----EGMEASIFVHVAUSD 879
 Db 732 HVHLSKSKNGQHPSATLFLVATLSLD 756

RESULT 3
 PID1_RAT
 PID1_RAT STANDARD; PRT; 756 AA.
 AC p10688: 090VD3: 090VD4: 090VD5;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (phospholipase C-delta-1) (PLC-III),
 GN PLCD1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68270495; Pubmed=3390863;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.";
 RL Cell 54:161-169(1988).
 RN [2]
 RP SEQUENCE OF 50-57, 128-140 AND 728-738.
 RC TISSUE=Brain;
 RX MEDLINE=92202192; Pubmed=1313009;
 RA Katematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
 RA Iwanaga S., Hirata M.;
 RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
 cytosol.";
 RL J. Biol. Chem. 267:6518-6525(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 12-130.
 RX MEDLINE=96107342; Pubmed=8521504;
 RA Ferguson K.M., Lemon M.A., Schlessinger J., Sigler P.B.;
 RT "Structure of the high affinity complex of inositol trisphosphate
 with a phospholipase C pleckstrin homology domain.";
 RL Cell 83:1037-1046(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 205-756.
 RX MEDLINE=96378790; Pubmed=8784353;
 RA Grobler J.A., Essen L.-O., Williams R.L., Hurley J.H.;
 RT "C2 domain conformational changes in phospholipase C-delta 1.";
 RL Nat. Struct. Biol. 3:788-795(1996).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 133-756.
 RX MEDLINE=96186608; Pubmed=8602259;
 RA Essen L.-O., Perisic O., Cheung R., Katan M., Williams R.L.;
 RT "Crystal structure of a mammalian phospholipidase-specific
 phospholipase C delta.";
 RL Nature 380:595-602(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 133-756.
 RX MEDLINE=97215812; Pubmed=9062102;
 RA Essen L.-O., Perisic O., Lynch D.E., Katan M., Williams R.L.;
 RT "A ternary metal binding site in the C2 domain of phospholipidase-
 specific phospholipase C-delta1.";
 RL Biochemistry 36:2753-2762(1997).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DICYCLIGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.

```

CC      -|- COFACTOR: Calcium.
CC      -|- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC      PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC      -|- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC      -|- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC      -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M20637; AAAA1886.1;  -
CC      PIR: B28821; B28821.
DR      PDB: 1DUJ; 07-JUL-97.
DR      PDB: 1DUH; 07-JUL-97.
DR      PDB: 1DJ1; 07-JUL-97.
DR      PDB: 1DJW; 23-JUL-97.
DR      PDB: 1DJY; 07-JUL-97.
DR      PDB: 1DJZ; 07-JUL-97.
DR      PDB: 2ISD; 07-JUL-97.
DR      PDB: 1MAI; 08-NOV-96.
DR      PDB: 1QAS; 12-FEB-97.
DR      PDB: 1QAT; 12-FEB-97.
DR      InterPro: IPR000008; C2.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR001849; PH.
DR      InterPro: IPR001192; PI_PLIC.
DR      InterPro: IPR000909; PI_PLIC_Xdom.
DR      InterPro: IPR001711; PI_PLIC_Y.
DR      Pfam: PF00036; efhand; 2.
DR      Pfam: PF00168; C2; 1.
DR      Pfam: PF00169; PH; 1.
DR      Pfam: PF00387; PI-PLC-Y; 1.
DR      Pfam: PF00388; PI-PLC-X; 1.
DR      PRINTS: PR00360; C2DOMAIN.
DR      PRINTS: PR00390; PHPLIPASEC.
DR      ProDom: PD001202; PI_PLIC_Y; 1.
DR      SMART: SMO0239; C2; 1.
DR      SMART: SMO0233; PH; 1.
DR      SMART: SMO0148; PLICX; 1.
DR      SMART: SMO0149; PLICY; 1.
DR      PROSITE: PS00018; EF_HAND; 2.
DR      PROSITE: PS50003; PH_DOMAIN; 1.
DR      PROSITE: PS50004; C2_DOMAIN_2; 1.
DR      PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR      PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
KW      Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;
KW      3d-structure.
FT      DOMAIN                21      130      PH.
FT      CA_BIND              153      164      EF-HAND 1 (POTENTIAL).
FT      CA_BIND              189      200      EF-HAND 2 (POTENTIAL).
FT      DOMAIN              296      440      DOMAIN X.
FT      DOMAIN              492      609      DOMAIN Y.
FT      DOMAIN              630      720      C2 DOMAIN.
FT      ACT_SITE            311      311
FT      ACT_SITE            356      356
FT      ACT_SITE
SQ      SEQUENCE              756 AA; 85962 MW; E33F2313AC81E9F9 CRC64;

Query Match      19.7%; Score 1258; DB 1; Length 756;
Best Local Similarity 35.8%; Pred. No. 3,2e-54;
Matches 308; Conservative 131; Mismatches 273; Indels 148; Gaps 19,

QY      44 AMOEGOMYKLGSGSLGYRFTYLDHRCIRMRPSRK-----NEKAKISIDISQIEYSBGR 99
DB      21 ALKGSQQLKLVKSSSRRRERYKIQDCKTI-WQESRKVRSPESOLEFIEDIQEVRGMKH 79
QY      100 GSEFVRPDGSDPDCSCFSIYHGSHRESIDLVSTSEVAFRTVGTGLRLMAGISDEDSL 159
      ::: ::: : |||| | : |||:: | |:: ||| : | :

```

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Db 80 RTEGLEKFA-RDIPEDRCFSIVFKDORNTLIDLAPSPADAQHWVGLRKI---IHHS GSM 135
QY 160 ARROTRDQWLTQTFEDKADKNGDLSIGEVYQLHLKLNVLPRQRYKQKREND---TD 216
Db 136 DQROKLO-HWHSCLRKADKKDKKMKFELKDKTLEKNTQVDDGVARKIFRECDHSQTD 194
QY 217 DHQGTGFCFCAFYKMMSTRDLYLMLTYSNKHDLDAASLQRFLOVEOK--MAGVTL 274
Db 195 ---SLEDELETFYKMLTORAEIDRAFEEMAGSAETLSVERLVTFTLQHQREENGAPAL 250
QY 275 ESCODITEOPPCENKSGILGIDGTNTYTRSPAGIIFPNEHHVQDMTOPISHTFT 334
Db 251 ---ASTLERPESETAKAQRQMKDQKGLMLLSDAGNAFSLAHRRYQDDMDQPLSHYLS 308
QY 335 SSHNTYLVGDQMSQSRVDMYAWTLQAGRCVCEYDCWDGPDGPPIYHGGYTLTKILFKD 394
Db 309 SSHNTYLVLEDDTGPSSTEAIRALCKGCHCLDQWDGNGEPPIYHGGYTLTKILFKD 368
QY 395 VIETINNYAPIKNEYPIYLSIENHCSTYQOKKMAQYITLILGKLDLSSVSSBDATPLPS 454
Db 369 VLRAIRDYAFKASYPVILSLLENHCSELDQRYVARHLRALIGPLI-LDQPLDGVTSLS 427
QY 455 POMLKGILYKGRK---LPANISEDAEVEGEVDESDADRIDCKILNDASTNKRRE 510
Db 428 PEOLKGIILKGGKGLPAGENGSEATDVSEVABAMEDEAV-----RSQVQ 478
QY 511 NTAKRKLDSLIKESKIRDCEDPNNSVSTLSPSGKLGRKSKADEVEDSEGDAGASRNGR 570
Db 479 H-----KPKED----- 484
QY 571 LVVGSFRRKKKSKLKAASVEBEGQDSPGQSGRQATROKTKMLKLSALSDLYKTK 630
Db 485 -----KTLVPELSDMLTYK 500
QY 631 SVATHDIEEAASS---WOVSFSETKAHQILQOKPAQYLRFNOQLSRIFSSYVDS 687
Db 501 SVHGFSSPGTSGQAFYEMASFSERARLRLQESNGVRHNVGSLNITPAGKWTDS 560
QY 688 NYRPFNMAGCOMVALNTOSEBRLQLRKATFSANGGGYTLKPCGM--COGVENPSE 745
Db 561 NYSFVEMMNGGQYVALNFTQPEPPEYVLGEGQDGGGYLKPFLDPTTFENSRAL 620
QY 746 DPLPGQJLQVLYRLISGOOLPKPRDSMLGDRCEITDPVEVEIIGLPVDCSREGORVVD 805
Db 621 TQGFMRPRLRVRILISGQLPKVN---NNSTVDPVYIEHIGVGDTSROTAVIT 676
QY 806 DNGFNTEETLVFMYHMEIALVRLVWDHPDIPGR-DEIGQRTLAFFSSMMPGTYHYVL- 863
Db 677 NNGFNRMMEFEFEVTVLDLALVRPMVDDYSSSKNDPFGOSTIPMNSLKQYRHVHL 736
QY 864 ---EGMEASIFVHAASD 879
Db 737 SKNGDQHPSATLFFVKISID 756

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RX MEDLINE=88270495; PubMed=3390863;
RA Sun P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.";
RL Cell 54:161-169(1988).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: calcium.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M20638; AAA30710.1; -.
DR PIR: C28821; C28821.
DR HSSP: P10688; IMAT.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000909; PL_PLC_Xdom.
DR InterPro: IPR001711; PL_PLC_Y.
DR Pfam: PF00036; efhand; 2.
DR Pfam: PF00166; C2; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00387; PI-PLC-Y; 1.
DR Pfam: PF00388; PI-PLC-X; 1.
DR ProDom: PD001202; PL_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00148; PLCxc; 1.
DR SMART: SM00149; PLCyc; 1.
DR PROSITE: PS00018; EF_HAND; 2.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
DR HydroLase; Lipid degradation; Transducer; Calcium-binding; Repeat.
FT NON_TER 1
FT DOMAIN 1
FT CA_BIND 92 103 PH.
FT CA_BIND 128 139 EF_HAND 1 (POTENTIAL).
FT DOMAIN 235 379 EF_HAND 2 (POTENTIAL).
FT DOMAIN 431 548 DOMAIN X.
FT DOMAIN 567 659 DOMAIN Y.
FT ACT_SITE 250 250 C2 DOMAIN.
FT ACT_SITE 295 295 BY SIMILARITY.
SQ SEQUENCE 695 AA; 78685 MW; 4239CD606076186 CRC64;

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Query Match 19.4%; Score 1235.5; DB 1; Length 695;
Best Local Similarity 36.1%; Pred. No. 3, 6e-53;
Matches 236; Conservative 122; Mismatches 252; Indels 151; Gaps 18;

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QY 83 EKAKISIDSIQSEVSEGRSEVFOR---PDGSFDDNCCFSYHSHRSLSLVSSSEY 138
Db 2 ESQLEFIEDIQEVRMGHRTGLEKFAVDPE-----NRCFSYFKQDRTWLDLAPSPAD 56
QY 139 ARTWVTGLRTLMAGISDEDSIARORTDQWLTQTFEDKADKNGDLSIGEVYQLHLKLN 198
Db 57 AQHWVQGLGKRI---IHHS GMDQOKLR-HWHSCLRKADKKDKKMKFELKDKTLEKNT 112
QY 199 VNLPRQRYKQKREND---TDHQGTGFCFCAFYKMMSTRDLYLMLTYSNKHDLHD 255

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DB 113 IQVDSDYAKKIRKEDHSTO-----SLEDELETETFKILTQKKEIDRPEATGSKETLS 168
 QY 256 AASLQFLQVEOK--MAGYTLBSCODIIOQEPCEPNKSKGLIGDFNTRRAGDIF 313
 DB 169 VQDLVTFLOHQOREEAGPAL--ALSLTEREPSEETAKKOROMTDGFMVLLSADGSNF 226
 QY 314 NPEHHVHODMOTPLSHYITSSHNMTLVYDQMLMSOSRDVAMVLOACRCVEVDCMDG 373
 DB 227 DLADRRVODMDQPLSHYLVSSSHNTYLEDQTPSSREAVIRALCKGCRLELDGMDG 286
 QY 374 PDGEPIVHHGYTLTKILFKDVIETINKYATKNEYPVLLSIENHCSTIQOKMAQYLTLD 433
 DB 287 PNEPIIHYGYTFSTKILFCVDYRAIROYAFKASPPYLLSEHNCSTLEQORVMAHRLRT 346
 QY 434 ILGDKLIDSSVSESDATTPSPOMLKGKTLVKGKTLPAINISDAEBCG-----VSDSDSD 489
 DB 347 ILGPM-LDRPLDGYVTSLSPEQLRGKTLGKGLGGLPPGEGGEPATVYVSDDEDA 405
 QY 490 EIDDDCKLNGDASTNRKRENTAKRKRLSLIKESKIRDCEDPNNFSVSTLSPSGRLGRK 549
 DB 406 EMEDEAV-----RSVOYQHS-----KEDKLR----- 426
 QY 550 SKAEDEVEGEDAGASRRNGRLVYVSFSRRKKGSKLKAAVYEEDEGDSFGGSRGA 609
 DB 427 ----- 426
 QY 610 TROKTKMKSRLASDLVYKTKSVATHDIEMEAS-----MOVSSFETKAHQLIOQPAQY 666
 DB 427 -----LAKELSDMYTKSVHFRGFPSSGTSGAFTEMSSFENKRLRLLOEGNSF 478
 QY 667 LRFNOQSLRITPYSRYVSDSNYNPQFVNAGCOMVANTQSEGRMLQUNRAKFSANGCC 726
 DB 479 VRNHNVLNSTIYACGMWTDSSNTPVEMNNGCOYVALNFTPGSEMDYVQGRFLNGAC 538
 QY 727 GYVLKPGCCM--CGGVFNPSDEDLPQOLKQVLRITISGQLKPRKPSMLGDEGEIIPR 784
 DB 539 GYVLKPAFLDPNSTFNSRLALAGPMTFRLVRYVTSQQLPRVKN-----NNSTVDPK 554
 QY 785 VEVEIILPYDCSREOTRVVDNDGNFTMEETLVFWVHMPAILVRLVMDHPIGR-DF 843
 DB 595 VYVEIHVGTGVASRQTAVYTNNGFNWMTLEFEVAVPELALVRYVEDIYDASSKND 654
 QY 844 IGORTLAFSSMMPGRIHYVL-----EGMEASIFVHYAVSD 879
 DB 655 IGQSTIPLKSLKQGYRHIHLKNGDHPATLFLVKVALOD 695

RESULT 5
 ID PIG1_BOVIN STANDARD; PRT; 1291 AA.
 AC P08487;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II)
 DE (PLC-148).
 GN PLCG1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RX MEDLINE=88156963; PubMed=2831461;
 RA Stahl M.L., Ferenz C.R., Kelleher K.L., Kriz R.W., Knopf J.L.;
 RT "Sequence similarity of phospholipase C with the non-catalytic region
 of src.";
 RL Nature 333:269-272(1988).
 RN [2]
 RP PHOSPHORYLATION SITES.

RX MEDLINE=90154080; PubMed=1689310;
 RA Kim J.W., Slim S.S., Kim U.H., Nishibe S., Whal M.I., Carpenter G.,
 RA Rhee S.G.;
 RT "Tyrosine residues in bovine phospholipase C-gamma phosphorylated by
 the epidermal growth factor receptor in vitro.";
 RL J. Biol. Chem. 265:3940-3943(1990).
 RN [3]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE=90154081; PubMed=1689311;
 RA Whal M.I., Nishibe S., Kim J.W., Kim H.K., Rhee S.G., Carpenter G.;
 RT "Identification of two epidermal growth factor-sensitive tyrosine
 phosphorylation sites of phospholipase C-gamma in intact HSC-1
 cells.";
 RL J. Biol. Chem. 265:3944-3948(1990).
 RN [4]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE=91208680; PubMed=1708307;
 RA Kim H.K., Kim J.W., Zilberstein A., Margolis B., Kim J.G.,
 RA Schlessinger J., Rhee S.G.;
 RT "PDGF stimulation of inositol phospholipid hydrolysis requires
 PLC-gamma 1 phosphorylation on tyrosine residues 783 and 1254.";
 RL Cell 65:435-441(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 663-759.
 RX MEDLINE=94236690; PubMed=8181064;
 RA Pascal S.M., Singer A.V., Gish G., Yamazaki T., Shoelson S.E.,
 RA Pawson T., Kay L.E., Forman-Kay J.D.;
 RT "Nuclear magnetic resonance structure of an SH2 domain of
 phospholipase C-gamma 1 complexed with a high affinity binding
 peptide.";
 RL Cell 77:461-472(1994).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-3D-myo-inositol 4,5-
 bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL; Y00301; CAA68406.1; -.
 DR PIR; S00666; S00666.
 DR PDB; 2PUD; 26-JAN-95.
 DR PDB; 2PLE; 26-JAN-95.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_Xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 2.

DR pfam; PF00018; SH3; 1.
 DR pfam; PF00168; C2; 1.
 DR pfam; PF00169; PH; 2.
 DR pfam; PF00387; PI-PLC-Y; 1.
 DR pfam; PF00388; PI-PLC-X; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 2.
 DR ProDom; PD001202; PI-PLC-Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00233; PH; 2.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCY; 1.
 DR SMART; SM00326; SH2; 2.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS50001; SH2; 2.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 DR PROSITE; PS50004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KM Hydrolase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 Repeat; Calcium-binding; Phosphorylation; 3D-structure.
 FT DOMAIN 27 142
 FT CA_BIND 165 176
 FT 320 464
 FT DOMAIN 489 523
 FT 550 657
 FT DOMAIN 668 756
 FT 791 851
 FT DOMAIN 895 931
 FT 953 1070
 FT DOMAIN 1075 1177
 FT ACT_SITE 335 335
 FT ACT_SITE 380 380
 FT MOD_RES 771 771
 FT MOD_RES 783 783
 FT MOD_RES 1254 1254
 FT SEQUENCE 1291 AA; 148312 MW; 9F31C7DMA3F8EA77 CRC64;
 Query Match 15.8%; Score 1009; DB 1; Length 1291;
 Best Local Similarity 26.1%; Pred No. 7.8e-42;
 Matches 308; Conservative 151; Mismatches 317; Indels 404; Gaps 35;

Db 401 AFVASEPVILSTEDHCSIAQQRNNAQYFKKVLGDTL-ITKPYDIAADGLSPNOLKRI 459
 QY 463 LVKCKLPA-----NISDAEAG----- 480
 Db 460 LTKKTLAAGSAVEEVPYTSVMYSENDISNKGILLYEDPVNHHMYPHYVLTSSKIY 519
 QY 481 -EYSDSDADEIDDOCKTLNG--DASTNKRY-----ENAKKILDS----- 519
 Db 520 SEETSSDQNEDEBEERKASSTELSHNKKRPHGKLAGRGRHIAERILTEYCIEGAP 579
 QY 520 ---LIKES-----KIRDC----- 529
 Db 580 DGSFLVRESETPVGYDYLTFMWENKGVQCHRIHSRODAGTPKFFLLDNLVPSLDLTHY 639
 QY 530 ----- 532
 Db 640 QGVPLRCNEFEMRLSEPVQTNHRSKEMYNHSLTRAQAEHMLNRPDGAFLVKKRNEP 699
 QY 533 NNEVS----- 538
 Db 700 NSYALSPFAEGKIKKCRVQEGQVYMLGNSEPSLDLISYEKHPLYRKMKLRYPINEE 759
 QY 539 -----TSPS-GKL--GR-----KSKAE 554
 Db 760 ALEKIGTAEPDYGALYEGRNPGFYVEANPMPFKCAVALLDYKAQREDELFTKSAIIQ 819
 QY 555 DYSEGE-----DAGASR----- 566
 Db 820 NVEKQGGMMGDDGGKKQLWFPSTNYEEMVSPALBPEREHLNDSPLGLRGVLDVP 879
 QY 567 -----RNGRLVYGSFRRKKKSKLTKKASVE-----GDEGQDSPGQSR 607
 Db 880 AQQLAVREGKNNRLFYFISIMASVAHSLDVAADSOEILDWYKKTREAAQADARLITE 939
 QY 608 CATRKKTAKLSKRALSDLVYTKSVATHD--TEMEAASMOVSSFSSTKAHQLIQ-KPA 664
 Db 940 GKMMER-KKATALEISELVYVCPRVPEDEKIGTERACYRDMSSFPETKAEKYNNKAKG 998
 QY 665 QYLRNQQQLSRIYPSRYVDSNYPNPFNNACQVVALNYOEGMIDLNRAKPSANG 724
 Db 999 KFLQYNRQLSRIYPKGORLDSSTYDPLPMWICGSQLVAINFOTPDPMOMNALFLAG 1058
 QY 725 GCGYVLKPGCMGCGVFNPNSEPLPGQLKQVLYRLIISGOLLKPRDSMGDGEIIDP 784
 Db 1059 HCGYVLQPSVARDPAFDPFKSSIRGLEPCALICEVIGANHLK-----NGNG-IYCPF 1111
 QY 785 VEVELIGLPVDCSREQRYVDNNGFNPTW--EETLVVWHPMETALVFLWDDPIG-RD 842
 Db 1112 VEIVAGAEYDSIKQKTEFYVDNGLNVPWPAKPFHFOISNPEFAFLRFVYEEEDMSDN 1171
 QY 843 FIGORTLAFSSMMPGYRHV-----YLEGMEASIFVVAV 877
 Db 1172 FLAQATFPVKGKLTGYRAVPLKNNYSGLFLASLVLKIDV 1211
 RESULT 6
 ID PIR4_HUMAN STANDARD; PRT: 1175 AA.
 AC Q15147; O9J02; O9B0W5; O9B0W6; O9B0W8;
 DT 15-JUN-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_Taxid=9606;
 RX [1]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=96079091; PubMed=8530101;

RA Alvarez R.A., Ghalayini A.J., Xu P., Hardcastle A., Bhattacharya S.,
 RA Rao P.N., Petteanti M.J., Anderson R.E., Beehr W.;
 RT "cDNA sequence and gene locus of the human retinal phosphoinositide-
 RT specific phospholipase C beta 4 (PLCB4).";
 RL Genomics 29:53-61(1995).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Delucas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Dearden R., Dhali P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvalho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachle L.J., McIay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1, 2 (shown here) and
 CC 3; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC
 CC EMBL, AL031652; CA21068.1;
 CC EMBL, AL023805; CAC34525.1;
 CC EMBL, AL023805; CAC34527.1;
 CC EMBL, AL023805; CAC34528.1;
 CC EMBL, LA1349; AAB02027.1;
 CC HSSP: PI0688; IDJX.
 CC GeneW: HGNC:9059; PLCB4.
 CC MIM: 600810;
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR001192; PI_PLC.
 CC InterPro: IPR000909; PI_PLC_Xdom.
 CC InterPro: IPR001711; PI_PLC_Y.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00387; PI_PLC_Y; 1.
 CC Pfam: PF00388; PI_PLC-X; 3.

DR PRINTS: PR00390; PPHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00148; PLCxc; 1.
 DR SMART: SM00149; PLCxc; 1.
 DR PROSITE: PSS0004; C2_DOMAIN_2; 1.
 DR PROSITE: PSS0007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PSS0008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolase; lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 313 463
 FT 565 681
 FT 688 786
 FT 328 328
 FT ACT_SITE 375 375
 FT ACT_SITE 375 375
 FT VARSPLIC 154 167
 FT VARSPLIC 154 167
 FT VARSPLIC 1 268
 FT CONFLICT 447 447
 FT CONFLICT 757 757
 FT CONFLICT 787 787
 FT CONFLICT 840 840
 FT CONFLICT 902 902
 SQ SEQUENCE 1175 AA; 134463 MM; AB208B99EF57357 CRC64;
 Query Match 15.7%; Score 999.5; DB 1; Length 1175;
 Best Local Similarity 29.2%; Pred. No. 2e-41;
 Matches 295; Conservative 131; Mismatches 308; Indels 275; Gaps 32;
 99 ROSEYFQRTPDGS--FDRNCGSIYH-----122
 18 QGAVFDRYEESFVEFPCLEKVFDEFFLTWRSEGEQVLECSLINSRGAIPDP 77
 123 -----GSHRESID-----LVTSSEVARTWVTLRLMAGIS 154
 78 KILALEANGKSENDLEGIYVCSTGLVYNSTFYMAENEYVKQVEGRSIIHNR 137
 155 DEDSLARRQRTDQWIKQTFDEADYNGDSLSIG-----VLQILKLANVL 201
 138 -ANNVSPMTCLEKHHMKLAF--MTNTNGKIPVRSITRTFASGKTEKYFQALKEI--GL 191
 202 PRQRVKQMRREDTDOHOT--LGFERPCAFYKMGSTRDLYLMLTYSNHK--DHDAASL 259
 192 P-----SGRNDIEPTLAFSEKFEYELTKICPRDIDELFKINGDKTDYTLVQL 242
 260 QRELYEQKMAQVT-----LESCDILIEQEPCEPKNSKGLGIDGFTYTRSPAGD 311
 243 VSTLNHODPRNLNELLFFYDAKRAMQIIEYEPEDLKKGLISDQFCRYLMSDENA 302
 312 IFNPEHHVADTOPLSHFITSSHNITLVGDOLMSQSRVDMYAVLQAGRCYEVDCW 371
 303 PVLIDRLLEYQEMDHLAFYFSSHNITLVGQFGSKSVEMRYVLLAGRCVELDCW 362
 372 D--GPGSEPVVHNGYLLTKLFKVDIETINRYAFIKNYEYVILSTIENHCSYIQQKMAQ 429
 363 DKGGEQEPITTGKAMCTDILFKVDYQAIKEAFYTSERYVILSEPHNSCKTYQYQKMK 422
 430 YLTDLIIGD--KLDLSVSSSEDAITLPSQMLKGLILVGRKL-----469
 423 YCEDLFGDILLKQALSHPLEPRALPSPDILKRLILKNNKRLKPEVEKKOLEALSRMME 482
 470 -----PANTSEDAEGEVSDESDAIDDDCKL--LNGDASTNNKRENTAKKRLDLSL 520
 483 AGESASPAANTLEDNEEIEISADQEEBAHEFFKGNELSDDDLGHKEAVANSYKGLVTV 542
 521 IKESKIRDCDPNNFVSSTLSPSGKLGKRSKAKADEVESGDCACASRNRLVYGSPSRK 580
 543 -----EDEBAMASRYKY-----555
 581 KKGSKLKAASVEGDEGQDPSGQSGRATROKTKMLSRALSDLVYTKSVATDIEH- 639
 556 -----GA-----TNIIHPLSTMTINVAQPVAFQCFQFHA 583

DR SMART; SM00149; PLCYC; 1.
 DR SMART; SM00252; SH2; 2.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS0001; SH2; 2.
 DR PROSITE; PS0002; SH3; 1.
 DR PROSITE; PS0003; PH_DOMAIN; 2.
 DR PROSITE; PS0004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS0007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS0008; PIPLC_Y_DOMAIN; 1.
 DR Hydrolyase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KW Repeat; Calcium-binding; Phosphorylation; 3D-structure; Polymorphism.
 FT DOMAIN 27 142
 FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 530 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT ACT_SITE 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 813 813 I -> T (IN DBSNP:753381).
 FT VARIANT 813 813 /FTID-VAR.011908.
 SQ SEQUENCE 1290 AA; 148531 MW; AE05ABE2A18EDDAC CRC64;
 Query Match 15.6%; Score 997.5; DB 1; Length 1290;
 Best Local Similarity 25.1%; Pred. No. 2.8e-41;
 Matches 306; Conservative 157; Mismatches 331; Indels 423; Gaps 35;

QY 74 IRNPSPKNEKAKISIDSEVSGRSEVFOR-PCGSF--DPNCFSTYHGS--HRES 128
 DB 60 ITWRSRGADLEGALDIREIKREIRPKTSRDFRQEDPARPPOSCEVLLYGEEFLKT 119
 QY 129 LDVSTSEVARTVWGLGRLTLAGISDEDSF-ARRQRTPOMLKOTDEADKNGDSL 187
 DB 120 LSLQATSEDEVNMWIKLITMLM-----EDTLQAPTLPIQIERMLKQFYSVDRNRKEDISA 174
 QY 188 GEVLQHLKLNLVLPQRVYQMFREADTDHOGTLGFEFCAYK--WMSTRDLVLLML 245
 DB 175 KDLKNNLSQVYRVYRPNRFLRE-RLTDLQKSGDITYGQFAQLYRSLMYSAGKTMDLPTL 233
 QY 246 TYS---NHKDHLDASLQRF-----LQVEQKAGVTLSCODITIQFE 285
 DB 234 EASTLRAGERPELCRVSLPEFOFLLDYQGLMAVDRLQVDFMLSLRDLPLREIEEPPY- 292
 QY 286 PCPENKSKGLGIDGFTNYTRSPAGDIFNPENHHVHOD-MTQPLSHYFITSNHTYLVGD 344
 DB 293 -----FLLDEFTYFLFSKENSVMNSDLAVCPDTMNNPISHWISSNHTYLVGD 342
 QY 345 QLMQSRYDVAWVLQAGRCVEVDCGDPGERPIVHGGYTLTKILFKVDIETINKYAF 404
 DB 343 QFSSSESLAVARCLRMGCRCIEIDCDGPGMGPVIVHGHLLTKIKFSDVLTATIKCHAF 402
 QY 405 IKNEPVTLSTENHCSYVQOKKMOYLTLGDLKIDLSVSSSEDAATLPSOMLKGKTIY 464
 DB 403 VASEPVTLSTEDHCSTIAQORNMAYRKVGLDTL-LTKPEVISAQGLPSPNOLKRLILI 461
 QY 465 KGRKL-----PAN-----ISE 475
 DB 462 KHKKLAEASVAYEVPYTSWMSYENDISIKNGILYLEDPVNHEWPHYFVLTSSKIYSE 521
 QY 476 DA-----EGEVSDEDSABEIDDCKLNGDASTNKKRPNNAKRLDS----- 519
 DB 522 ETSSDOGNEDEEPEKREVSSTELHSNEKWFHGLGAGHDG-RHIAERLLTEYCIETGAPD 580
 QY 520 ---LIKES-----KIRDC----- 529

DB 581 GSELVRESEETVGYDTLTSFMNGKVVQCHRIHSRODAGTPKFFLNDLVPSLDLTHRYQ 640
 QY 530 -----EDPN 533
 DB 641 QVPLKCNFEEMRLSEPPVQTNHESKEWYHSLTRQAQEHMLMVPYPRDGAFLVRRNEDPN 700
 QY 534 NFSVS----- 538
 DB 701 SYAISFRAGKIKHCRVOOEGQTVMLGNSFSDVLDLSYEEKHPLKMKLRYPINEEA 760
 QY 539 -----TSPS-GKL--GR-----SKAEED 555
 DB 761 LEKIGTAEPDYGALYGRNPGTYVEANMPPTPKCAVKALFDYKQAREDELFIKSAIQN 820
 QY 556 VESGE-----DAGASR----- 566
 DB 821 VEKQSGMWRGYYGKKQKLMFSPSYVEEVNVALEPEREHLDENSPLGDLRGVLDVPA 880
 QY 567 -----RNGRLVYGSFSSRRKKGSKLKAASVE-----GEGQDSFGQSGRG 608
 DB 881 COIATRPECKNNRLFFVFSISMAVSALDVAADSOEELQDMWKKIRREVAAOTARLREG 940
 QY 609 ATRQKTKMLSRALSDLYTKRSVATHD--IEMEAASSWVSSFSETRAHQILQD-KPAQ 665
 DB 941 KIMERN-KKIALELSELVYICRPVPEDEKIGTERACTRDNMSFETPAEKYVNAKAKKK 999
 QY 666 YLRFNQOQLSRTPSSRYVDSNTYNPQPPMNAQGMVALNTQSEGRMLQNLNKAESANGG 725
 DB 1000 FLQYNNLQSLRIVPKQORLSDSNYDPLPMWICGSLVALNFQTPPKPMQMNALPMTGRH 1059
 QY 726 CGYVLKPGCMCGVFPNPNEDPLPGOLKQVLYRIISQOLPKRPDSMLGDSGELIIDPFV 785
 DB 1060 CGGVLOPSTMRDEAFEPFEDKSSLRGEPCAISIEVGAHHLK-----NGHG-TVCPFV 1112
 QY 786 EVELIGLPVDCSREQTRVYDNDGNGFNPTM--EETLVPMHPEIALVFLVMDHPDG-EDF 843
 DB 1113 EIEVAAAEVDSIKQKTEFEVVDGNLNPVPAKPFHQIISPEAFPLRFVYEEEDMSDQNF 1172
 QY 844 IGORTLAFSSMMGCVRYH-----YLEGMEASIEYHVAV----- 877
 DB 1173 LQATFPVGLKGYRAVPLKNNYSDELASLILIKIDIFPAKENGDSLSPFSGTSLRENG 1232
 QY 878 SDISCKVYKQALGLKLF 894
 DB 1233 SDASGQLFHGRAREGSF 1249

RESULT 8
 PIB4_RAT
 ID PIB4_RAT STRAND: PRT; 1175 AA.
 AC Q9QW07; Q920G6; O88356;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE=94012687; PubMed=8407970;
 RA Lee C.-W., Park D.J., Lee K.-H., Kim C.-G., Rhee S.-G.;
 RT "Purification, molecular cloning, and sequencing of phospholipase C-
 beta 4".
 RU J. Biol. Chem. 268:21318-21327(1993).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE=93343926; PubMed=7688223;

RA Kim M.J., Baik Y.Y., Min D.S., Lee S.J., Ryu S.H., Suh P.G.;
 RT "Cloning of cDNA encoding rat phospholipase C-beta 4, a new member of
 RT the phospholipase C.";
 RL Biochem. Biophys. Res. Commun. 194:706-712(1993).
 RN [3]
 RP SEQUENCE OF 447-1175 FROM N.A. (ISOFORM C).
 RC TISSUE-BRAIN;
 RX MEDLINE=99132015; PubMed=9931434;
 RA Adamski F.M., Jims K.M., Shieh B.H.;
 RT "A unique isoform of phospholipase C-beta 4 highly expressed in the
 RT cerebellum and eye.";
 RL Biochim. Biophys. Acta 1444:55-60(1999).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYME. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate +
 CC H2O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L15556; AAK13557.1; -
 DR EMBL: U57836; AAD10403.1; -
 DR EMBL: AF031370; AAC98145.1; -
 DR EMBL: AF027571; AAC24984.1; -
 DR HSSP: P10688; IDUX.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI_PLC_Y; 1.
 DR Pfam: PF00388; PI_PLC_X; 1.
 DR PRINTS: PR00390; PPHILIPASEC.
 DR PRODOM: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 DR HydroLase: lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing;
 KW DOMAIN 313 463
 FT DOMAIN 565 681
 FT DOMAIN 688 786
 FT ACT_SITE 328 328
 FT ACT_SITE 375 375
 FT VARSPPLIC 1013 1022
 FT VARSPPLIC 1023 1022
 FT VARSPPLIC 1154 1175
 FT VARSPPLIC 1175 1175
 FT CONFLICT 255 255
 FT CONFLICT 308 308
 FT CONFLICT 417 417
 FT CONFLICT 470 470
 FT CONFLICT 504 504
 FT CONFLICT 545 546
 EQ -> M (IN REF. 2).
 R -> A (IN REF. 2).
 Q -> E (IN REF. 2).
 E -> K (IN REF. 2).
 A -> AA (IN REF. 1).
 EQ -> DE (IN REF. 2).

FT CONFLICT 734 734 I -> L (IN REF. 2).
 FT CONFLICT 741 741 R -> H (IN REF. 2).
 FT CONFLICT 764 764 L -> M (IN REF. 2).
 FT CONFLICT 766 776 D -> N (IN REF. 2).
 FT CONFLICT 828 828 F -> L (IN REF. 1).
 FT CONFLICT 843 843 S -> Y (IN REF. 2).
 FT CONFLICT 852 852 Q -> T (IN REF. 3).
 FT CONFLICT 916 916 W -> C (IN REF. 3).
 FT CONFLICT 1024 1024 L -> M (IN REF. 3).
 FT CONFLICT 1043 1043 A -> V (IN REF. 3).
 FT CONFLICT 1057 1057 L -> V (IN REF. 3).
 FT CONFLICT 1067 1067 S -> C (IN REF. 3).
 FT CONFLICT 1084 1084 S -> C (IN REF. 3).
 SQ SEQUENCE 1175 AA; 134496 MW; 7379CB8B95B8FCED CRC64;
 Query Match 15.6%; Score 96.5; DB 1; Length 1175;
 Best Local Similarity 29.3%; Pred. No. 2.8e-41;
 Matches 294; Conservative 135; Mismatches 310; Indels 265; Gaps 31;
 QY 99 ROSEFORPDS--FDRPCSTIYH-----LSTSEVARTYVGLRTYLMAGIS 154
 DB 18 QGAVFDRYEESFVEFPCNLFKVFDFGLTWKSGEGVLECSLINSIRLAIPDP 77
 QY 123 -----GSHRESLD-----LSTSEVARTYVGLRTYLMAGIS 154
 DB 78 KILALESGKSENDLEGRILCYCGSTLVNIGFTYVAENPEITKQWESLRIHNR 137
 QY 155 DEDSLARRORRDLQKOTFDEADKNGDSLSIG-----VLQLLKLVNL 201
 DB 138 -ANNVSPTCLKHKMKLAF--LNTSGKIPVNSITRTFASGTEKVIQALNEL--GL 191
 QY 202 PQRQKQFREADTDDGDTIGFEFECFAFKMSTRDULYMLTYSNK-DHIDAASIQ 260
 DB 132 PGRKDEIRPAFT-----YEFYELQKICPRDIEDLEFKKINGKTDYTLVDLV 243
 QY 261 RFLVQEKMAQVT-----LESCDITIEFEPCEPKSKGLIGDFTYTRSPAGDI 312
 DB 244 SELNHRQDPRINELIFPFYDAKRAMQIEMYPEDEELKKGLISGFCYKLSMDENAP 303
 QY 313 FNPENHHQDMOTPLSHYFTTSSHNITLVGDQLMSQSRDYMVYLQAGRCVEVDQMD 372
 DB 304 VFLDLLELYQEDHPLAFYFSSSHNYTLTGROGKGSVMYQVYLACRCVEILDQMD 363
 QY 373 --GPDSEPTVHGYTLTKILFKDVIEETINKAFITKNEYVPIYLSIENHGSVYLOOKMAQY 430
 DB 364 GKGEQDEPILTHGKAMCDILFKVIOAKETAVTSEYPIYLSFENHCKSYOQYOMSKY 423
 QY 431 LTLTLDG---KLDISSVSSSEDATTLPSDQMLKGIIVKGRKL----- 469
 DB 424 CEDLFGLDLKQALESHPLPGRIPLSPNDLKRILIKNRKLRPEVEKKOLEALKSMEA 483
 QY 470 -----PANISEDAGEVSDSDAIEDDOCKL---LNGASINRKRYENTARKKLDLSL 521
 DB 484 GESAAPASILEDNEDEETIESADQEEHAPKPEKGNELISADDFSHKAVANSVKGLVTV- 542
 QY 522 KESKIRDCEDPNPNVSSTLSPSGKIGRKSRAEDEVGSDGACASRRGRVLVGSFSRRK 581
 DB 543 -----EDQAMMASIKYV----- 555
 QY 582 KGSILKKAASVEEDDEGDSBGOSRGATNOKTMTKLSRLSDLVYTVSVATHDEM-- 639
 DB 556 -----GA-----TWNHPLYSITMIVYADQVFKQGFHVAE 584
 QY 640 EAASMOVSSFSETKAHQIIOQKPAQVILRENOOLSTIYSSRYDVSSYNTNPQFPNAGC 699
 DB 585 ERNHHYMSFNSFNSVGIGYKTAHIEFVNNTKROMSKRITPKGRVSSNMPDIFNNAC 644
 QY 700 QMVALNTQSEGRMLQLNRAKFSANGGCVYLKPGCMQ--GVFNPNSEPLPQOLKOLV 757
 DB 645 QMVALNTQSEGRMLQLNRAKFSANGGCVYLKPGCMQ--GVFNPNSEPLPQOLKOLV 757
 QY 758 LRTISGQLKPPKPSDMLGDEGLIIPPEVEYIIGLPVDCSRQ--TRVVDNGCFNFTW-E 814
 DB 758 LRTISGQLKPPKPSDMLGDEGLIIPPEVEYIIGLPVDCSRQ--TRVVDNGCFNFTW-E 814

Db 705 VQVISO-----FLSDK--IGTYEVDMXGLPTDITREKFRMANNGLNPVYNE 754
 QY 815 ETLVTF-MVNMPELALVFLVMDHPDIGNRFGICORTLAFSSMPGRHYVL--EGMEEAS- 870
 Db 755 ESFVEFKVILPDIAVLRLVYDNN--NKLIGQRILPLDGLAGRNHLSLRNKGKPLSL 811
 QY 871 --TFVAVH--VSDISGVKQALGLKGLFLR-----GPKPGSL 903
 Db 812 PTFCHVILKTYPPDFGDIYDALSPKKFLLSTTEKRAQDLRMGTETSDIADVPSDTSK 871
 QY 904 DSHAAGRPAPSPV---SQRILRTASAPTKSOKPGRKGPPELV 944
 Db 872 NDKKGRANPAKANVTPOSSSELPTTTAALGSGQAKKGI-ELI 914
 RESULT 9
 ID PIG1_RAT STANDARD: PRT; 1290 AA.
 AC P10686;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II)
 DE (PLC-148).
 GN PLCG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-88289733; Pubmed-2840660;
 RX Sub P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Inositol phospholipid-specific phospholipase C: complete cDNA and
 RT protein sequences and sequence homology to tyrosine kinase-related
 RT oncogene products.";
 RT Proc. Natl. Acad. Sci. U.S.A. 85:5419-5423(1988).
 RL -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-Inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-Inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PPM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
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 CC or send an email to license@isb-sib.ch).

DR InterPro: IPR001192; PI-PLC.
 DR InterPro: IPR000909; PI-PLC_Xdom.
 DR InterPro: IPR001711; PI-PLC_Y.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 2.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 2.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; PHPLIPASC.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 2.
 DR ProDom: PD001202; PI-PLC_Y; 1.
 DR SMART: SM00238; C2; 1.
 DR SMART: SM00239; PH; 2.
 DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCY; 1.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS0001; SH2; 2.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KM Hydrolyase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KM Repeat; Calcium-binding; Phosphorylation.
 FT CA_BIND 165 176 EF_HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT DOMAIN 1075 1177 C2 DOMAIN.
 FT ACT_SITE 1075 1177 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
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 Query Match 15.4%; Score 985; DB 1; Length 1290;
 Best Local Similarity 25.6%; Pred. No. 1,1e-40;
 Matches 303; Conservative 157; Mismatches 313; Indels 410; Gaps 36;
 QY 74 IRRPSSKRNKAKISID--SIOEVSERGESEVQRY-PDGSF--DPNCCFSIYHGS--HR 126
 Db 60 ITW--SGADKIGSIDIREIKRIRKTSRDRQDEPAPFDPQSHCFVILYGEFRLL 117
 QY 127 ESDLDVSTSESVARTWVGLRYLMAGISDESL-ARRQRTROWLKOTDEADKNDGSL 185
 Db 118 KTLSTQTSDEVMVMKIGLTLWLM-----EDTQAATPLQIEKMKQFYSDVRNREDEI 172
 QY 186 SIGVYLQLLKLNWNPVPROVKQMFREADTDHGO--GLTGFEECAFYK--MMSTRRDY 241
 Db 173 SAKDLKMLSLQVNRVYNNR---FLRRLTDFDRSGDIIYGFPAQLYRLSLMSAKTMD 229
 QY 242 LLMV---TYSNHRDLDAASLQRF-----LQVEKMGAGVTLESQDII 281
 Db 230 LPFLFTNLTNRGERPELCQVSLSEFQGLLEYQGLWAVDRQLVOEFMLSLFDPLEIRE 289
 QY 282 EQFEPCEPKNSKGLGLDGCTNNTTRSPAGDIFNPENHNH--HQMTOPLSHYFTTSSHNTY 340
 Db 290 EPy-----FFLDELVTFLFSKENSVMNSQDAVCPETMNNPLSHYWTSSSHNTY 338

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QY 341 LVGDLMGQSRVMTAMVLAQCRCVEVDCMDGPDGEPYHNGYTLTKLIFKDIETIN 400
DB 339 LTGQDFSSSESLFAYARLRCMGCRCIEIDCWDPGMVYIHGHTLTTLTKIFSDVLT 398
QY 401 KYAFKNEYPVITLIEHNCVIOCKKMAOYLTDILGDKLDLSSVSSSDATLTPSPMLKG 460
DB 399 EHAIVASSTPYITLIEHNCVIOCKKMAOYLTDILGDKLDLSSVSSSDATLTPSPMLKG 457
QY 461 KILVKKKLLPA-----NISDAEAG----- 480
DB 458 KILKHKKLLAGSAVEEPTSVMTSENDISNISKNGILYLEDPVNHHEWYHYVLSKSI 517
QY 481 ---EVSDSDADEIDDCCKLLNGASTNRKRV-----ENTAKKLDL----- 519
DB 518 YVSETSDSDGNDDEEPEKASSTELHSEKKEHGLAGRDGRHIAERILTEYCIENG 577
QY 520 -----LIKES-----KIRDC----- 529
DB 578 APDGSFLVRESEVVDYTLTFMRNKGVCYCHRHSDAGTPKFLTDNLVFDLDTIT 637
QY 530 -----E 530
DB 638 HYQOVLRCNEFEMRLSEPVOTNAHESKEWYHASLTRAQAEHMLKRPDGAFLVRKN 697
QY 531 DPNNEFVSTLSPSGK-----LGRSK----- 551
DB 698 EPPSYAIS-PRAGCKIKCHVQOEGQVLMGNSEPDVLDTISYEKHPILYRKMLRYP 756
QY 552 -----AEDD-----VESG----- 559
DB 757 NEBALEKIGTAEPDYGALYGRNPGFYVEANPMTFCANVKAFLDYKAQREDELITTKSA 816
QY 560 -----EDAGASR----- 566
DB 817 IIONVEKODGQWNRG DYGGKKQLMPPSNYVEEMINPAILEPEREHIDENSPLGDLRGVL 876
QY 567 -----RNGRLVYGSFRRKKKSKLKAAYEE-----GREGDPSG 604
DB 877 DVPACQIARPECKNNRLVFYSISMPSVAMQSLDVAADQDELDQWVKKIREVAQADAR 936
QY 605 QSGGATROKKTMLRALSDLYKTVSVATHD--IEMEAASSVOVSSSETRAHOTILOO- 661
DB 937 LIEGKMMERR-KKIALELELVELVYCRPVEFDEKIGTERACRDNSSFPETKAKEYNKA 995
QY 662 KPAQVLRFNQOOLSRITPSSYRVDSNYPPOFPMNAGCOMVALINOSBEKMLQLRAKFS 721
DB 996 KKKKFLQVNRLOLSRITPSSYRVDSNYPPOFPMNAGCOMVALINOSBEKMLQLRAKFS 1055
QY 722 ANGCGYVLRPGCMQGVFNPNSEDEPLPGOLKQVLRILISGOQLPKPRDSMLGREGIIT 781
DB 1056 AGGHGCGYVLRPGCMQGVFNPNSEDEPLPGOLKQVLRILISGOQLPKPRDSMLGREGIIT 1108
QY 782 DPFVEVEIIGLVDCSRETRVVDNGFPPVY-EEVLVPMVMPREILAIVRLVMDHPDG 840
DB 1109 CFEVELEVAAGAYDSTKTEFVVDNGFPPVYPAKPFHIOJNSPFAFLRFVYEDMFS 1168
QY 841 -RDFIGORTLAFSSMMPGYRHY-----YLEGMEASIFVHAV 877
DB 1169 DQNFIAQATFFYKGLKGTGRRAVPLKNNYSEDLIASLILIKIDI 1211

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OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=90094370; PubMed=2557343;
RA Emori Y., Homma Y., Sorimachi H., Kawasaki H., Nakanishi O.,
RA Suzuki K., Takenawa T.,
RT "A second type of rat phosphoinositide-specific phospholipase C
RT containing a src-related sequence not essential for phosphoinositide-
RT hydrolyzing activity."
RL J. Biol. Chem. 264:21885-21890(1989).
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CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. IT IS A CRUCIAL ENZYME IN TRANSMEMBRANE SIGNALING.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: Calcium.
CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
CC SYSTEM RECEPTORS.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC
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CC
CC EMBL: J05155; AAA1896.1;
CC PIR: A34163; A34163.
CC HSSP: P08487; 2PID.
CC
CC InterPro: IPR000008; C2.
CC InterPro: IPR001849; PH.
CC InterPro: IPR001192; PL_PLC.
CC InterPro: IPR000909; PL_PLC_Xdom.
CC InterPro: IPR001711; PL_PLC_Y.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC Pfam: PF00017; SH2; 2.
CC Pfam: PF00018; SH3; 1.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00169; PH; 2.
CC Pfam: PF00387; PL_PLC-X; 1.
CC Pfam: PF00388; PL_PLC-Y; 1.
CC PRINTS: PR00390; PHPLIPASEC.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD000066; SH3; 1.
CC ProDom: PD000093; SH2; 2.
CC ProDom: PD001202; PL_PLC_Y; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00233; PH; 2.
CC SMART: SM00148; PLCCX; 1.
CC SMART: SM00149; PLCYC; 1.
CC SMART: SM00325; SH2; 2.
CC SMART: SM00326; SH3; 1.
CC PROSITE: PS50001; SH2; 2.
CC PROSITE: PS50002; SH3; 1.
CC PROSITE: PS50003; PH_DOMAIN; 1.
CC PROSITE: PS50004; C2_DOMAIN; 2; 1.
CC PROSITE: PS50007; PL_PLC_X_DOMAIN; 1.
CC PROSITE: PS50008; PL_PLC_Y_DOMAIN; 1.

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CC or send an email to license@isb-slb.ch).

CC
DR EMBL: X14034; CAA32194.1; -
DR EMBL: M37238; AAA60112.1; -
DR PIR: S02004; S02004.
DR HSSP: P08487; 2PBD.
DR Genew: HGNC:9066; PLCG2.
DR MIM: 600220; -
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DR InterPro: IPR001849; PH.
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DR InterPro: IPR001711; PL_PLC_X.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00017; SH2; 2.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00169; PH; 2.
DR Pfam: PF00387; PI-PLC-X; 1.
DR Pfam: PF00388; PI-PLC-Y; 1.
DR PRINTS: PR00390; PHPLIPASEC.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR ProDom: PD000093; SH2; 2.
DR ProDom: PD000202; PL_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00233; PH; 2.
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DR SMART: SM00249; PLCYC; 1.
DR SMART: SM00252; SH2; 2.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50001; SH2; 2.
DR PROSITE: PS50002; SH3; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS50004; C2_DOMAIN; 2; 1.
DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolyase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
KW Repeat; Calcium-binding; Phosphorylation.
FT DOMAIN 20 131 PH.
FT DOMAIN 312 456 DOMAIN X.
FT DOMAIN 532 635 SH2 1.
FT DOMAIN 646 735 SH2 2.
FT DOMAIN 769 829 SH3.
FT DOMAIN 930 1044 DOMAIN Y.
FT DOMAIN 1059 1152 DOMAIN Y.
FT ACT_SITE 327 327 C2 DOMAIN.
FT ACT_SITE 372 372 BY SIMILARITY.
SQ SEQUENCE 1252 AA; 146119 MW; 6F63F051621EEB64 CRC64;

Query Match 14.9% Score 950.5; DB 1; Length 1252;
Best local similarity 25.1% Pred. No. 5, 2e-39;
Matches 292; Conservative 164; Mismatches 310; Indels 399; Gaps 34;

QY 74 IRRRSRKNKKAISIDSIQEVSEGRQSEVFQRPDGSFDPCCSFYSH--RESIDL 131
DB 52 VAMSKRADRIEFGIDIMEIKETIRPKNSKDFEAKAVRQKEDCCFTILXGTFVLTSL 111
QY 132 VSSSEVATWGLRYLMAAGISDEDSLARKQRTDOMLKQTFDEADKNGSGSLIGEV 191
DB 112 AADSKEDAVNMISGLKIL---HDEMASTPTIIESWLKQIYSDVDRRNSISLREIK 167
QY 192 QLLHLNVLPRQR-VKQFREADTDHOGTLGFEEFCAFYKMM-----STRDL 240
DB 168 TLPLINFEVSAAFLKQKFEVIGL--HKDELSEFOHFIKKLMEQOKSLIDEFKKDS 225
QY 241 YLLMTYSNKHNDASL---QRF-----QVEKMAVLTLESCODITE 282
DB 226 SVFLL---GMDRPDASAVYLHDFORFLIHQEHMAODLKKVRRMTKFTDDIMRETAE 282
QY 283 QEPREPKSKGLIGDGTFTYTRPADIDFIRENNHN--QDMTPRLSHYITTSHTNYL 341

DB 283 PF-----LVDEFLTYLFSRENSIMDEKYADVMDQNNPFLSHWISSHTNYL 331
QY 342 VGDQIMQSRYDVAWYLAQACVEYDCWDGDPGRYIHGGYTLKSLFLFDVITFK 401
DB 332 TGDQLRSESSPEAVINLRMGCKCIELDCWDGDPGRYIHGGYTLKSLFLFDVITFK 391
QY 402 YAFIKNEYPIYLISIEHCSYTOOKKAAQYLTDLGDKLDSVSSBDATTLSPQMLKGR 461
DB 392 HAFVTSFPVILISIEHCSVEQORHMAKAFKEVFGDL--LTKPTASADQLPSPGLRKK 450
QY 462 ILVKKKL-----PANI-----SEDAEGBVSDEDAE-----IDDD-- 494
DB 451 IILKKKLLGRGVYDVNAMEDKDEKQGEELTYMDSIDQKWTGRHYCAIADAKLSFSDIE 510
QY 495 -----CKLLNDASTNRKRVNTAKRKL-----DSLKESEK--- 525
DB 511 QTMEEVPODIPPTELHFGKEMFKKVEKRTSAEKLQYCMETGKXOTPLVRESFPP 570
QY 526 ----- 525
DB 571 NDYTLSEFMSGRVQHCRISTMEGTLKYLYLNDLFRRMVALIQHRETHLPACAEFLR 630
QY 526 -----INDCEDPNNESYSTLSPGK 545
DB 631 LTDPVPNPNHESKPYIYDLSRGAEDMLRIPDGAFLIKRREGSDVAL-TFRARGK 689
QY 546 L-----GR-----KSKAEEDV 556
DB 690 VAKCRINRDGRFVLGTSAFESLVELSVYKHSILYRKMRLRYVPPELLEBRYNTEDI 749
QY 557 ESGEDAG-----ASRRN-----GRLYVGSFSRKKKGSGL-----KKAASVEEG 595
DB 750 NSLYDSKRYVPSELNPMQRYKALDYKAKSDLSFCRGALIHNVSKREGQWKKG 809
QY 596 DEG-----QDSP-GGQSRG----- 608
DB 810 DVGTRIQQYFSPSYVEDISTADFEELKQIIEDNPLGSLCHGILLDNTYNYKAPQCKQ 869
QY 609 -----ATRO-----KTKMLLSRA 621
DB 870 KSFVILIEPKRGDPPEVPAIDRYEELFEWQSIRETITWKIDSKENMKYWEKQSIATIE 929
QY 622 LSDLYKTKYSVATHDIEMEASMSQVSSSETKAKQILQKPAQYLFENQOOLSRIPSS 681
DB 930 LSDLYVYCKPTSKYKDNLENDPEIRISFVETKADSIIRQRPVLLKYNQKGLRVRYPKG 989
QY 682 YRVSSNNPQPFNNAGQWALNYOSGRMLQINRAKFSANGCGYVLRPGCMQCGVFN 741
DB 990 QRVSSNIDPRLMLCGSQWALNLFOTADKYOMNHALLFSINGRTGYLQPESEW----R 1044
QY 742 PNEEDPLRGLQKQ---LVLRITISGOQLPKPRDSMLGDGEIITDPVEVEITGLPVDGS 797
DB 1045 TEKDYPMPEESQKILMLTYKVLGARHLR-----LG--RSIACRVEVEIGCAEYGNV 1097
QY 798 REQIRYVDNCKFNPTW---EETLVYVNMPEIALVRLVMDHDPIG-RDFIGORTLAFFSS 853
DB 1098 KFKTIVVNDNLSPIMATQEKVTEFIYDNLAFIRVVVEEDMFSPNPLAATYPIKA 1157
QY 854 MAPGYRVH-----YLQEMEASIFV 873
DB 1158 VKSGFRSVPLKNGISEDIELASLIV 1182

RESULT 12
PIPL_DROME
ID PIPL_DROME STANDARD; PRT: 1312 AA.
AC P25455: O9VFN9;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-phosphatidylinositol-4,5-disphosphate phosphodiesterase classes I and II (EC 3.1.4.11) (Phospholipase C).
GN PLC21C OR PLC-21 OR CG4574.

OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=91286274; PUBMED=206123;
 RA Shortridge R.D., Yoon J., Lending C.R., Bloomquist B.T.,
 RA Perdev M.H., Pak W.L.,
 RT "A Drosophila phospholipase C gene that is expressed in the central
 RT nervous system".
 RL J. Biol. Chem. 266:12474-12480(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (CLASS II ISOFORM).
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Nelson C.R., Miklos G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.H.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rehett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CLASS I AND CLASS II (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: NEURONAL CELL BODIES OF THE OPTIC LOBE,
 CC CENTRAL BRAIN, AND THORACIC GANGLIA IN ADULTS, AND THE BRAIN OF
 CC LARVAE.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: M60452; AAA2881.1; -
 CC EMBL: M60453; AAA28820.1; -
 CC EMBL: AE003589; AAF51507.1; -
 CC PIR: BA0879; B40879.
 CC HSSP: P10688; 10AS.
 CC Flybase: FBgn0004611; Plc21C.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR001192; Pl_Plc.
 CC InterPro: IPR000909; Pl_Plc_xdom.
 CC InterPro: IPR001711; Pl_Plc_Y.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00387; Pl_Plc-Y; 1.
 CC Pfam: PF00388; Pl_Plc-X; 1.
 CC PRINTS: PR00390; PHPLIPASEC.
 CC ProDom: PD001202; Pl_Plc_Y; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00148; PLCXC; 1.
 CC SMART: SM00149; PLCYC; 1.
 CC PROSITE: PS50004; C2_DOMAIN_2; 1.
 CC PROSITE: PS50007; Pl_Plc_X_DOMAIN; 1.
 CC PROSITE: PS50008; Pl_Plc_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Transducer; Alternative splicing.
 CC FT DOMAIN 318 466
 CC FT DOMAIN 599 715
 CC FT DOMAIN 722 820
 CC ACT_SITE 333 333
 CC ACT_SITE 378 378
 CC VARSPIC 1057 1063
 CC CONFLICT 508 508
 CC G -> A (IN REF. 1).
 CC SEQUENCE 1312 AA; 145717 MW; B8DD0EFA8C2665 CRC64;
 Query Match 14.8%; Score 945.5; DB 1; Length 1312;
 Best Local Similarity 25.3%; Pred. No. 9.7e-39;
 Matches 324; Conservative 190; Mismatches 434; Indels 335; Gaps 42;
 44 AMEGMQMVK-----LNGSGGLVRFYLDENRSCIRMPRSKRNEKAKISIDS 91
 19 ALDQGEKIRIMDDSGTGTPYKAVDAKGF-LYWDQN-----NELDIDYAT 66
 92 IQEVSEGRQS-----EYFORYPGSGDPNCSYIGSHRESLIDS---TSSEA 139
 67 IRDVTGGYARRPRDNKLRQIVTLGPDQTLER-TYVCHGSDFVNMTFVNFCIRRDIA 125
 140 RHWWTGLYLMAGISDEDSLARORTDQWLKOTFD-----EADKNGDSLISGEVLQDLH 195
 126 QLTWDGL-----IKLAVSLAQLNGSALMFLQKHTKLCLOVYKS--GRIPVNIILKPA 177
 196 K-----LNV-NLPRQVRKMFREADTDDHOGTLGFEFCAFYKAMSTRRLYL 243
 178 QKEDRKREKALDVTGIPSGKVDSI-----SVSKFQEFDFYNYKYLTRSEVER 229
 244 M-LTYSNKHDLDAASQRLQVLEOK-----MAGVTLESQODIIFQFECPEKNSK 293
 230 FDSIVNSKRKMSIAQVLEFLNKTQRDPRLNELLYANPARKELIQEYFNKRAOK 289
 294 GLIGIDGFNTYRSPAGDIFNPENHHVHODMTOPLSHYFITSNHTYLVGDQLMSGRVD 353
 290 QGLSIDGFRLYMGSDNRIAPSKRLDQDDMDQPSHSYFINSHTYLVGHLQKSSVE 349
 354 MRAWYLQACRVEVDQDPDGEPIYHNGTLLSKILFKVITIKYAFIKREYVYL 413
 350 IYRQCLAGCRVEVDENNGTEPEYVHGYTVEIPFAKVLEALIASAKTSEYVIL 409
 414 SIENHSVYQKKMAYLIDILIGRL---DLSSVSEDDATLPSQMLKGIIVKGR--- 467
 410 SEENHCNPRQAKIANCYCEIFGMDLDRPDSHLEPNDMLPPAMLRRIILKNNKH 469

QY 468 -----KLPANISEDAEERGVSDSDADEIDDDCKLINGASTNRKRENTAKRKLD 518
 Db 470 HHHHHHHHKKRPAQVGPRAANNKLTITANSVD----- 500
 QY 519 SLIKESKIRIOCEDNNNSVSTLSGKLGKRSKAEEDY---ESGEDGASR--RNGHLYV 573
 Db 501 -----AKAAQVGLSASHEDEGVYRSTANGVDAT 529
 QY 574 GS-----FSRRKKKSKLKKAASVEBG--DEGDDSGGSGRATRG 612
 Db 530 GTGTGSAAGTAGHAPLQIROSQKSDSTGSDSSSDSLNTPTNLPDSGNEPPPERKA 569
 QY 613 KTKTKLRALSDLYTKYKSAVATHDEMEAAAS---WQVSSFETAKHQLIQKPAQYLR 668
 Db 590 QKETAGAEISALVNVQPI--HFSFEENAEKKNRCYEMSSFDKQATTLTKRPIEFV 647
 QY 669 FNOOLSRITPSRYVSDSVNPNOPFNACCQVVALNYSEGRLQLNKRAKFSANGCGY 728
 Db 648 YNKHQLSRVYPAQTRDSSNFMQLTNACQVLALNFOTLDIAMQNLGIFETYNARSGY 707
 QY 729 VLKPCCKCG--VFNPNSEDPLPGOLKKOLVLTIIISGOOLPKPRDSMLGDRGEIIDPVE 786
 Db 708 LKLPERRRDRRLDPEFAESTVDGIAGVSTVLSGQFLDKR-----ANTVE 757
 QY 787 VEIIGPVDCSRE--QTRVYDNGFNPWT--EETLV--WYHPEIALVFLVDHDPIDGRD 842
 Db 758 VDMYGPADIVYKFKRTKTVKMDGNMPLVDEEPYFKVYVLELASSIRAAVEE--GSK 814
 QY 843 FICQRTLASMMQPGYRHYVLEGEERASTFVHVAASDISGKQKQALGLGLPL--RGP 898
 Db 815 LIGHRYLPIYIGLPGYRHY-----NLSEVGQPIALASLTLVYVVDY 857
 QY 899 KPSLDSHAAGRPAPRSVSOHLIRTAAPTKSQKPRGREGPELVLTGRDNGSKVAD 958
 Db 858 VPDDELNFA-----EALANPKYQSELEKRDIOISVLTDEEALGSAD 901
 QY 959 VYPPGPGAPPAQEGPGSGSPRGKAPAAVAEKSPVRVRYVDPGPPAGMA----- 1012
 Db 902 DLKSGCGKKEKLRPVESLAT--SPKRPSTISAANAASVYTVTRTGCGEISIVAPSI 960
 QY 1013 -----ATCMKCYVGS----- 1022
 Db 961 QHSHLSDSVSTIQVSSSQFVDVLAEPLEKILDRHYSEKRLMEKLESLRKHD 1020
 QY 1023 -----CAGVNTGGLQREPPSPGPASROAIPRQPRADSLGAPCCGLDHAITGRSRE 1077
 Db 1021 KEKIKIAGOKSSPLEGKRP-----KFAITNKLYKLSKSLNC--LSPHSEPG--VE 1068
 QY 1078 APKGGAMROGPGSGSGSSSSSDSPSGIPERSFWEPE---GACRQPGALGEMSALE 1133
 Db 1069 IPACP--LDLDDSEESAADAAGEDLAGSSSLDGRQESRLRSACR-----Y 1115
 QY 1134 AOKLEIRSK--SPWFSAGKPL 1154
 Db 1116 TSQYREIQEKYHEALYSAAEVYL 1138

RX MEDLINE=88270495; PubMed=3390863;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.";
 RL Cell 54:161-169(1988).
 RN [2]
 RP ACTIVITY, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX MEDLINE=93203266; PubMed=8454637;
 RA Zhou D.-Y., Lee H.-H., Park D., Lee C.-W., Lee K.-H., Yoo O.J.,
 RT "Cloning, sequencing, purification, and Gq-dependent activation of
 phospholipase C-beta 3";
 RL J. Biol. Chem. 268:6654-6661(1993).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DINGICGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- CORRECTOR: Calcium.
 CC -1- SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
 CC -1- TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
 CC parotid gland, liver, uterus, lung, heart, adrenal gland and
 CC ovary. Not detected in spleen, pancreas, intestine, thymus or
 CC kidney.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; M20636; AAA41885.1; -
 DR PIR; A28821; A28821.
 DR HSSP; P10688; IDJX.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_Xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00387; PI_PLC-Y; 1.
 DR Pfam; PF00388; PI_PLC-X; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXG; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PSS0004; C2_DOMAIN_2; 1.
 DR PROSITE; PSS0007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PSS0008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467
 FT DOMAIN 540 656
 FT DOMAIN 663 761
 FT ACT_SITE 331 331
 FT ACT_SITE 378 378
 FT MOD_RES 887 887
 SQ SEQUENCE 1216 AA; 138344 MW; 92F23691781F788E CR64;
 Query Match 14.8%; Score 945; DB 1; Length 1216;
 Best Local Similarity 26.0%; Pred. No. 9.4e-35;
 Matches 293; Conservative 153; Mismatches 325; Indels 274; Gaps 38;
 QY 44 AMQEGNQWYK-----LNGSGKLVRFYIYIDHRS-----CIRMRP 78
 Db 21 SLKGTGKFKVKKMDSDSTIVTPIILRTDPGGF--FYWTQNKETELLDLSLVKADARGCKHAK 79

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QY 79 SRNREKAKISIDISIOVSEGRSEVFORYPDGSFDPNCCFSIYHCSHRESIDLVSSTSEV 138
DB 80 APDPLRELD-----VGNIGHLEGRNITYVYGPD-----LVNISH---LNLVAFQEEV 126
QY 139 ARTWVTGLRYLMAGISDEDSLARROTRDQMLKOTFFDADKNGDGLSIGVLOLMLKLN 198
DB 127 AKEMTNEV-----FSLATNLLAQNMSRDAFLKAYTKL-----KLO 162
QY 199 V-----NLPRQRYVMKREADTDHOGTLGFEFECAFYKMMSTR-----DLYLLM 244
DB 163 VTEGRPIPLKNYRLF-SADKRKREVAL---EACS---LPSRNSITQEDPTPVYRVF 215
QY 245 LTVSNHDKHLD-----AASLQRFLOEQKMGAVTL-----ESCQDII 281
DB 216 LNNICPEPEIDNIFSEGRKSKRYLTFVDDMDPFINLKORDPRLNELLYPRLKQEOVOYLI 275
QY 282 EOPREPCENKSKGLGIDGTNTYTRSPADGINPREHHVHODMOTPLSHYFTSSHNTYL 341
DB 276 EKEPNNSLAKKQOMSVDFMRILSGEENGVSPEKLDINEDMSQPLSHYFTSSHNTYL 335
QY 342 VGDOLMSQSRDYMAYLQACRCVENDCDG--PDGEPIVHGYTLTKILFKDVIETI 399
DB 336 TAGOLAGNSVEMRYOVLISGCRVCLDCKMGTAEPEVITHGFTMTETSEFKEVIEAI 395
QY 400 NKVAFIRNEYPVVILSTENHC-SYIQOKKAAQYLTDLGDKL---DLSSVSEDAATLPSR 455
DB 396 AECAFKTSPPFILLFSEFNHVSPOKQAKMAYRCLIFGDLMLPELEKPLSEGVLPSP 455
QY 456 QMLGKTLVYGGKRLPANISEDAERGEVSDSDADEIDDDCKLNGDASTNRKREVENTAR 515
DB 456 MDLMTKILVKKK-----KSKHSESGSKK-----KSKHSESGSKK 480
QY 516 KIDSLINKSIRDEDPNNSVSTLSPSGKLGRKSKAEVEYSEGEDAGASRRNGRLVGS 575
DB 481 KLS-----EQASNRYSDSSVFEPPSPGAGADRESDDDDDDDD-----519
QY 576 FSRKRRKSKLAKKASVEEGDEGDDSPGCGRGATROKTKMLSRALSDLVKTKSVATH 635
DB 530 -----CKSSMDGEGAGSEAM-----ATEE-----MSNLVNTIOPYKFE 553
QY 636 DIE--MEASGNOVSPSESTRAHQTLOOKPAQYLRFNOOQLSRIPSYSTVSDSNINPQ 693
DB 554 SEFTSKKKNKSPSEMSFEYTGDLQTSKPYEYNNMQLSRIPYCTRVSDSNINPQ 613
QY 694 FNNAGCQVYALNYOSEGRMLQNLRAKFSANGCGCYLKGPGMCO--GVFNPSNEDPLPGQ 751
DB 614 FNNAGCQVYALNYOTVDLAMOINMGMYNKGSGRLKPEFMRPRDKHFDPTFGIYDGI 673
QY 752 LKKOLVLRITISGOQLPKPRDSMLGDRGEIIDPEVEVEIIGLVPDCSRE--QTRVVDNGF 809
DB 674 VANITLSVKITISGO-----FLSDK--VGYYVEVDEFGLPVPTRRKAFKTSQGNAY 723
QY 810 NPTW-EETLVF-MVHMPETALVRLVMDHDPGRDFTQORLASSMMGRHRYLSEME 867
DB 724 NPWEEEPVYFVKVYLPJSLACLRIAAEE--GKFIQHRIILPVQAIRPGHITCLNRK 780
QY 868 E-----ASIFVHAVSD-----ISGKVR-----QALGLKGLFLRGKPGSL 903
DB 781 NQPLMLPAFVYIEVDYDPDYADYIELNSPIRYVNLMEGRAKQALALTLIED-----834
QY 904 DSHAAGPPAPSVSORILKRTASAPTKSQKGRGKGPBLVIGTDTSKGVADYVPPG 963
DB 835 -----EEVKKKADPGTSESEAPSE-----TRTPAENGVNHTATLA 871
QY 964 PGAPAPAP-AQEGPGSGSPRCAPA 987
DB 872 PKPPSOAPHOSAPAGS---VKAPA 892

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RESULT 14
PIB4_BOVIN
ID PIB4_BOVIN STANDARD; PRT; 1023 AA.

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AC 007722; 007721; 007723; 007724;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta 4
DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4) (Fragment).
GN PLCB4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Retina;
RC MEDLINE=93317620; PubMed=8327481;
RA Ferreira P.A., Shortridge R.D., Pak W.L.;
RT "Distinctive subtypes of bovine phospholipase C that have preferential
RT expression in the retina and high homology to the norpa gene product
RT of Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 90:6042-6046(1993).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -1- COFACTOR: Calcium.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: 1A, 1B (SHOWN HERE), 2A
CC AND 2B; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L13936; AAA30699.1; -
CC EMBL: L13935; AAC37304.1; -
CC EMBL: L13937; AAA30700.1; -
CC EMBL: L13938; AAA30701.1; -
CC HSSP: P10688; 1OAS.
CC InterPro: IPR000008; C2.
CC InterPro: IPR001192; PL_PLC.
CC InterPro: IPR000909; PL_PLC_Xdom.
CC InterPro: IPR001711; PL_PLC_Y.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00387; PL_PLC-Y; 1.
CC Pfam: PF00388; PL_PLC-X; 1.
CC PRINTS: PR00390; PHPLIPASEC.
CC PRODOM: PD001202; PL_PLC_Y; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00148; PLCXc; 1.
CC SMART: SM00149; PLCTc; 1.
CC PROSITE: PS50004; C2_DOMAIN_2; 1.
CC PROSITE: PS50007; PL_PLC_X_DOMAIN; 1.
CC PROSITE: PS50008; PL_PLC_Y_DOMAIN; 1.
CC HydroLase; Lipid degradation; Transducer; Phosphorylation; Calcium;
KW Alternative splicing; 1.
KW NON_TER 1.
FT DOMAIN 149 299 DOMAIN X.
FT DOMAIN 413 529 DOMAIN Y.
FT DOMAIN 536 634 C2 DOMAIN.
FT ACT_SITE 164 164 BY SIMILARITY.
FT ACT_SITE 211 211 BY SIMILARITY.
FT VARSPIC <1 104 MISSING (IN ISOFORM 2A AND ISOFORM 2B).

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FT VASPLIC 372 383 MISSING (IN ISOFORM 1A).
 VASPLIC 372 383 MISSING (IN ISOFORM 2A).
 SEQUENCE 1023 AA; 117109 MW; 416D700C2095748C CRC64;

Query Match 14.7% Score 937.5; DR 1; Length 1023;
 Best Local Similarity 33.4%; Pred. No. 1.8e-38;
 Matches 258; Conservative 110; Mismatches 258; Indels 147; Gaps 25;

QY 224 FEBCATAYKMKSTRDLYLLMTYNSHK-DHLDASTQRFQVEOKMAGVT-----L 274
 DB 42 YEKYEELQKICPRTDIEDFKKINGKIDYLVFDVLSPLNHQDPLNELLEPFYDA 101
 QY 275 ESCDIIIEPCEPENSKGLIGDFTNTYTRPADINDPENHIVHODMTPSLHYFTT 334
 DB 102 KRAMQIIEMEPEDDLKQGLISSDGCRLMSDENAPFLDLRLCYQEMDPLAHYFIS 161
 QY 335 SSHNTYLVGQMSQSHVDYAWYVLOAGRCVEVDMD--GPDGEPIVHGHTLSKILF 392
 DB 162 SSHNTYLVGQFGKSSVEKRYVLLAGRCVEVDMDGKDEPITTHGKAKCTDILF 221
 QY 393 KDVIETINKYAFIKNEYPVLTSTENCSYIOOKKAAQYITDILGD--KLDLSVSSDA 449
 DB 222 KDVIQAKETAEVTSSEPVLTSTENCSKYQYKMSKCEDLFGDILLKQALESHPLEPG 281
 QY 450 TLPSPQMLKGLVY-----GKRL-----PANISEDAEFGVSDED 486
 DB 282 RPLSPNDLKRILIKQTEVEVEKQLEALSMMEAGESAAPVNLLEDNEEIESAE 341
 QY 487 SAEIDDDKL---LNGDASTRKREVTAKRKLDLSEKIRDCEDPNFVSSTLSPS 543
 DB 342 QEEHAEPEKRYGNSADLGHKEAIVSVK----- 372
 QY 544 GKLRKSKAEEDVESGEDAGARRNGRLVYGSFSRRKKSKLKAASVERGSDGSDSPG 603
 DB 373 -----KASDLE-----HENSCKG-----LVYVE--DQAMMAS 399
 QY 604 GSGRATRKTKTKMSRLSLDYTKSVANTHDEM--EAASSQVVSFSETKAHQILQO 661
 DB 400 YKVGQ-----TTNHPYLSITMINAOPVKQGFHVAEERINHYNMSSPNSVGLYLKT 454
 QY 662 KPAQYLRNOCOLSRIVSSRYVDSNNPQPFVNNAGGOWALVYSGEGLMQLNRAKFS 721
 DB 455 HAIEFVNANKRQMSRIYKGGRVSSNMPDIFNNSGOWSLVYQPLDAMLONGKFE 514
 QY 722 ANGGGCVYLAGGCMQ--GVFNPSDEPLPGQLKOLVRLIISGQOUPKPRDSMLGDRGE 779
 DB 515 YNGSGGYLLKDPFKRRPDRPFDPESETPVDGVIAATGCVGVISQ-----FLSDKR 565
 QY 780 IIDEFVEVEIIGLPVDCSREQ--TRVYDDNGFNTW--EELVLF-VYHMEPIALVRLVMD 835
 DB 566 -IGTYVEVDMLGLPTDITRKEFRTRMANNGLNPNVNESEFVRKYLIDPLAVRIAAYD 624
 QY 836 HDPIGRDPIGORTLAFSSMPGYRHYV--EGMEEAS--IFVHVA-----VSDISKVVO 886
 DB 625 DN---NKLIGQRIPLDGLGAGYRHLISLRNEGKPLSLPTIFCNILYKTYVDPGEGDIYD 681
 QY 887 ALGLKGLFLNGPKRGLSDHSAAGRPAPRSVSGRIILRTASAPTKSQKGRNG 939
 DB 682 ALSDPKKFL-----SITERRADQMRAMGLETSDI-----ADVPSPTSKNDKKG 724

RESULT 15
 ID PIR1 HUMAN STANDARD; PRT: 1216 AA.
 AC G9N065; G9N065; G9NTH4; O60325; G9H4H2; G9B0W2; G9U0P6;
 AC G9U0M6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).
 GN PLCB1 KIAA0581.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE-Brain;
 RX PubMed-11118617;
 RA Caricose A., Sala C., Roncarati R., Formenti E., Terstappen G.C.,
 RT "Cloning and characterization of the human phosphoinositide-specific
 RL phospholipase C-beta 1 (PLCBeta1)."
 RP Biochim. Biophys. Acta 1517:63-72(2000).
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE=20225428; PubMed-10760467;
 RA Perruzzi D., Calabrese G., Faenza I., Manzoli L., Matteucci A.,
 RT "Identification and chromosomal localisation by fluorescence in situ
 RT hybridisation of human gene of phosphoinositide-specific phospholipase
 RL C beta 1".
 RP Biochim. Biophys. Acta 1484:175-182(2000).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagduly C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead D.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Graham D.V., Griffiths S., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvallo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell U.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMuray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RP Rogers J.
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).
 RC TISSUE-Testis;
 RA Koehner K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RL code for large proteins in vitro.";
 RC DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.

CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AJ278313; CAB98142.1; -
 DR EMBL; AJ278314; CAB98143.1; -
 DR EMBL; AY004175; AAF86613.1; -
 DR EMBL; AL031683; CAC16181.1; -
 DR EMBL; AL050315; CAB56498.1; -
 DR EMBL; AL049632; CAB46663.1; -
 DR EMBL; AL137267; CAB70666.1; -
 DR EMBL; AB011153; BAA25507.1; -
 DR HSSP; P10688; IDJX. -
 DR Genew; HGNC:15917; PLCB1.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 2.
 DR Pfam; PF00387; PI_PLC_Y; 3.
 DR Pfam; PF00388; PI_PLC_X; 2.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 DR HydroLase; Lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 316 467 DOMAIN X.
 FT DOMAIN 540 656 DOMAIN Y.
 FT DOMAIN 663 761 C2 DOMAIN.
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT ACT_SITE 378 378 BY SIMILARITY.
 FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 FT VARSPIC 1142 1216 LEVELDEYODKRRRLPLELLEFVQAMGKISSEDSHSA
 FT PLSLSDPGKVNHRKTSSEELGDIPEKFEFPL -> GEG
 FT SSSFLSETHCHEDPSVSPNTPPPQALKM (IN ISOFORM
 FT B)
 FT MAGAOPGVHALLQKPYCVSDSLKTKFYKAMD -> MGS
 FT LOGIATKILIRLISDALIKRETDLKS (IN REF. 2).
 FT CONFLICT 1 34
 FT CONFLICT 189 189 L -> M (IN REF. 2).
 FT CONFLICT 203 203 P -> L (IN REF. 2).
 FT CONFLICT 216 216 L -> F (IN REF. 2).
 FT CONFLICT 221 221 P -> L (IN REF. 2).
 FT CONFLICT 226 226 L -> P (IN REF. 2).
 FT CONFLICT 309 309 P -> T (IN REF. 2).
 FT CONFLICT 320 320 Q -> R (IN REF. 2).
 FT CONFLICT 352 352 V -> A (IN REF. 2).
 FT CONFLICT 366 366 K -> R (IN REF. 2).
 FT CONFLICT 393 393 E -> K (IN REF. 2).
 FT CONFLICT 983 983 P -> S (IN REF. 1; CAB98143).
 FT SEQUENCE 1216 AA; 138566 MW; 6F4265D1A50C6FD1 CRC64;
 Query Match 14.7%; Score 937; DB 1; Length 1216;
 Best Local Similarity 28.4%; Pred. No. 2,3e-38;
 Matches 297; Conservative 155; Mismatches 318; Indels 276; Gaps 40;

QY 44 AMOEGOMVYK-----LKGSGKLVREYYLDEHNS-----CIKRRP 78
 Db 21 SLKGTGKVKKDDSTIVTPILRTDPQGF-FYWDQNKETELLDSLVDKACGHNAR 79
 QY 79 SRKEKAKISIDISQVSEGESEVFPQYRPGSDPPCCSIYHSGRESLIDVYSSEV 138
 Db 80 APKDFKLEELD-----VGNIGRLQRMITVYVGP---LVNISH---LNLAFQEEV 126
 QY 139 ARVWTGRLVIMAGISDEDSLARQRTPDQMLKOTPEADKNGDGSISGEVLQHLKN 198
 Db 127 AKETNEY-----FSLATNLAAQMSDAFLERAYKRL-----KLO 162
 QY 199 V---NIPROVKOMFREDATDDHOGTLGFEFCFAFKMSTRD-----LYLM 244
 Db 163 VTPEDRIPLKNIYRLF-SADRRVETAL---EACS---LPSRRSDSIPOEDFPEYRVF 215
 QY 245 LYSNKHRLD-----AASIQRFLOVQKAGVTL-----ESGDI 281
 Db 216 LNNLCPREIDNITSEFGAKSPYLTVDQMDFTNLKORPRLNELIYPLKQEOVYLI 275
 QY 282 EQFEPCEPNKSKGLGIDGFTNYTRSPAGDI.FNDEHHVHODMTQPLSHVFTSSHTYL 341
 Db 276 EKEPENSLARKQISVDGFMRLYLSGEENGVSPEKLDLNDMSQPLSHFTINSHTYL 335
 QY 342 VGDQMSQSRVDMTAVMLQAGRCVEYDCWDG--PDGEPIYHGGYTLTKLFDVYETI 399
 Db 336 TAGQLAGNSVEMYRQVLLSGRCVELDCMKGRFAESEPVTYHGTMTETISFEVIEAI 395
 QY 400 NKVAFIKNEYVPIYLSIENHC-SVIOQKMAOYLNDILGDKT---DLSSVEDATTLTSP 455
 Db 396 ACACAKTSFPLFLTFENHVDSPKQAKMAEYCRILFDALMLPELEYPLESGVPLSP 455
 QY 456 QMLKGIYVKGKRLPANISSEAESEVSDSDAIDDDCKLNGDASTNRKRVENAKR 515
 Db 456 MDLAKIKLYKNK-----KSHKSESGSGK 480
 QY 516 KIDSLIKESKIDCEDPNPFVST--LSPSGKLGKKAEDVESEGEDAGASRRNGRLVY 573
 Db 481 KISE-----QASNTYSDSSSMFEPSPGAGEATESEDDDDDD-----519
 QY 574 GSFRRKKKSKLKKAASVEEGDEGDSFGQSRGATROKTKMLSRALSDLYKTKSV- 632
 Db 520 -----CKSSMDEGTASSEM-----ATEE-----MSNLYNIQYVK 551
 QY 633 -ATHDIEMEAASSWOVSFSETRKAHOLLQOKPAOYLRFNCOOLSRITYSTRVDSSTNP 691
 Db 552 FSEFSEISKRRKNSFEKSEVETKGLEQLTKSVEFEYENKQLSIRYKGTGVSSNTMP 611
 QY 692 QPFWNAGCOMVALNTOSEBGMLOLNRAKFSANGGGYVAKPGCMCO--GVFNPSDEPL 749
 Db 612 QLEFWNAGCOMVALNTOSEBGMLOLNRAKFSANGGGYVAKPGCMCO--GVFNPSDEPL 749
 QY 750 GOLKQVLIIRISGOOLPAPRDSMLDRGEIIDPEVEYELIPLVDCSRE--QTRVVDN 807
 Db 672 GIYANLSTVKIISGQ-----FLSDK--VGTIYEDVMFLPVDTRKAKKRTSGCN 721
 QY 808 GGNPTV-EETLVF-VWHPEDIALVRFVWDHPDIGHDFGQRTLAFSSMPGTRAVYL-- 863
 Db 722 AVNPVEEPIYKVKVTLACLRIVAYE--GGEKFGHRIPLVQALRPYHICLN 778
 QY 864 ---EGMEASIPVHVAVSD-----ISGVK-----CALGKGLFLGPKRG 901
 Db 779 ERNQPILPLAVFYITVKDVPDVTYADVLEALSNPRIYVNLMEQRKQALALTLDEDEV 838
 QY 902 SLDSHAAGRPAPRPSVSORILKRTASAPTKSOKPGRGPELVLTGTRDTGSGVADVVP 961
 Db 839 KKEADGETSEAPSEA-----RTTPAEN-----GVNHT-----TLT 871
 QY 962 PGGPAPEAPAPQPGSGSPGKAPA 987
 Db 872 PKP-PSQALHSOPAPS---VAPA 892

Mon Mar 31 11:07:17 2003

us-09-927-112-2.rsp

Page 20

Search completed: March 28, 2003, 13:49:37
Job time : 43 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:47:05 ; Search time 54 Seconds
(without alignments)
2148.782 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPPTAGPLPGPALPDPEDPG.....ALYPHCLRLGTLPLWLACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524.5	23.9	997	1	phosphoinositide-s
2	1517	23.8	1096	1	inositol 1,4,5-tri
3	1459	22.9	764	1	1-phosphatidylinos
4	1297	20.3	895	2	hypothetical prote
5	1287	20.2	745	1	1-phosphatidylinos
6	1285	20.1	756	1	1-phosphatidylinos
7	1258	19.7	756	1	1-phosphatidylinos
8	1244	19.5	709	2	1-phosphatidylinos
9	1009	15.8	1291	2	1-phosphatidylinos
10	997.5	15.6	1290	2	1-phosphatidylinos
11	997	15.6	1176	1	1-phosphatidylinos
12	986	15.5	1236	1	1-phosphatidylinos
13	985	15.4	1290	2	1-phosphatidylinos
14	968.5	15.2	1265	2	1-phosphatidylinos
15	950.5	14.9	1252	2	phospholipase C (E
16	947.5	14.8	1312	1	phospholipase C (E
17	945	14.8	1216	1	1-phosphatidylinos
18	943	14.8	1305	2	phospholipase C (E
19	939	14.7	751	1	1-phosphatidylinos
20	937.5	14.7	1023	2	phospholipase C (E
21	936	14.7	1216	2	1-phosphatidylinos
22	928.5	14.6	1418	2	phospholipase C (E
23	925	14.5	801	1	1-phosphatidylinos
24	915.5	14.4	1210	2	phospholipase C (E
25	911	14.3	1234	2	1-phosphatidylinos
26	908.5	14.2	1181	2	1-phosphatidylinos
27	908	14.2	1095	1	phospholipase C (E
28	903	14.2	1173	1	1-phosphatidylinos
29	900	14.1	1234	2	phospholipase C-be

30	887.5	13.9	913	2	T46339	hypothetical prote
31	881.5	13.8	1211	2	S68251	phospholipase C, I
32	880	13.8	1299	2	T24299	hypothetical prote
33	872	13.7	1217	2	A45493	phospholipase C-be
34	870.5	13.6	899	2	S51092	probable phosphoin
35	867.5	13.6	1051	2	S27002	phospholipase C (E
36	865.5	13.6	899	2	S55075	1-phosphatidylinos
37	857	13.4	875	1	S66672	phosphatidylinosil
38	852	13.4	1898	2	T42440	phospholipase C ho
39	832.5	13.1	1922	2	T21581	hypothetical prote
40	682.5	10.7	869	1	A47257	1-phosphatidylinos
41	677	10.6	1099	2	T18257	phospholipase C -
42	649	10.2	565	2	T07424	phosphoinositide-s
43	623	9.8	600	2	T06420	phosphoinositide-s
44	609.5	9.6	581	2	T50841	phosphoinositide-s
45	604.5	9.5	551	2	T06777	phosphoinositide-s

ALIGNMENTS

RESULT 1

154390 phosphoinositide-specific phospholipase C (EC 3.1.4.-) epsilon - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: 154390

R:Kohno, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota, Hum. Mol. Genet. 4, 667-674, 1995

A:Title: Identification of a novel phospholipase C family gene at chromosome 2q33

A:Reference number: 154390; MUID:9535973; PMID:7633416

A:Accession: 154390

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-997 <RES>

A:Cross-references: GB:D42108; NID:g780121; PIDN:BAA07688.1; PID:g780122

C:Genetics:

A:Gene: GDB:PLCE; PLC-L

A:Cross-references: GDB:699207; OMIM:600597

A:Map position: 2q33-2q33

C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinositol domain Y homology

C:Keywords: phosphoric diester hydrolase

F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

Query Match 23.9% Score 1524.5; DB 1; Length 997;

Best Local Similarity 36.2% Pred. No. 1.9e-70;

Matches 348; Conservative 158; Mismatches 279; Indels 177; Gaps 20;

QY	41	CMGAMQEGMNVKLNKSGKGLVFFYLDEHNSCIRWDRSKN-EKAKISIDSIQVSGR	99
DB	13	CISPMQACELKKVRNRSIRYRFFLDLQALHWEPSKDLERAKIDISAKIRIRGK	72
QY	100	QSEVFRQRYDGSFD--PNCCTSIYHSGHRESLDIVSSSEVAFRTWGLRLTMGIDS	156
DB	73	NETTFPN--NGLADQICECAFSILHGENYESLDLVANSADVANIWVSGRLVRSRKP	130
QY	157	-DSIARQRT-RDQWLKQTFDEADKNGDSLSIGEVLDLRLKLVNLPORRYKQMFREAD	214
DB	131	LPMENQNTPRHWMKATYFEADVDGNGIMLEDVSLIKLNPFLKAKIRLKFKEIQ	190
QY	215	TDDHQT--LGEFECAFYKMMSTRDLVLLMTYISNKHDIADASLQRFLOVEQKMACV	272
DB	191	KSEKLTFTVTEFEFEACECELTREVEVFLVLOISKNEYDANDLMLFAEGGVTHI	250
QY	273	TLESCDIIIEFEPCEPKSKGLGIDFTNTYRSPAGIFPNHHVHODTOPLSHYF	332
DB	251	TEICDITIRRLSEGRKQGLAIDGFTTYLLSECDIFRDEQKVAQMDTQPLSHY	310
QY	333	ITSNHTYLVAGQILMSQSRDAYVVLQAGRCVDEKWDGPDGEFTYHNGYTLTKILF	392
DB	311	INSHMTYLLIEDQFRPADINGYITRALKMGCRSEVELVDGSDNEPILCRNNMTTHVSF	370


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OY 393 KQVIEIENKAYAFKNEYPIVILSIENHCYIOQKKMAOYITLDIGKLDLSSVSEEDATTL 452
Db 371 RSTIEVINKFAPVASEYPIILGLGNHCSLPQOKVMAQOKKVFGNKL-YTEAPLPSSEYL 429
OY 453 PSDOMLKGKILVKGKPLPANI SEDAEGEVSDSDSADEIDDDCKILNGASTNRKKEVENT 512
Db 430 PSPERKLRMIYKCKPLPSD--PDVLEGEVTDDB----- 461
OY 513 ANRKLDLSLKESKIRDCEDPNPFVSYTLSPSGKLGNKSAEDVEDSEGDAGSRNGRLV 572
Db 462 -----EEAOMSR----- 469
OY 573 VGSFNRKKKSKLKKAAVEBEGDEGODSPGQSRGATROKTKMLRALSDLVKTYKSV 632
Db 470 -----MSVDYNGE-----QOIRCRSLSDLVSKCSY 497
OY 633 ATHDIE--MEAASSMOVSESEETKAHOLLQOKPAOYLRFNNOOLSIITYSSSTRVDSSNYN 690
Db 498 QYRDEFLMSKQNTWEMCSFSETELSRIANEYPEDFVYNNKFLSLITYPSAMKIDSSNIN 557
OY 691 POFNNAGCOMVALNYQSEGRMLQNRKAFKSANGCGYLLKRCMCQOG--FNPNSEDTL 748
Db 558 PODEFNCGQOIAAMNFQEPGMMDLHTGWFLONGCGGYLBRPSIMRDEVSYESANTKGL 617
OY 749 POLKCOLVLRITISGOOLPKPRDSMLGDGELIIDPFVEVEITGLVDDGSRBQTRVYDDNG 808
Db 618 PGVSPALAHIKITISQONPKFKGACA--KGDIYIDVYCLEIHGIPADCSQOQTKTVQONS 675
OY 809 FNPVTEELVPMVMPHETALVRFVLWDDPIGRDIFIGRTLAFSSMNGYRRVLYEG-- 865
Db 676 DNPIDDEFEEFOVNLPELAMIHFVLLDDYIGDEFIIGYTTIPFECIOGGRYHVRPSFVG 735
OY 866 --MEBASIFVHAVSDISG-----KVQALGKGLFLR-----GP 898
Db 736 DIMEHVTLFVHAIATNRSGCGAKOKRSLSVRMGKKVREYTMRLNRIGLKTIDIDIFIAVHP 795
OY 899 KPGSLD-----SHAAGRPARPSQRLRRTASAPYKSQKPG-----RKGP 941
Db 796 LREALDMENNONALIVSITKEIGLGPPI-ASLKQCCILLTSSRLTSDNTPSVSLVAKDSFP 854
OY 942 EL 943
Db 855 YL 856

```

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RESULT 2
562358      1inositol 1,4,5-trisphosphate-binding protein, 130k - rat
N:Alternate names: phospholipase C delta 1 homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S62358; PMID:569328
R:Kamenatsu, T.; Miumori, Y.; Wetanabe, Y.; Ozaki, S.; Koga, T.; Iwanaga, S.; Ikehara, Y.
A:Title: A new inositol 1,4,5-trisphosphate binding protein similar to phospholipase C-delta 1
A:Reference number: S62358; PMID:8546702
A:Accession: S62358
A:Molecule type: mRNA
A:Residues: 1-1096 <KANI>
A:Cross-references: EMBL:D45920; NID:g1183843; PIDD:BAAB08351.1; PID:g1183844
A:Accession: S69328
A:Molecule type: protein
A:Residues: 172-191;228-242;1024-1034 <KAN2>
C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinositol-4,5-bisphosphate
domain Y homolog
F:401-543/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog
F:585-705/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

Query Match      23.88;      Score 1517;      DB 1;      Length 1096;
Best Local Similarity 36.18;      Pred. No. 5.2e-70;
Matches 349;      Conservative 161;      Mismatches 278;      Indels 180;      Caps 22;

```

[illegible]

RESULT 3
S1413
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-2 - bov
N;Alternate names: phosphoinositidase C; phospholipase C-delta-2; triphosphoinositide

C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Jun-2000
 C:Accession: S14113; S04944
 R:Meldrum, E.; Kriz, R.W.; Totty, N.; Parker, P.J.
 Eur. J. Biochem. 196, 159-165, 1991
 A:Title: A second gene product of the inositol-phospholipid-specific phospholipase C-delta
 A:Reference number: S14113; M0ID:91160548; PMID:1848183
 A:Accession: S14113
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-764 <ME2>
 A:Experimental source: brain
 R:Meldrum, E.; Katan, M.; Parker, P.
 Eur. J. Biochem. 182, 673-677, 1989
 A:Title: A novel inositol-phospholipid-specific phospholipase C. Rapid purification and
 A:Reference number: S04944; M0ID:89325315; PMID:2753038
 A:Accession: S04944
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 528-541, 'X', 543-553; 659-669 <ME2>
 A:Experimental source: brain
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosphate
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog; pleckstrin repeat homology; duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signal
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signal
 F:13-122/Domain: pleckstrin repeat homology <PLK>
 F:134-166/Domain: calmodulin repeat homology <EF1>
 F:170-202/Domain: calmodulin repeat homology <EF2>
 F:293-435/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog
 F:489-609/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
 F:611-725/Domain: protein kinase C C2 region homology <KC2>

Query Match 22.98; Score 1459; DB 1; Length 764;
 Best Local Similarity 39.28; Pred. No. 3e-67; Mismatches 263; Indels 134; Gaps 21;
 Matches 342; Conservative 133;

29 FLNANILPVERRCGAMQEGMVKLRGSGKGLVRFYLLDEHNSCIKMRPKNRKA-- 86
 3 YLGGRLPINDLL-LMGKTMKRVKSKKRLRFRLLDDGWTW-VHARQAGRAKPS 60
 87 ISIDISGVSEGRSEVFORPPDSFDPNCCFSYHSGHRESLDIVTSSEVARTWTGL 146
 61 FSIISVDIVRGEHSELRLNLA-EFPLEOGFTVFHGRSNDLDVANSVOEQATWMOGL 119
 147 KTLMAIGDEDESLARORTDQWLKQTFDEADKNGDSLISGEVLOLHLKLNVLPRQRY 206
 120 QLLVGFVNMND---QQRLLDQWLSDFQRKQKQDGMSEGEVQRLLHLMNVMDQETA 175
 207 KQMFREADTDHOGTLGEEFCAFYKMWSTRDLYLLMLIYSNKHDLDAASLQRFQVE 266
 176 FQLFGFADT-SQSGTLEGEFEVFKSLTORPEVELEFEKFSDDGQKLTLLFVDFLOEE 234
 267 QKMAVGTLESODDIEGEPCEPKSKGLGIDGFTNTRSPAGDIFNPEHNHNDMTQ 326
 235 QKEGERASDLALDLRPESESGKRLHYLSMDGFLGLYSKDDGDFNPTCHPLXDMTQ 294
 327 PLSHYFTSSHTNYLVGQDLMSQSRVDYAWYLQAGRCVDEWCDGPGEPYVHGTYL 386
 295 PLNHVYINSHTNYLVGQDLGCGSSVEGYIRALKRCRCVEVDIMDGSGEPYVHGTYL 354
 387 TSKILKDYETINKAFYKNEYRPLYSLENICSYIOQKMAOVYTLTDLGKLLDSSVSS 446
 355 TSTRIPKDVVAALGOYAFQTSYPIVLSLENICSWEDDEIYRHLTEILGQDLTTLALDG 414
 447 EDATTLPSQMLKGLIVGKRLPANISDAEGEVSDESDADEIDDDCKLLNGDASTNR 506
 415 QPTQLPSPEDLKGTLVGGKRLMLEEEDEEAELEAQA-RLDLEQL----- 464
 507 KRVENTAKRRLDLKESKIRDCEDNNFVSSTLSPGKLGKKAEEVEGEGDAGASR 566
 465 -----ESRFD-----LSP-----RSED----- 477
 567 RNRLLVGSFRRKKKSKLKAASVEEDGDDSPGGSGRATROKTKTKLSRLSLDLY 626

478 -----KKKKPKAI-----LCRALSALV 494
 627 KYTKSVA-----PHDIEMEAASSNOVSSESTKAHOLLOOKPAOYLRFNOOLSRTPSSY 682
 495 VYKAVTFYSFTH-SREHYHETSSSESTKAHLKEADGEFQVHANOQLSNVPSGL 552
 683 RYDSNVNPOPEWNAAGCQVAVLNTQSEGRMLQJLNRAKTSANCGCYLPGCM-CQGVF 740
 553 RTDSNVNPOPEWNAAGCQVAVLNTQSEGRMLQJLNRAKTSANCGCYLPGCM-CQGVF 740
 741 NPNSDEPLPGLKOLY-----LRITSGOQLKRPDMSMLGDEGLIDPFVEYELGLPYD 795
 613 HP-ERFISPFKAQTLIDPEWLVISGOOLPRKVDNT--KEQSTVDPLVREILGVKRPD 667
 796 CSRQRTFVNDGNFNPWEETLVFVWMPDIALVRFVWDHPDR-DFTGORTLAFSSM 854
 668 TTRQETISVENNGFNPMWGOTLCFRLVLEFALIRRVAVDYDMKSRNDPILGQYTLPMSCM 727
 855 MPGRHYVL--EG--MEASIFVHVAVSDIS 881
 728 QQGYRHHLLSKQGLSLHPASIFVHICTQEV 759

RESULT 4
 T32374
 hypothetical protein K10F12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
 C:Accession: T32374
 R:Wohlmann, P.; Beck, C.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of C. elegans cosmid K10F12.
 A:Reference number: 221157
 A:Accession: T32374
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-895 <WOH>
 A:Cross-references: EMBL:AF025462; PIDD:AA871005.1; GSPDB:GN00021; CESP:K10F12.3
 A:Experimental source: strain Bristol N2; clone K10F12
 C:Genetics:
 A:Gene: CESP:K10F12.3
 A:Map position: 3
 A:Intons: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1;
 C:Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
 F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 20.3%; Score 1297; DB 2; Length 895;
 Best Local Similarity 35.0%; Pred. No. 7.3e-59;
 Matches 310; Conservative 138; Mismatches 266; Indels 172; Gaps 23;

38 VERCMGAMQEGMVKLRGSGKGLVRFYLLDEHNSCIKMRP-SKKNRKAISIDSIOEVS 96
 46 VSDCMWYMQTGSDFYKLNQTRNFRFPFLDADLSYIMWTNNKPKHARLADIEIR 105
 97 EGRQSEVPQRYDDGSP---DPNCCFSYHSGHRESLDIVTSSEVARTWTGLYLMAGI 153
 106 LQANTLL-RSSDEVFTDQECLESIYGNVETLIDLASGDANLWYTGMAALNSNK 164
 154 SD-EDSLARORTDQWLKQTFDEADKNGDSLISGEVLOLHLKLNVLPRQRYKQFRE 212
 165 YECKPSSQFATLKRERISVDFEFTKNGHLDQTFKALHINSRISHRLTNLKE 224
 213 ADTDDHOGTLGPE-----PCAFYKMWSTRDLYLLMLIYSNKHDLDAASLQRF 262
 225 V-----TGAESERSGIKESHFYDLTKETIGRPEYFLWRYAN-KDTLSQDRLRF 276
 263 LQYEQKMAVGTLESODDIEGEPCEPKSKGLGIDGFTNTRSPAGDIFNPEHNHNVQ 322
 277 LREOGWVGYTTCNCTLLQYVPCSEARBNMLVDTGFTSPLFSPDGVDPNHRVVTM 336
 323 DMQPLSHYFTSSHTNYLVGQDLMSQSRVDYAWYLQAGRCVDEWCD---GPDEP 378

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Db 337 DMKQFSSKXFTSSSRKSLYVEDOL-GPSSSDGFSALKRNCRLFEDIMDNPENADGTER 395
QY IVHHGYTLTKLFRDVIETINKYAFIKNEYPVLSTIENHCSVYQOKMAOYTLIDGDK 438
Db 396 MVWNGQATSKITITSSALRITREPAERSRYPLLLKVSVCSTDMOKVAMLYTHIGTR 455
QY 439 LDL---SSVSEDAATLPSQMLKGLTVKGLLPANISEDAEAGEVSDSDADEIDDC 495
Db 456 LYLKRPNDPTMWDDEKNCPTPMDPQNRIIVGKLD---NDOTSGEVSDEED-DSL----- 506
QY 496 KLNGDASTNKKRVENAKRLDLSLKEKIROCED-----PNNFSYTLSPSGKLGKRS 550
Db 507 -----ASTRR-----KSKRIQCKELSDLVPEFVFNKTLN----- 537
QY 551 KAEDVES---GEDAGARRNGRLVVSFSRRKKSGSKLKAASVEBGDGDGDSPPGQSR 607
Db 538 ---DLSTAPGSTTMSRRK-----LASVTESTCLRMHTVATNERG 575
QY 608 GATROKTKMLSLRLSDLVYTKSVATHDIEMEAASSWVSFSETKAHQILOQKPAQYL 667
Db 555 -----LASVTESTCLRMHTVATNERG 575
QY 668 RFNQOOLSRITPSSSYRVDSSNTNPOPFWMAGCOMVALNTQSEGRMLQLNRAKFSANGCG 727
Db 576 QATRNCAVRFEPNPSRVDSNLNPOEFMNGVAVCLNTQPELMDLOEGKFSNDGCG 635
QY 728 YVLRPGCMCGVNPNSDEPLPQOLKQVLRLITISGOQLPKPRDSMLGRGETIDPEFV 787
Db 636 YVLRPVMMDMFPSPDRPFTSPQI---LHLRLISGOQLPRPGS--NAKGSADPEFV 690
QY 788 EILGLPVDSCREQTRVVDNGFNPTEETLVFVHMPETALVRLVMDHPIDRGDTIGOR 847
Db 691 EYVGLPGDCAEERTKRVVNDINSPFDESFOQVSVPELALVFLVLDYIGDDFIGQY 750
QY 848 TLAFSSMFPGRHYV---EG---MEASIFVAVASDI--SGKVRQ 886
Db 751 TLPECLDGPYRHYLYLNEGDPLEHATLFLVAVATNRRGSGKAKK 796

RESULT 5
PC4183
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 - Chinese
M:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide ph
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: PC4183
R:Leclercq, M.A.; Silbert, D.F.
Biochem. Biophys. Res. Commun. 224, 382-390, 1996
A:Title: Genomic organization of the hamster phospholipase C-delta1 gene: Differential l
A:Reference number: PC4183; MUID:96295498; PMID:8702399
A:Contents: fibroblast
A:Accession: PC4183
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-745 <LEO>
A:Cross-References: GB:U50564
C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosph
C:Genetics:
A:Gene: PLCdelta1
A:Introns: 56/1; 132/2; 175/3; 253/1; 320/2; 368/3; 418/3; 471/3; 525/1; 564/1; 623/3; 6
C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat homol
F:8-117/Domain: pleckstrin repeat homology <Plex>
F:129-161/Domain: calmodulin repeat homology <EF1>
F:165-197/Domain: calmodulin repeat homology <EF2>
F:287-429/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:480-601/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:603-713/Domain: protein kinase C C2 region homology <KC2>

Query Match 20.2%; Score 1287; DB 1; Length 745;

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Best Local Similarity 35.8%; Pred. No. 1,9e-58;
Matches 307; Conservative 128; Mismatches 279; Indels 144; Gaps 16;

QY 44 AMOEGMAYKLVKNGSGKLVRFYLDHRSCTIWRRSRK-----NEKAKISIDSIQEVSGR 99
Db 10 ALLKSGQLKLVKSSSSRRRRRTKLOEDCKTI--WQSRKWRSPESQLSIEDIQEVRMGH 68
QY 100 QSEVFQRPDGSFDPNCCSIYHSGHRESLDIVTSSEVAFRTWVGLRYLMAGSDSDSL 159
Db 69 RTEGLEKFA-RDIPEDRCPSIYFKDQNTLDLILASADAGQHWVGLAKTI---IHSQSM 124
QY 160 ARROTRDQWLKQTFDEADKNGDSSLSGEVYLQHLKLVNLPKRVKQMFREAD---TD 216
Db 125 DQROKIQ-HWISCLARKADKNKDNKNEKFLDKELKELINIOVDYSARKIRRECDHSQTD 183
QY 217 DHQGLTGEFEEPCAFKMSSTRDLVLMITVSNHNDHDAASLQRFLOVEKMGAVILES 276
Db 184 ---SLEDEIRTFYKMLQRAEIDRVFAEAGSAETLSVKLVTFQHQOOREAPAL 239
QY 277 CODIIEQFEPCEPKNSKGLLIGDFTNTYTRSPAGDIFNPEHHVHODTQPLSHYFTSS 336
Db 240 ALSLIEREPESETAKAQAQOMTKDGFIMYTLSDAGSAFSLAHRRVYQDMDQPLSHYVSSS 299
QY 337 HNTYLVGDOLMSOSRVDMYAVWLQAGRCVYDCWDGDPYVHNGYTLTKLFRDVI 396
Db 300 HNTYLVLEQQLGSPSTETAYITALCKGCRCLDWDGDPNDEPIYHGYTFSKILFYDVL 359
QY 397 ETINKYAFIKNEYPVLSTIENHCSVYQOKMAOYTLIDGKLDLSSVSEDAATLPSQ 456
Db 360 RAIRDYAFKASPPYVILSTENHCSLEEQOVVARRLKLKIML-LDPLDGVYMSLSP 418
QY 457 MLKGLIIVKGGK-----LPANISEDAEAGEVSDSDADEIDDCKLNGASTNKKRVEN 512
Db 419 OLKGLIIVKGGKFGGLPAGENGPEPTVDSDDEAAEMDE----- 460
QY 513 AKRKLDSLKSKIRDCEDPNPNSVSTLSPSGKLGKRSKAEEDVSEGDAGARRNGRLV 572
Db 461 -----A 461
QY 573 VGSFRRKKKSKLKAASVEBGDGDGDSPPGQSRGATROKTKMLSLRLSDLVKTKSV 632
Db 462 VRSVOOKSKEDKLNVAP-----LSMDVYICKSV 491
QY 633 ATHDIEMEAAS---WQVSSFETKAHQILOQKPAQYLRFNQOOLSRITPSSYRVDSNV 689
Db 492 HFGGFSNPSTSGCAFYMASFENRALRLIQEGCNFVRLNVSRLRTPAGKRTDSSNV 551
QY 690 NPQPFWMAGCOMVALNTQSEGRMLQLNRAKFSANGCGYVLRPGCM--COGYFNPNSDEP 747
Db 552 SPVEMNNGGQIVALNFOYPPGPMDDYLGFRDNGACGYLPAFLRDPDTAFNPRALQ 611
QY 748 LPQOLKQVLRLITISGOQLPKPRDSMLGRGETIDPEFVETIIGLPVDCSRQOTRVVDN 807
Db 612 GPWMAQKRLRVRYSOQLPKVKS-----KNSLVDPKTVVEHVGQDVASQRTAVTN 667
QY 808 GNPTEETLVFVHMPETALVRLVMDHPIDRG-DFTIGORTLAFSSMFPGRHYV--- 863
Db 668 GNPTEETLVFVHMPETALVRLVMDHPIDRG-DFTIGORTLAFSSMFPGRHYV--- 863
QY 864 ---EGMEASIFVAVASD 879
Db 728 NGDQHSATLFLKISLD 745

RESULT 6
A55943
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 (vav1
M:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: A55943
R:Cheng, H.F.; Jiang, M.J.; Chen, C.L.; Liu, S.M.; Wong, L.P.; Lomasney, J.W.; King,
J. Biol. Chem. 270, 5495-5505, 1995

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A:Title: Cloning and identification of amino acid residues of human phospholipase Cdelta
 A:Reference number: A55943; MOTID:95197554; PMID:7890667
 A:Accession: A55943
 A:Molecule type: mRNA
 A:Residues: 1-756 <CH>
 A:Cross-references: GB:009117; NID:9483919; PIDN:AAA73567.1; PID:9483920
 A:Experimental source: aortic smooth muscle
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphospho
 C:Genetics:
 A:Gene: GDB:PLCD1
 A:Cross-references: GDB:6075994
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
 phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat homol
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; signa
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:116-208/Domain: calmodulin repeat homology <EF2>
 F:298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
 F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 20.1%; Score 1285; DB 1; Length 756;
 Best Local Similarity 35.8%; Pred. No. 2.4e-58;
 Matches 308; Conservative 134; Mismatches 265; Indels 158; Gaps 19;

QY 44 AMOGMOMVLRGSGKGLVFEYLDHRSCTIRMPSPK---NEKAKISIDSIOEVSSEGR 99
 Db 21 ALLKGSOLIKVSSSWRRERFKLOEDCKTI-WQESRKVMKRPESLFSEIDIOEVRMGH 79
 QY 100 QSEVFOR---PDGSPDPCFSIYHSHRESLDVSTSEVARTWTGLRYLMAGISD 155
 Db 80 RTEGLEKFAVDPE---DRCFSIYFKDQKNTLDLIPSPADAQHMVGLNHT---IHH 131
 QY 156 EDSIARQRTRDOLKTPPEADKNGGSGSISEVQLLHKLVNVPQKVKOMPREAD- 214
 Db 132 SGMDOORCKLO-HWISCLRKADKNKNKMSFELOFLELNIQYDDSTARKIFRECH 190
 QY 215 --TDHOGTLGFEFCFAFYKMASTRDLYLMLTYSNHKNHDLDAISLORELOVEQKMGV 272
 Db 191 SOTD---SLEDELEAFYKMLQORVIEDTRPFAEAGPGTSLVDQVLFQHQOREEA 246
 QY 273 TLESCDIIIEFEPCEPKSKGLGIDGFTNYTRSPAGDIFNBEHHVHODMOPLSHYF 332
 Db 247 GPALALSLIEHYEESEETKAKORMTKDFLMTLLSADGSFSLAHRVYVDMQOPLSHYL 306
 QY 333 ITSSNHTLVDDLOMSORVMYAVIQAQRCVQVDCMGDPDEPIVHNGYTLTKTLF 392
 Db 307 VSSNHTLVLEDOLAGPSTATYTRALCKGRCLEDCMGDPNPEPIYHNGYTFSTKTLF 366
 QY 393 KDVETINKYAFIKNEYPVILISNHCSSVIOQKMAQYTFDILGDKL---DLSVSEDA 449
 Db 367 GCVLAIRIDYAFKASPYVILISNHCITLQOQRYMARHLHILGPMILNRPDLGVTN--- 423
 QY 450 TILSPQMLKGLIKYKGLKANTISEDAEAGE---VSDEDSADEIDDDCKLNGASTN 505
 Db 424 -SLSPEDQKGLIKGLKGLLPPEGGEGEPATVVSDEDAEMEDAEV----- 473
 QY 506 RKRVENTAKRKLDLSIKESKIRDCEDPNPNSVSTLSPSGKLGKRSKAEDVESGEDAGAS 565
 Db 474 RSRVQHKP-----KEDKLR----- 487
 QY 566 RNRGLVGSFSRRKKKSKLKAASVEEGDEGQDSPPGQSRGATROKTKMLSRALS 625
 Db 488 -----LAQELSDM 495
 QY 626 VKYTSVATHDIEMEA---SSMOVSFSETKAHQILQOKPAOYLRFNQOLSRITPSSY 682
 Db 496 VIYCKSVHFGGSSPGTPOQAYEMASSENKALFLILDESNGVFAHNVGLSLRIYAGW 555
 QY 683 RVDSNVNPOPMFAGCCQVVALNTOSEGRMLQILNRAKFSANGCGGYLPCGM--COGVF 740
 Db 556 RIDSSNVSYVEWMNGGQVALNFOGPPEKMDVYQDRQDNGACGYLKPALFRLDPNGTF 615

QY 741 NPNSDEPLRGOLKQDLYLRISGQQLPKPRDSMLGDKCEITIDPEVEYETLPPDCSREQ 800
 Db 616 NPRLAQGPWMAKRRLNIRIVISGOOLPKVKN---NKNSIVDPKVTYHISVSDVARSQ 671
 QY 801 TRAYVDNGNRPVTEELVYVNMPELALVRLVMDHDIRG-DFIGQRTLFSSMMGQYR 859
 Db 672 TAVITNNGNPNMDEFEAEVVPDIALTRFLVEDYDASSKNDFIGOSTIFLNSIKQYR 731
 QY 860 HVLV-----EGMEASIFVHVAUSD 879
 Db 732 HVHLSKNGDQHSATLFPKISLQD 756

RESULT 7

B28821
 N:Alternate names: phospholipase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 02-Jun-2000
 C:Accession: B28821; 155942
 R:Sub, P.G.; Ryu, S.H.; Moon, K.H.; Sub, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A:Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MOTID:88270495; PMID:3390863
 A:Accession: B28821
 A:Molecule type: mRNA
 A:Residues: 1-756 <SUH>
 A:Cross-references: GB:M20637; GB:J01316; NID:9206219; PIDN:AAA4186.1; PID:9206220
 A:Experimental source: brain
 R:Yagisawa, H.; Tanase, H.; Nojima, H.
 J. Hypertens. 9, 997-1004, 1991
 A:Title: Phospholipase C-delta gene of the spontaneously hypertensive rat harbors pol
 A:Reference number: 155942; MOTID:92098966; PMID:1684614
 A:Accession: 155942
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411, 'M', 413-422, 'S', 424-462, 'D', 464-626, 'A', 628, 'K', 630-667, 'A', 669-756
 A:Cross-references: GB:S74591; NID:9241276
 A:Note: this translation is not annotated in Genbank entry S74591, release 113.0
 A:Note: spontaneous hypertensive mutant
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphosph
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p
 phosphodiesterase domain y homology; calmodulin repeat homology; pleckstrin repeat ho
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; sl
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:176-208/Domain: calmodulin repeat homology <EF2>
 F:298-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
 F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y
 F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 19.7%; Score 1258; DB 1; Length 756;
 Best Local Similarity 35.8%; Pred. No. 5.8e-57;
 Matches 308; Conservative 131; Mismatches 273; Indels 148; Gaps 19;

QY 44 AMOGMOMVLRGSGKGLVFEYLDHRSCTIRMPSPK---NEKAKISIDSIOEVSSEGR 99
 Db 21 ALLKGSOLIKVSSSWRRERFKLOEDCKTI-WQESRKVMKRPESLFSEIDIOEVRMGH 79
 QY 100 QSEVFOR---PDGSPDPCFSIYHSHRESLDVSTSEVARTWTGLRYLMAGISDSDSL 159
 Db 80 RTEGLEKFA-RDIPDRCFSIYFKDQKNTLDLIPSPADAQHMVGLNHT---IHHSGM 135
 QY 160 ARQRTRDOLKOTFDEADKNGGSLSGEYVQLLHKLVNVPQKVKOMPREAD---TD 216
 Db 136 DORQKLO-HWISCLRKADKNKNKMSFELOFLELNIQYDDSTARKIFRECHSDTD 194
 QY 217 DHOGLTGFEEFCFAFYKMASTRDLYLMLTYSNHKNHDLDAISLORELOVEQK--MAGVT 274
 Db 195 ---SLEDELEIFYKMLQORVIEDTRPFAEAGPGTSLVDQVLFQHQOREEAPAL 250
 QY 275 ESCDIIIEFEPCEPKSKGLGIDGFTNYTRSPAGDIFNBEHHVHODMOPLSHYFIT 334
 Db 247 GPALALSLIEHYEESEETKAKORMTKDFLMTLLSADGSFSLAHRVYVDMQOPLSHYL 306

C:Keywords: phosphoric diester hydrolase
 F:322-464/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain x hom
 F:550-657/Domain: SH2 homology <SH21>
 F:668-756/Domain: SH2 homology <SH22>
 F:798-846/Domain: SH3 homology <SH3>
 F:952-1073/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain y hom

Query Match 15.8%; Score 1009; DB 2; Length 1291;
 Best Local Similarity 26.1%; Pred. No. 6.5e-44;
 Matches 308; Conservative 151; Mismatches 317; Indels 404; Gaps 35;

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OY 74 IRRPFRKNEKAKISIDISIOEVSEGRSEVFORV-PDGSF--DPNCCFSIYHGS--HRES 128
Db 60 ITWSRADKIEGADIREIKELRPGTSRDPFQEDPAFRPDQSHCFVILYGMERLKT 119
OY 129 LDVSTSEVARTWGLRYLMAGISDEDSL-ARRORTDQWLKOTFPDADKNGDGLSI 187
Db 120 LSLQATSEDEVNMWIRGLTWLM-----EDTLQAPPLQIERMLRKQFYSVDRNRREDRISA 174
OY 188 GEVLQLLHLKLVNLPRQVKOMFREADTDDHOGT--LGFEEPCAFYK--NMSTRDLYLL 243
Db 175 KDLKNNLSQVNRVPRNMR--FLREKLTLEQRTSDITTYGQFQRLYSIMYSQKTMPLR 231
OY 244 MLTVS-----NKKDHLDAASLQRF-----LQVEQKAGVLTSCODITIQ 283
Db 232 FLASALRAGERELCRVSLPEFQOFLLEYQELMAVDRLOQEFMLSLRDLPLREIEEP 291
OY 284 FEPCPEKNSKGLIGIDGFTNTYTRSPAGDIFNPEHHVHOD--MTQPLSHYFTSSNNTYLV 342
Db 292 Y-----FLDEFTYFLFSKENSISWNSQLDECCPDTMNNPLSHWISSSHNTYLT 340
OY 343 GDOLMSQRYDMYAWYLQAGRCVEVDWCMDGPDGEPIVHHGYTLTSKILFKVDYETINKY 402
Db 341 GDQFSSSSSEIATARCILRCMCRIEEDCWDGMPGVYIYGHLLTKIKESVDYLHTKEH 400
OY 403 AFIKNEYVILTSIENHCSVTIQKKMAQYLTDLIGDKLIDLSVSSSEDTATLPSPQMLKGI 462
Db 401 AFVASEPVLITIEDHCSIADQRMMAQYFKKVLGDTL-LRKPVDIADGLPSNQLKRI 459
OY 463 LVYGGKILPA-----NISEDAEAG----- 480
Db 460 LIRKKILAEBSAYEVPYTWYSNDSISNISKINCILYLEDPVNHEWPHYFVLTSSKIY 519
OY 481 -EVSDESDADEIDDDCKILNG--DASTNRKV-----ENTAKRKIDS----- 519
Db 520 SEETSPQGNDEDEPEKASGSETLHSNEKWFHGKLGAGRGRIARLLETCIETGAP 579
OY 520 ----LIKES-----KIRDC----- 529
Db 580 DGSFLVRESSETVGDYTLSEWRNCKVOCHIRSKODAGTRPKFPLTDLNLYPDSLITHY 639
OY 530 ----- 532
Db 640 QQVPLRCNEFERMLSEPVPTNAHESKEWYHASTLRAQAEHMLMRVPDCAFLVKKRNEP 699
OY 533 NNFVS----- 538
Db 700 NSYALSFAREGKIKHCRCVQOEGQTYMLGNSEFSLVDLISYERKHPYRKMKLRYPINEE 759
OY 539 -----TISPS-GKL--GR-----SKAAEE 554
Db 760 ALEKIGTAEPDYGALYEBRNPGFYVEANPMPTFKCAVYALFDYKAQRDELTFPKSAITQ 819
OY 555 DVEESGE-----DAGASR----- 566
Db 820 NVEKEGEGMMWRGDDYGGKQOLMPSPSYVEEMVSPALPEREHLIDNSPLGLLRKGLVDP 879
OY 567 -----RNGRLVGSFSRKKKSGSKLKAASVEE-----GDEGDDSPGQGSR 607
Db 880 ACQIAVREBKGNRRLEFVSISMAVHMSLDVAADSOEELQDWKIREVAQTAARLLE 939
OY 608 GATROKTKMKSRLASDLVYKTKSVATHD--TEMEAASWQVSSEFETKAHDILOO-RPA 664
  
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Db 940 GKMMERR-KKIALELSELVYCRPVPEDEKIGTERACRYCDMSSFPETKAEKYNKAKG 998
OY 665 QYLRFENOQOISRTIYSSRYVSDSNYNPQPFWMAGCQWALNYSOEGRMQOLNRAKESANG 724
Db 999 KFLDYNRQLSRIITPKQGRDSSNYDPLPMWIGSQVLNFGQPPKPMQMNQALFAGG 1058
OY 725 GCGVYLKPCGCMGCVFNPNSDEPLPGQLKKOLYKRIISGQQLKRPBSMLGDGEITIDP 784
Db 1059 HCGVYLQPSVYRDEAFEPFEDKSLRGLEPCACIEVGAHRLPK-----NGRG-IVCPF 1111
OY 785 VEVEITGLPVVCSRQRFVYVDNGFNPTW--BELTVFWVHPEILVRFVWHDHPIG-RD 842
Db 1112 VEIEVGADEVYSIQKTEFVVDNGLNVPWPAKPPHFOISNPEFAFLFVYEEDEMFSDON 1171
OY 843 FIGQRTLAESSMMPQRYHY-----YLGEEMERASIFVHAV 877
Db 1172 FLAQATFPVKGKLTGYRAVPLKNNYSEGLFELASILVYKIDV 1211
  
```

RESULT 10

A36466
 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 04-Feb-2000
 C:Accession: A36466
 R:Burgess, W.H.; Dionne, C.A.; Kaplow, J.; Mudd, R.; Friesel, R.; Zilberstein, A.; Sc
 Mol. Cell. Biol. 10, 4770-4777, 1990
 A:Title: Characterization and cDNA cloning of phospholipase C-gamma, a major substrat
 A:Reference number: A36466; MUID:90355993; PMID:2167438
 A:Accession: A36466
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1290

 A:Cross-references: GB:M34667; NID:q190037; PID:AAA36452.1; PID:q190038
 C:Genetics:
 A:Gene: GDB:PLCG1; PLC1
 A:Cross-references: GDB:120299; OMIM:172420
 A:Map position: 20q12-20q13.1
 C:Superfamily: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase II; 1-phosph
 A:Keywords: phosphoric diester hydrolase
 A:Keywords: phosphoric diester hydrolase
 F:322-464/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain x
 F:550-657/Domain: SH2 homology <SH21>
 F:668-756/Domain: SH2 homology <SH22>
 F:798-846/Domain: SH3 homology <SH3>
 F:952-1073/Domain: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase domain y

Query Match 15.6%; Score 997.5; DB 2; Length 1290;
 Best Local Similarity 25.1%; Pred. No. 2.5e-43;
 Matches 306; Conservative 157; Mismatches 331; Indels 423; Gaps 35;

```

OY 74 IRRPFRKNEKAKISIDISIOEVSEGRSEVFORV-PDGSF--DPNCCFSIYHGS--HRES 128
Db 60 ITWSRGADKIEGADIREIKELRPGTSRDPFQEDPAFRPDQSHCFVILYGMERLKT 119
OY 129 LDVSTSEVARTWGLRYLMAGISDEDSL-ARRORTDQWLKOTFPDADKNGDGLSI 187
Db 120 LSLQATSEDEVNMWIRGLTWLM-----EDTLQAPPLQIERMLRKQFYSVDRNRREDRISA 174
OY 188 GEVLQLLHLKLVNLPRQVKOMFREADTDDHOGTLCGFEEPCAFYK--NMSTRDLYLL 245
Db 175 KDLKNNLSQVNRVPRNMR--FLREKLTLEQRTSDITTYGQFQRLYSIMYSQKTMPLR 233
OY 246 TYS-----NKKDHLDAASLQRF-----LQVEQKAGVLTSCODITIQ 285
Db 234 EASTLRAGERELCRVSLPEFQOFLDYQELMAVDRLOQEFMLSLRDLPLREIEEPY 292
OY 286 PCPEKNSKGLIGIDGFTNTYTRSPAGDIFNPEHHVHOD--MTQPLSHYFTSSNNTYLV 344
Db 293 Y-----FLDEFTYFLFSKENSISWNSQLDAVCPDTMNNPLSHWISSSHNTYLTG 342
OY 345 QLSQSRVDMYAWYLQAGRCVEVDWCMDGPDGEPIVHHGYTLTSKILFKVDYETINKY 404
  
```


Db 551 ASYKYGA-----TTNIHPLSTMINVAQPVKFGFVHAEBRNHYNMSSFNESVGLYL 605
 QY 660 QOKPAQYLFEENOQSLSRIPSSYRVDSNTNPOPFWMAGCQVVALNTQSEGMLOLNRAK 719
 Db 606 KTHAIEFVYNNKROMSRIRPKGKRVDSNTNPOPFWMAGCQVVALNTQSEGMLOLNRAK 665
 QY 720 FSANGCGVYKPGCMQ--GVFNPNSEDEPLPGOLKQVLRTISGQOLPKPRDSMLGR 777
 Db 666 FEYNSGCVLLKPFDEKRRDRDTPPESETPVGVIAATCSVVISGQ-----FLSK 717
 QY 778 GEIIDEFEVEEILGLPDCSREQ--TRVVDNGFNPTM--EETLVF--MHPPEIALVRELY 833
 Db 718 K--IGYEVDMYGLPTDTRIRKEFTFVYNNMGLNPNVNESEFVRKYLIDPLAVLRIAY 775
 QY 834 WDHDPIGRDFIGORTLAESSMMPGRHYTL--EGMEAS--IFVHVA--VSDSGRY 884
 Db 776 YDGN---NKLIGORILPLDGLAGYRHISLRNEGNKPLPLPTFCIVLKYVYVDELGI 832
 QY 885 KQALGLKGLFLR-----GPKPGSLDASHAAGRPAPRSV--SOR 920
 Db 833 VDLSPDKFELSTTEKRAQDLRAMGIETSDIADVPDTSKNDKKKANPAKANVTPQSS 892
 QY 921 ILRTASAPTKSOKPGRKGPPELY 944
 Db 893 ELRPTTAAALGSGQEAKKGI-ELI 915

RESULT 12

A53970
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit
 C:Species: Drosophila melanogaster
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2000
 C:Accession: A53970
 R:Emori, Y.; Sugaya, R.; Akiyama, H.; Higashijima, S.; Shishido, E.; Saigo, K.; Homma, Y.
 J. Biol. Chem. 269, 19474-19479, 1994
 A:Title: Drosophila phospholipase C gamma expressed predominantly in blastoderm cells at
 A:Reference number: A53970; M0ID:94308233; PMID:8034716
 A:Accession: A53970
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1236 <EMO>
 A:Cross-references: GB:029806
 C:Genetics:
 A:Gene: plc-gamma4
 A:Cross-references: FlyBase:FBgn0003416
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphatidyl
 hodiesterase domain Y homology; SH2 homology; SH3 homology
 C:Keywords: phosphoric diester hydrolase
 F:326-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:589-688/Domain: SH2 homology <SH2B>
 F:701-789/Domain: SH2 homology <SH2>
 F:831-879/Domain: SH3 homology <SH3>
 F:979-1095/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y ho

Query Match 15.5%; Score 986; DB 1; Length 1236;
 Best Local Similarity 25.0%; Pred. No. 9.3e-43;
 Matches 315; Conservative 177; Mismatches 328; Indels 440; Gaps 42;

QY 30 LSANILPVERCMGMQGMVKLRGSGKLVFRFYDEHRCIR-----W-----RP 78
 Db 7 MSAPLIGMEEDITGLMELGTIVTKLQKORPRD-----RLMLIRERQLMKTATVQT 61
 QY 79 SRNKEKATISIDISQEVSEGRSEVFORYPDG--SFDPNCCFSYHSGH--RESIDLVT 134
 Db 62 PRIDEGAIQREIREIVGKHSKEFLFADDCQFESSKCFVILHGNHFKLKSFSVAL 121
 QY 135 SSEVARTVTGLRLYLMAGISDEDSLAKRQRT-R-DWLKQTF-----DEADKNDG 183
 Db 122 SEIEDNNVNRGLRYVY-----KDTLGARYPLQIDRMRLREYQLENVVTHSAKATQSPA 176
 QY 184 SLISGEVQLHLKLVNVLPROVRKOMFREADTDHQTGLGEFEFCAFYKM-----ST 236
 Db 177 QVTIKDFKFLAGVSCSKMTGKFMHFTEDVARRKH--LKPDDFSRLLQKLLPNGFASV 234

QY 227 RRDYLMLTYSNNKDHDAISLQFLQVEOK-----MAGVTLES--CODIIDQEPRE 289
 Db 235 LSGGVANFPESEDOQVYRRELKQFLETREGRDVSASEISMAIASPIRDFQOYE---R 291
 QY 290 NKSGLGIDGFPTVYTNPSPADIFNPENHHVQMTOPLSHYFTSSHNLYVGDQLMSQ 349
 Db 292 DVEEPYLFPEFVDFLEFSKNDLWNSKYDFMDMNLPLSSYMASSHNYLLTGDFPSE 351
 QY 350 SRVDYAVNVLQAGRCVVDGDDGDEPIVHGHGTLSKILFADVLETINKYAFINEX 409
 Db 352 SSCETAAHALMGKRCIPLDCMNGPDNLPIFPHGHTITSKIFMDVYIKTKIDHAFISSEY 411
 QY 410 PYLISIEHNSVYLOQKKAQYLTDLGDKLDSVSSSEDAATLPSQMLKGLIKVCKKL 469
 Db 412 PYLISIEQNSLEQGRNNAQALIEVFGDML-LTQPCDRNEQHLSPYQLRKRIILKHKL 470
 QY 470 P-----ANISEDAEG----- 480
 Db 471 PQFDDIANGISSTGSLGHRSSLGAGAGAGHGBDGENVRKVKGLLYFKDPVDSMNL 530
 QY 481 -----EYSEDSADEIDD-----CKLNG-----DASTN----- 505
 Db 531 QFVLTQELIYSSEINERNGNSEDDFCISSCSGLNMQOKOKDTSANDELHGENWF 590
 QY 506 -----RRVVENTAKR-----KL----- 517
 Db 591 HGKLEGKREADDLLKTKYHFGDGTFLVRESATFVGDYSLSEFWRNRNHRKIKHENG 650
 QY 518 -----DSL-----IKE----- 523
 Db 651 SKIKYLVENFVDSLXSLIVYRKMLNLSSESIILKEPVYQPKRHEQMFHPITTEQ 710
 QY 524 -----SKIRDE-----DPNNF----- 535
 Db 711 AEGGLYRLIEGSLVPSVOSINAFISPTINRKIKHCRIMQEGCLYGDITWNEFSLVSL 770
 QY 536 -SVSTLSP-----SGKLGRSKAE--DYEGS-EDAGAS----- 565
 Db 771 INYTRNPLRYNKLKSHPVSOELLRQALAEAGDHSGGHDNGASNTWGSLEENVTCK 830
 QY 566 -----RRNGRLVGSFSPRRKK--GSKLKRAASY----- 592
 Db 831 ALYSYANKPDELSPFKKALITNVQORDNSMMWIGDYGKIKKHLNANYKYVDSTTEQYN 890
 QY 593 ---EEGDEQ-----DSPG----- 603
 Db 891 SLNEEGTDRDTSIEIFGAVASLFESENPGIIFKLIQTPMQNPVIGFDNQETAYEMI 950
 QY 604 -----GQSGCATRQK--TKISRLASDLVYTKGVATHDIEMAASSW---QVSS 649
 Db 951 KATQEAALIASOLASERRKERTARVAKESDILITFRSVPRE-----HSNIFQEMSS 1004
 QY 650 FSETKAH-QLLQOKPAQYLFEENOQSLSRIPSSYRVDSNTNPOPFWMAGCQVVALNTQ 708
 Db 1005 FPETKAKQFQONTQFLSYHNNQISRYVYKQGRIDSSNPNMPPWNGSQMIALNTQT 1064
 QY 709 EGRMLQINRAKFSANGCGVYKPGCMQGVNPNSEDEL-PEQLKQVLVRLISQQLP 767
 Db 1065 GDKAMQJLNOAKFRNNGCGGILKPSFKSDSPFN--NPLCLDLSSEVKYSIRILARHLF 1122
 QY 768 KPRSMIGDGEIIDPEVEEILGLPYDCSREQTRVVDNGFNPTMEETLVFWHPEIA 827
 Db 1123 R-----GKSNPQIYVELIGASDTGVKRTKYIENGFPVYNNSESEFVYRNPORA 1174
 QY 828 LVRFVMDHDPGR-DFIGORTLAESSMMPGRHYTL--EGMEASIFVHVAVSDIS 881
 Db 1175 ILREYQDEDMFARTHTIAQACYPILTCIRQGYRSVILRNKFSSELEISLILINKIANVT 1234

RESULT 13

A51317
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) II - rat

Query Match 15.4%; Score 985; DB 2; Length 1290;
Best Local Similarity 25.6%; Pred. No. 1.1e-42;
Matches 303; Conservative 157; Mismatches 313; Indels 410. Gaps 36

[illegible]


```

Db 631 LTDPVNPNEPHESKPWYVDSLSRGAEEDMLMRIPDGAFLIRKRGSDSYAI-TPRARGK 689
QY 546 L-----GR-----KSKAEEDV 556
Db 690 VKHCRINEDGHRHVLGTSAYFESLVELVSYEKKSLYRKMRIRYPVPELLEIRYTERDI 749
QY 557 ESGEDAG-----ASRRN-----GRLVVGFSFSRRKKKSKL-----KKAASVEEG 595
Db 750 NSLDVSMYMPDSEINSMQRTYKALYDKAKRSDLSFCRGALLINVSKEPGGMWK 809
QY 596 DEG-----QDSP-GGQSRG-----608
Db 810 DYGTRIQQYFPSNYVEDISTADFELEKQILEDNPLGSLCRGILDNTYNYVKAPOGKNO 869
QY 609 -----ATRO-----KTKMLSRA 621
Db 870 KSEVFILLEPKEOGDPVPEFATDRVEELPEMFQSIREITWKIDSKENNMKYWEKNQSIATIE 929
QY 622 LSDLVKYYKSVATHDIEEAASSWQVSSFSSTKAHQILQCKPAQYLRPNQOQLSRIYPS 681
Db 930 LSDLVYVCKPFSKTKDNLENDFREIRSFVETKADSIIRQKPVDLKYNQKGLTRVYPKG 989
QY 682 YRVDSSNTNPOPEMNAGCOMVALNOSGEGRLQINRAKFSANGCGGYVLKPGCMQGVFN 741
Db 990 QRVDSNNDPEFRLMLCGSQMVALNFOTADKYMOMNHALFSLNGRTGYVLOPESM-----R 1044
QY 742 PMSDPLPGOLKKO-----LVLRITISGOQLPKPRDSMTGDRGEIIDPFVEVELIGLPVDCS 797
Db 1045 TEKTDPMPEPESQKILMTLTIVKLGARHLPK-----LG--RSIACPVEVEICGAEYGN 1097
QY 798 REQTRVYDDNGFNPTW--EETLVFMVHMPETALVRFLVWDHPDG--NDFIGORTLAFSS 853
Db 1098 KFKTTVYVNDGLSPIWAPTQEKVTEFYDPMIAFLRFVVEEDMFSDPNLAHATYPIKA 1157
QY 854 MMGGRHY-----YLEGMEBASIFY 873
Db 1158 VKSGFRSVPLKNGYSEDEIELASLLV 1182

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Search completed: March 28, 2003, 13:52:36
Job time : 66 secs

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 13:39:09 ; Search time 80 Seconds
(without alignments)
2010.419 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 6379
Sequence: 1 MAPRAGPLPAPLPEDPG.....ALYWHICRLGTLPLWACGP 1207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	6092.5	95.5	1239	23 ABB08205	Human lipid metabo
2	4941	77.5	1619	23 AAU077498	Human lipid metabo
3	3225	50.6	621	23 ABB07493	Human lipid metabo
4	3163	49.6	1014	23 ABB08001	Human lipid metabo
5	2343	36.7	787	22 ABB073659	Novel human diapo
6	2343	36.7	787	22 AA017367	Human phospholipid
7	1524.5	23.9	997	23 AA017367	Human phospholipid
8	1517	23.8	1096	22 AA01596	Novel human phosph
9	1441	22.6	762	22 AA010440	Novel human phosph
10	1441	22.6	762	23 AA014268	Human phospholipid

11	1439	22.6	828	23 ABB08008	Human lipid metabo
12	1432	22.4	762	23 AAU076816	Human phospholipid
13	1385.5	21.7	759	23 AA014270	Human phospholipid
14	1372.5	21.5	785	23 AA014269	Human phospholipid
15	1325.5	20.8	731	23 ABB07492	Human lipid metabo
16	1290	20.2	789	22 AAG03220	Amino acid sequenc
17	1279.5	20.1	736	22 AAB47516	Human phospholipid
18	1278.5	20.0	736	23 AA021821	Human phospholipid
19	1277.5	20.0	794	23 ABB06693	Human novel polype
20	1277.5	20.0	794	23 ABB066721	Human novel polype
21	1258	19.7	756	21 AA01394	Rat phospholipase
22	1256.5	19.7	466	22 AAB05125	Human protein sequ
23	1106	17.3	677	22 AAB94673	Human protein sequ
24	1085.5	17.0	608	23 AAU076817	Human phospholipid
25	1006.5	15.8	1093	23 ABB08201	Human lipid metabo
26	1002	15.7	567	22 AA011925	Human CG121 (or C5
27	990	15.5	1236	22 ABB060480	Drosophila melanog
28	985	15.4	1290	17 AAB00583	Phospholipase C-ga
29	945.5	14.8	1312	22 ABB07055	Drosophila melanog
30	939	14.7	1216	22 AAU079193	Human protein sequ
31	939	14.7	1216	23 ABB08204	Human lipid metabo
32	931	14.6	178	23 ABB05980	Human DITRP polype
33	896.5	14.1	1058	22 AAB01177	Human protein sequ
34	852	13.4	1898	23 ABB07352	Amino acid sequenc
35	841	13.2	1579	23 ABB06735	Human novel polype
36	840.5	13.2	1809	22 AA013101	Human phospholipid
37	723.5	11.3	1054	23 AAU01619	P. patens signal t
38	719	11.3	214	22 AAU07352	Novel central nerv
39	713	11.2	214	22 AAU03569	Human polypeptide
40	685.5	10.7	628	23 AAU01620	P. patens signal t
41	682.5	10.7	869	15 AA053732	S. cerevisiae Plc1
42	622	9.8	324	22 AAU07205	Novel central nerv
43	599.5	9.4	306	22 AAB94419	Human protein sequ
44	593.5	9.3	561	17 AAB91932	Phosphatidylinosit
45	522.5	8.2	340	22 AA011930	Human CG121 (or C5

ALIGNMENTS

RESULT 1
ABB08205
ID ABB08205 standard; Protein: 1239 AA.
XX ABB08205;
XX 04-MAR-2002 (first entry)
DE Human lipid metabolism enzyme-5 (LME-5).
XX
XX Human: LME-5; lipid metabolism enzyme-5; cytosolic; neuroprotective;
KW immunosuppressive; anti-inflammatory; cardiovascular; gene therapy;
KW enzyme therapy; cancer; neurological disorder; autoimmune disorder;
XX inflammatory disorder; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200185956-A2.
PD
XX 15-NOV-2001.
PF 11-MAY-2001; 2001WO-US15210.
XX
XX 11-MAY-2000; 2000US-203511P.
PR 25-MAY-2000; 2000US-207903P.
PR 07-JUN-2000; 2000US-210150P.
PR 23-JUN-2000; 2000US-213392P.
XX
PA (TNCY-) INCTE GENOMICS INC.
XX
XX Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;
PI Khan FA, Gandhi AR, Au-Young J, Lal P, Kearney L, Elliott VS;
PI Ding L, Thornton M;

XX WPI: 2002-089794/12.
 DR N-PSDB: ABA96005.
 XX
 XX New lipid metabolism enzymes useful for diagnosing, treating and
 PT preventing cancer, neurological disorders, autoimmune/inflammatory
 disorders, and cardiovascular disorders.
 PS
 XX Claim 1; Page 114-116; 122pp; English.
 XX
 XX The sequence represents a novel human lipid metabolism enzyme (LME-5) of
 CC the invention. The invention relates to novel human LME's, and the
 CC polynucleotides which identify and encode them. The enzymes of the
 CC invention have cytosolic, neuroprotective, immunosuppressive,
 CC anti-inflammatory, and cardiovascular activity. The polypeptides and
 CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
 CC metabolism enzymes are useful in the diagnosis, treatment and prevention
 CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
 CC cardiovascular disorders, and in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
 CC for compounds that modulate the activity of LME. Polynucleotides encoding
 CC LME may be used for somatic or germline gene therapy, to detect and
 CC quantify gene expression in biopsied tissues in which expression of LME
 CC may be correlated with disease, to generate a transcript image of a
 CC tissue or cell type, to generate hybridization probes useful in mapping
 CC the naturally occurring genomic sequence, and for screening libraries of
 CC compounds in drug screening techniques. The polypeptide sequences may be
 CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
 CC primers derived from polynucleotide sequences encoding LME may be used to
 CC detect single nucleotide polymorphisms.
 XX
 SO Sequence 1239 AA:
 Query Match 95.5%; Score 6092.5; DB 23; Length 1239;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 1166; Conservative 0; Mismatches 0; Indels 73; Gaps 2;

QY 509 VENTARKKIDSLIKESKINDCEDPNNFVSSTLSPSGKLGKRSKAEDVESGEDAGASRRN 568
 DB 541 VENTARKKIDSLIKESKINDCEDPNNFVSSTLSPSGKLGKRSKAEDVESGEDAGASRRN 600
 QY 569 GRIVGSFRRKKKSKLKAASVEEGEDGDSFGSGSGATROKTKYKLSRALSDLVKY 628
 DB 601 GRIVGSFRRKKKSKLKAASVEEGEDGDSFGSGSGATROKTKYKLSRALSDLVKY 660
 QY 629 TRSVATHDTEMAASWQVSFSETRKAHIIQOKPAOYLRFENQOOLSTYSSRYVDSN 688
 DB 661 TRSVATHDTEMAASWQVSFSETRKAHIIQOKPAOYLRFENQOOLSTYSSRYVDSN 720
 QY 689 YNPQPPNAGCCOMVALNTQSEBRLQLNBAKFSANGCGYVLKPCMCQGVFNPSDDPL 748
 DB 721 YNPQPPNAGCCOMVALNTQSEBRLQLNBAKFSANGCGYVLKPCMCQGVFNPSDDPL 780
 QY 749 PQOLKKQVLRLTISGOQLPKPADSMIGRGETIDPFVEVEITIGLVPDCSREOTVYDNG 808
 DB 781 PQOLKKQVLRLTISGOQLPKPADSMIGRGETIDPFVEVEITIGLVPDCSREOTVYDNG 840
 QY 809 FNPWEETLVFVHMPETALVFLWMDHPDPIGRDFTGORTLAFSSMMPGYRHVYLEGME 868
 DB 841 FNPWEETLVFVHMPETALVFLWMDHPDPIGRDFTGORTLAFSSMMPGYRHVYLEGME 900
 QY 869 ASIFVHAVVSDISGKVKKALGLKGLFLGPRPGSIDSHAARPPARPSVORILRTASA 928
 DB 901 ASIFVHAVVSDISGKVKKALGLKGLFLGPRPGSIDSHAARPPARPSVORILRTASA 960
 QY 929 PTKSOKPGRRGPELVLTGDTGSGVADVPVPPGPPAPAPAOEGSGSGSPGKAPAA 988
 DB 961 PTKSOKPGRRGPELVLTGDTGSGVADVPVPPGPPAPAPAOEGSGSGSPGKAPAA 1020
 QY 989 VAEKPPVVRPPVLTGSGPAGMAATCKCYVSGACVNTGGLQREBPPSPGASROAAI 1048
 DB 1021 VAEKPPVVRPPVLTGSGPAGMAATCKCYVSGACVNTGGLQREBPPSPGASROAAI 1080
 QY 1049 RQOPARADSLGAPCCGLDPAHITPGRSREAPKGGANROGGSGSSSSSPDSFGIP 1108
 DB 1081 RQOPARADSLGAPCCGLDPAHITPGRSREAPKGGANROGGSGSSSSSPDSFGIP 1140
 QY 1109 ERSPPWPBACROPGALOGESALFAOKLEIRNSKSPMSAGKPLPCVYLPHAPGAGP 1168
 DB 1141 ERSPPWPBACROPGALOGESALFAOKLEIRNSKSPMSAGKPLPCVYLPHAPGAGP 1200
 QY 1169 GSPAAASAMTVSPRYLVVALYPWHCLRGTLPLWLAGCP 1207
 DB 1201 GSPAAASAMTVSPRYLVVALYPWHCLRGTLPLWLAGCP 1239

RESULT 2
 ID AAU77498 standard; Protein; 1619 AA.
 XX
 AC AAU77498:
 DT 05-JUN-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme, LME-6.
 KW Human; lipid metabolism enzyme; LME-6; immune system disorder;
 KW neurological disorder; developmental disorder; cancer; nootropic;
 KW cell proliferative disorder; immunomodulator; neuroprotective;
 KW cytosolic; enzyme.
 XX
 OS Homo sapiens.
 PN
 PN W0200216597-A2.
 XX
 XX 28-FEB-2002.
 PD
 PF 22-AUG-2001; 2001WO-US26365.
 XX

23-NOV-2000; 2000US-227429P.
 PR 08-SEP-2000; 2000US-231370P.
 PR 15-SEP-2000; 2000US-233212P.
 PR 29-SEP-2000; 2000US-236885P.
 XX
 XX
 PA (INCYTE GENOMICS INC.
 PI Griffin JA, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;
 PI Walla NK, Hafalla AJA, Ding L, Tribouley CM, Das D, Thornton M;
 PI Lai P;
 DR MPI: 2002-280936/32.
 DR N-PSDB: ABK12390.
 XX
 XX
 PT New lipid metabolism enzymes, useful for diagnosing, treating or
 PT preventing immune system disorders (e.g. Crohn's disease), neurological
 PT disorders (e.g. Parkinson's disease), or cell proliferative disorders
 PT (e.g. cancers) -
 XX
 XX
 PS Claim 50; Page 113-117; 122pp; English.
 CC
 CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LME) designated LME-1 to LME-6, and the
 CC polynucleotide sequences encoding them. The LME polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LME, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LME-6.
 CC
 XX
 SO Sequence 1619 AA:
 Query Match 77.5%; Score 4941; DB 23; Length 1619;
 Best Local Similarity 84.2%; Pred. No. 0;
 Matches 973; Conservative 2; Mismatches 14; Indels 166; Gaps 5;
 QY 9 LRPALRPEDPGDPRESRMFLFSLANTLPV-VERCMGAMOGMOMVLRGSGKLVFFYL 67
 Db 473 LRQVAAPP-----LTVASLPCPVERKMGAMOGMOMVLRGSGKLVFFYL 519
 QY 68 DEHRSCIRWPRSRKNEKAKISIDISIOEVSEGRQSEVFORYPDGSFPDNCFSITYHSHRE 127
 Db 520 DEHRSCIRWPRSRKNEKAKISIDISIOEVSEGRQSEVFORYPDGSFPDNCFSITYHSHRE 579
 QY 128 SLDLVSTSSVAVRTWTGRLTYLMAGISDEDSLARKQRTDQ----- 168
 Db 580 SLDLVSTSSVAVRTWTGRLTYLMAGISDEDSLARKQRTDQ----- 639
 QY 169 -----MLKOTFDEADKNGDGLSISGEVYLQLLHKLNVMLPRQRYK 207
 Db 640 PWGGLSFRAGSHTEGVAGQRYEMLKOTFDEADKNGDGLSISGEVYLQLLHKLNVMLPRQRYK 699
 QY 208 QMER-----EADTDHOGTLGFEFCARFYK 234
 Db 700 QMERVAGHAWLEOGKILACSODRALVEVPMGTQGLALOEADTDHOGTLGFEFCARFYK 759
 QY 235 STRDYLMLLTYSNKHNDLDAASIOREFLOVEOKMAGVTLESODIIEOEPPEPKSKS 294
 Db 760 STRDYLMLLTYSNKHNDLDAASIOREFLOVEOKMAGVTLESODIIEOEPPEPKSKS 819
 QY 295 ILGIDGFTNTYRSPAGDIFNPENHNHVDMTOPLSHYFITSHNTYLVGDOLMSOSRVD 354
 Db 820 ILGIDGFTNTYRSPAGDIFNPENHNHVDMTOPLSHYFITSHNTYLVGDOLMSOSRVD 879
 QY 355 YAWVLQAGRCRCVEVDCWDGDERPTVNHGTYLTKILFKQVIEFINKYATIKNEYPTLS 414
 Db 880 YAWVLQAGRCRCVEVDCWDGDERPTVNHGTYLTKILFKQVIEFINKYATIKNEYPTLS 939
 QY 415 IENHCSTVIOQKKMAQYLTLDLIGDKLDSVSSSEDAATLTPSPOMLKGILVKGKLPANIS 474

|||||
 Db 940 IENHCSTVIOQKKMAQYLTLDLIGDKLDSVSSSEDAATLTPSPOMLKGILVKGKLPANIS 999
 QY 475 EDAREGEVSDSDGADIEDDDCKLLNGDASNNRRKRVETARAKLDSLKESKINDCEDPNN 534
 Db 1000 EDAREGEVSDSDGADIEDDDCKLLNGDASNNRRKRVETARAKLDSLKESKINDCEDPNN 1059
 QY 535 FSVSTLSPSGKLGK----- 549
 Db 1060 FSVSTLSPSGKLGKRVAKKVTPLMPTGPPDSQPVGPPPNRGSVQAGPQMGERRAAV 1119
 QY 550 -----SKAEDEVEGEDAGARRGRVYGS 575
 Db 1120 GAVCCGVAERERVYVMATYASLQCCSGIQCGRSKAEDEVEGEDAGARRGRVYGS 1179
 QY 576 FSRKKKSKLTKAASVEEGDEGDSFGGSRGATROKTKMKSRLALSDLVKTKSVATH 635
 Db 1180 FSRKKKSKLTKAASVEEGDEGDSFGGSRGATROKTKMKSRLALSDLVKTKSVATH 1239
 QY 636 DIEMEAASWQVSFSETKAHQILQOKPAQYLRENNQQLSRIPSSYRVDSNNPQPF 695
 Db 1240 DIEMEAASWQVSFSETKAHQILQOKPAQYLRENNQQLSRIPSSYRVDSNNPQPF 1299
 QY 696 NAGCOMVALNTQSEGRMLQNRKAFSANGCGYVLRKCMQGVFNNSDPLPGOLKQ 755
 Db 1300 NAGCOMVALNTQSEGRMLQNRKAFSANGCGYVLRKCMQGVFNNSDPLPGOLKQ 1359
 QY 756 LVLRITISGQQLPKPRDSMLDGRGELIDPFVEVEILGLPVDCSRQRTVYVDNGFNPTWE 815
 Db 1360 LVLRITISGQQLPKPRDSMLDGRGELIDPFVEVEILGLPVDCSRQRTVYVDNGFNPTWE 1419
 QY 816 TLVFWVHMPETALVFLVWDHDPGRDPTGORTLAFSSMMGYNHYLLEGKEASIFVHV 875
 Db 1420 TLVFWVHMPETALVFLVWDHDPGRDPTGORTLAFSSMMGYNHYLLEGKEASIFVHV 1479
 QY 876 AVSDISGVKQALGLKGLFLRGPKPGSLDSSHAAGRPAPRSVSORILRTASAPTKSO 935
 Db 1480 AVSDISGVKQALGLKGLFLRGPKPGSLDSSHAAGRPAPRSVSORILRTASAPTKSO 1539
 QY 936 GRGPELVLTGRTDTSKGVADVVPPGPPAPPAEAPAOEGSGSPKGAAPAAVAEKSPV 995
 Db 1540 GRGPELVLTGRTDTSKGVADVVPPGPPAPPAEAPAOEGSGSPKGAAPAAVAEKSPV 1599
 QY 996 RYRPPRVLDGPPAG 1010
 Db 1600 RYRPPRVLDGPPAG 1614
 RESULT 3
 ABB07493
 ID ABB07493 standard; Protein: 621 AA.
 XX
 XX ABB07493;
 DT 23-APR-2002 (first entry)
 XX
 DE Human lipid metabolism molecule (LME) polypeptide (ID: 2965233CD1).
 KW Lipid metabolism molecule; LME; cytosolic; neotropic; neuroprotective;
 KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;
 KW cardiovascular; anti-HIV; antiemetic; antiallergic; hypertensive; human;
 KW cancer; gene therapy; protein therapy.
 OS Homo sapiens.
 XX
 XX WO200204490-A2.
 XX
 XX 17-JAN-2002.
 PD
 XX
 XX 06-JUL-2001; 2001WO-US21432.
 PF
 XX
 XX 07-JUL-2000; 2000US-216801P.
 PR
 XX
 PR 07-JUL-2000; 2000US-216803P.
 PR

PR 14-JUL-2000; 2000US-218233P.
PR 21-JUL-2000; 2000US-220046P.
PR 26-JUL-2000; 2000US-220739P.
PR 04-AUG-2000; 2000US-222824P.

XX (INCY-) INCYTE GENOMICS INC.

PI Tang YT, Asimzai Y, Das D, Thornton M, Lu DAM, Tribouley CM;
PI Yue H, Ganahi AR, Walla NK, Khan FA, Lu Y, Yao MG, Hafalia ATA;
PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugh MR;
XX WPI: 2002-164631/21.

DR N-PSDB; ABA94696.

PT Lipid metabolism molecules useful in diagnosing, treating or preventing
PT cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
PT skin and cardiovascular disorders

PS Claim 1; Page 112-113; 128pp; English.

XX The invention provides human lipid metabolism molecule (LM) polypeptides
XX and polynucleotides. The LM polypeptides can be expressed by standard
XX recombinant methodology. The LM polypeptides are useful for diagnosing
XX or treating a condition or disease associated with the expression of LM,
XX or screening for compounds that specifically bind to or modulate the
XX activity or expression of LM. They are also used to generate antibodies
XX and assess the toxicity of test compounds. The LM polypeptides,
XX modulators and antibodies are specifically useful for diagnosing,
XX treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
XX melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
XX cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/
XX inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
XX or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
XX esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
XX disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
XX disorders (e.g. hypertension, arterial dissections, vascular tumours, or
XX thrombolysis). The present sequence represents a human LM polypeptide
XX sequence.

SO Sequence 621 AA:

Query Match 50.6%; Score 3225; DB 23; Length 621;
Best Local Similarity 99.0%; Pred. No. 1.2e-241;

Matches 614; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAPPTAGPLPGALPPDPGPPPPESRWLFLSANILPVVERCGAMQEGMVKILGSGSG 60
DB 2 MAPPTAGPLPGALPPDPGPPPPESRWLFLSANILPVVERCGAMQEGMVKILGSGSG 61

QY 61 LVRFYLLDEHRSICIMRPSRKNEKAKISTDSIOEVSEROSFVRYPDGSFDPNCCFSI 120
DB 62 LVRFYLLDEHRSICIMRPSRKNEKAKISTDSIOEVSEROSFVRYPDGSFDPNCCFSI 121

QY 121 YHGSRESLIDVSTSEVARTWVGLRLVLMGISDEDSIARRORTDQMLKOTFEADKN 180
DB 122 YHGSRESLIDVSTSEVARTWVGLRLVLMGISDEDSIARRORTDQMLKOTFEADKN 181

QY 181 GDGSISIEVQLHLKLVNLPORVKRMFEADTDHOGTLGFBECATFKMSTRDL 240
DB 182 GDGSISIEVQLHLKLVNLPORVKRMFEADTDHOGTLGFBECATFKMSTRDL 241

QY 241 YLLMLTYSNHDHDAASIQRFLOVEKMAVTLSESCDITIEOPPEPENSKGLIGDG 300
DB 242 YLLMLTYSNHDHDAASIQRFLOVEKMAVTLSESCDITIEOPPEPENSKGLIGDG 301

QY 301 FTNTRSRAGIIFNDEHHVHODMTOPISHYFTSSNHTYLVGDQLMSOSFVDMYAVWLQ 360
DB 302 FTNTRSRAGIIFNDEHHVHODMTOPISHYFTSSNHTYLVGDQLMSOSFVDMYAVWLQ 361

QY 361 AGRCVVDKDPDGPDIYHGGTILSKILFKVYETINKYATIKNEYPIVLSIENHCS 420
DB 362 AGRCVVDKDPDGPDIYHGGTILSKILFKVYETINKYATIKNEYPIVLSIENHCS 421

QY 421 VIOQKMAQYLTDLIDGKIDLSSVSEDAATLPSQMLKGLVYKGLPANISEDAEG 480
DB 422 VIOQKMAQYLTDLIDGKIDLSSVSEDAATLPSQMLKGLVYKGLPANISEDAEG 481
QY 481 EYSDSDADEIDDDCKLNGDASTNRKRENTARKKIDLSIKESIRCEPPNPFVSTL 540
DB 482 EYSDSDADEIDDDCKLNGDASTNRKRENTARKKIDLSIKESIRCEPPNPFVSTL 541
QY 541 SPFGKIGRKSAAEDVEGSDAGASRRNGRLVYGSFSRRKKSGLKKAASVEGDEGOD 600
DB 542 SPFGKIGRKSAAEDVEGSDAGASRRNGRLVYGSFSRRKKSGLKKAASVEGDEGOD 601
QY 601 SPFGSGRGTATRKKTMTKSR 620
DB 602 SPFGSGRGTATRKKTMTKSR 621

RESULT 4
ABR08001

ID ABR08001 standard; Protein: 1014 AA.

AC ABR08001;

DT 27-AUG-2002 (first entry)

DE Human Lipid metabolism enzyme (LME)-1 (Id: 7472210CD1).

KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective;
KW noctropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;
KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antitumoral;
KW gene therapy; protein therapy; enzyme.

OS Homo sapiens.

PN WO200229036-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US31302.

PR 06-OCT-2000; 2000US-238388P.

PR 13-OCT-2000; 2000US-240616P.

PR 02-NOV-2000; 2000US-245719P.

PR 08-NOV-2000; 2000US-247503P.

PR 17-NOV-2000; 2000US-249503P.

XX (INCY-) INCYTE GENOMICS INC.

PI Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;

PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;

PI Lal PG, Tribouley CM;

XX WPI: 2002-315862/35.

DR N-PSDB; ABL60537.

PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,

PT diagnosing and treating e.g. cancer, Alzheimer's disease and

PT Creutzfeldt-Jakob disease

PS Claim 1; Page 110-113; 127pp; English.

XX The invention relates to human lipid metabolism enzymes (LMEs) and

XX encoding polynucleotides. The LMEs can be expressed by standard

XX recombinant technology. The LME polypeptides, polynucleotides and

XX modulators may be used in the prevention, diagnosis and treatment of

SQ Sequence 1014 AA:
 Query Match 49.6%; Score 3163; DB 22; Length 1014;
 Best Local Similarity 63.5%; Pred. No. 1.7e-236;
 Matches 607; Conservative 141; Mismatches 172; Indels 36; Gaps 9;
 29 FLNANLTPYERQMGOMVLRGSGKGLVRYLDERSCIRMPKRNKAKIS 88
 18 FLVNDNSVFYERCMVSMQSTQWIKRKTKRGTGKGLVFLYDERHTRLRMPKRSKSEKATL 77
 89 IDSIOEVSERQSEVFORYPDGSFDPNCCFSIYHGSRESLQVSTSEVARTWTGLRY 148
 78 IDSIYVTERGSEIFHQAEGNFDPSCFTIYHGNHMSLDLITSNPEARTWITGLAY 137
 149 LMAIGSDESLARQRTQDMLKQTPDEADKNGDSLIGEVQLQHLKLNVLPRQRYKO 208
 138 LMAIGSDESLARQRTQDMLKQTPDEADKNGDSLIGEVQLQHLKLNVLPRQRYKO 197
 209 MFRPADDDHOGTIGFEFCAPYKMASTRDYLMLTYSNKHDLDAASLQFLOVEOK 268
 198 MFOBADIDENOGTLTFEFCVFKKMSLRDYLILLSTSDKKDHLVLELAQFLKVEOK 257
 269 MAGVTLSECDIIEQEPCEPKSKGLIGDTFTNTSPAGDIFNPEHHVHODMTOPL 328
 258 MNVYTTDYCDIIEKFEVSEENKKNVGLIEGFTNMRSPACDIFNPLHEVYQDDOPL 317
 329 SHFITSSHTYLVQQLMSQSRVDYAWVLAQGCVEVDCMDGPDGEPYVHHGYTIS 388
 318 CNVYIASHNTYLVQQLMSQSRVDYAWVLAQGCVEVDCMDGPDGEPYVHHGYTIS 377
 389 KILFKDVIETINKYAFIKNEYPVILSTENHCYVLOOKMAQVLTDLIGDKLDSVSSSD 448
 378 KILFKDVIETINKYAFIKNEYPVILSTENHCYVLOOKMAQVLTDLIGDKLDSVSSSD 437
 449 ATTLPSQMLKGLVKGKLPANISDAEVEGSDSDADEIDDOCKL-LNDASGNRK 507
 438 CKOLPSPQSLKGLVKGKLPYHGLGDAEVEGSDSDADEIDDOCKLFLHNGTTEH 497
 508 RVEHTARKLDSLIESKIRNDCEDPNFVSSTLSPSGKLKRS--KAEEDV-ESGEDAGA 564
 498 QVESFIRKTESLKEQIRNDCEDPNFVSSTLSPSGKLKRS--KAEEDV-ESGEDAGA 553
 565 SRNRGLVSGFSRKRKSKGLKRAASVEGDEGDS--PGQSGRATNOKTKTMSRA 621
 554 -KSHGRSLMTNFKHKKTKTSKRSYSTDEDEDTQOSTGEGCOLYLRGRRKTKMLCRE 612
 622 LSDLVYTKSVATHDIEEAASSQVSSFTSKAHOILQOKPAQYLRPNQOOLSRIYPS 681
 613 LSDLVYTKSVATHDIEEAASSQVSSFTSKAHOILQOKPAQYLRPNQOOLSRIYPS 671
 682 YRVDSSNYPQFVWAGGQVYALYQSEGRMLQLNRAKFSANGGCGVYLRPGCMCGVFN 741
 672 YRVDSSNYPQFVWAGGQVYALYQSEGRMLQLNRAKFSANGGCGVYLRPGCMCGVFN 731
 742 PNESEDPLRGQKQVLVRIISGQOLPKPRDSMLDREGITIDPVEVETIGLPVCCSRQT 801
 732 PNESEDPLRGQKQVLVRIISGQOLPKPRDSMLDREGITIDPVEVETIGLPVCCSRQT 791
 802 RYVDNDNGFNPMTEFLVPMVMPETALRYLWMDHPIGRDPIGORTLAFSSMMPGYRHV 861
 792 RYVDNDNGFNPMTEFLVPMVMPETALRYLWMDHPIGRDPIGORTLAFSSMMPGYRHV 851
 852 YLEGLTEASIFVHTITNEYKWSPLILNPSTYILHFGATRNKROLOGLFKFNKPHS 911
 862 YLEGLTEASIFVHTITNEYKWSPLILNPSTYILHFGATRNKROLOGLFKFNKPHS 901
 902 SLDSNAGRPAPRPSVQRIILRTASATPKSQPKRGRPELYLGTROGSGVAD 957
 912 SSENNS--HYVRRKSIIGRIILRTASAPAKGRKSKMGFQEMV-BIKDSVSEATPD 964

RESULT 5
 ABG13669

ID ABG13669 standard; Protein: 787 AA.
 XX
 AC ABG13669;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13660.
 XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 PI N-PSDB; AAS77856.
 DR WPI, 2001-639362/73.
 DR N-PSDB; AAS77856.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID No 44028; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 787 AA:
 Query Match 36.7%; Score 2343; DB 22; Length 787;
 Best Local Similarity 61.4%; Pred. No. 6.4e-173;
 Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;
 239 DLYLLMLTYSNKHDKDLDAASLQFLOVEOKMAGVTLSECDIIEQEPCEPKSKGLIGI 298
 1 DLYLLMLTYSNKHDKDLDAASLQFLOVEOKMAGVTLSECDIIEQEPCEPKSKGLIGI 60
 299 DGFNTYRSPAGDIFNPEHHVHODMTOPLSHFITSSHTYLVQQLMSQSRVDYAWV 358
 61 EGFNTYRSPAGDIFNPEHHVHODMTOPLSHFITSSHTYLVQQLMSQSRVDYAWV 120
 359 LQAGRCVYDCMDGPDGEPYVHHGYTISKILFKDVIETINKYAFIKNEYPVILSTENH 418


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Db 121 LQEGRCVEVDCWDGPDGEFVHHGYTLTKILFRDVEETINKNAFVKNPEFVILSTENH 180
Qy 419 CSVYIOOKKMAQYLTDLIGDKLDSVSSSEDATLTPSPQMKGKILVYGGKILPANISED 478
Db 181 CSTIOOKRIAYLIGTIGDKLDSVDTGECQKLPSPQSLKGLVYGGKILPYHLGDAD 240
Qy 479 EGEVSDSDADEIDDDCKL-LNGDASTNRKRVENTAKRKIDSLIKESKIRDCEDPNNSFV 537
Db 241 EGEVSDSDADEIDDECKFKLHYNSGTTEHVESFIRKLESILKESQIDKEDPDSEFTV 300
Qy 538 STLSPSGKILGRKS--KAEDV-ESGEDAGASRRNGRLVVGFSRRKKSGSLKAASVEE 594
Db 301 RALKAKTHIEGLNAHLKQSPVKSBSG----KSHGSLMTNFGKHKKTKTTSRKSXYSTD 355
Qy 595 GDEGDS---PGQSRGATROKTKMLSRALSDLYTKTSVATHDIEMASSWQVSSFS 651
Db 356 EEDTQOSTGKEGQLYRLGRRRKTKMLCRLSDLYVTNSVAADI-VDDGTGTVLSFS 414
Qy 652 ETKAHQILQOKPAQYILRFNQOOLSRIPSSYRVSSSNYNPQFPMNAGCOMVALNTQSEGR 711
Db 415 ETKAHQVVOOKSEQFMITYNOKQLTRIPSAVYRIDSSNPNLPYMNAGCOLVALNTQSEGR 474
Qy 712 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKKQLVLRITISGQLEPKRPD 771
Db 475 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKKQLVLRITISGQLEPKRPD 534
Qy 772 SMIGRGEIIDPFVEVEIIGLPVDCSREQT RVVDNGFNPTEETLVFWHMEIATLVF 831
Db 535 SMIGRGEIIDPFVEVEIIGLPVDCSREQT RVVDNGFNPTEETLVFWHMEIATLVF 594
Qy 832 LVVDHPRIQDRIQORTLAPSSMMQGRVRYLEGEAEATIFVAVASDISG----- 882
Db 595 LVVDHPRIQDRIQORTLAPSSMMQGRVRYLEGEAEATIFVAVASDISG----- 882
Qy 883 -----KVKQALGLKGLFLRGPCKPSLDSHAAGRPAPRPVSQRIILRRFASAPRK 931
Db 655 STYTLHFLGATNKRQLOGKGLFNKNPRHSSSENN--HYAKRSLGRIILRRFASAPRK 712
Qy 932 SOKPGRGPELVLTGRDQSGKVAD 957
Db 713 GRKSKMGFOEMV-EIKDVSSEATRD 737

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RESULT 6
AAE14673
ID AAE14673 standard; Protein; 787 AA.
XX
AC AAE14673;
XX
DT 26-JUL-2002 (first entry)
XX
DE Human phosphatidylinositol-specific phospholipase C-1-like enzyme.

XX
KW Human: phosphatidylinositol-specific phospholipase C-1-like enzyme;
KW PI-PLC-like enzyme; chromosome 3; asthma; cancer; central nervous system;
KW CNS disorder; Parkinson's disease; dementia; COPD; protein therapy;
KW chronic obstructive pulmonary disease; gene therapy; vaccine.
XX
OS Homo sapiens.

XX
PN MO200226996-A2.
XX
PD 04-APR-2002.
XX
PE 24-SEP-2001; 2001WO-EP11012.
XX
PR 27-SEP-2000; 2000US-235552P.

XX
PA (FARB) BAYER AG.
XX
PI Zhu Z;
XX

DR WPI; 2002-372128/40.
DR N-PSDB; AAD31081.
XX
PT Isolated polynucleotides encoding human phosphatidylinositol-specific
PT phospholipase C-1-like enzymes, useful for preventing, diagnosing and
PT treating e.g. asthma, cancer, a CNS disorder or chronic obstructive
PT pulmonary disease -
PS
XX Claim 25; Fig 2; 125bp; English.

CC The invention relates to polynucleotide encoding human
CC phosphatidylinositol-specific phospholipase C-1-like enzyme
CC (PI-PLC-like enzyme). Human PI-PLC-like enzyme gene is located on
CC chromosome 3. The PI-PLC-like enzyme polypeptide and
CC polynucleotide may be used in the prevention, diagnosis and
CC treatment of diseases associated with enzyme dysfunction,
CC e.g. asthma, cancer, central nervous system (CNS) disorder (e.g.
CC Parkinson's disease, dementia) and chronic obstructive pulmonary disease
CC (COPD). The polynucleotide and polypeptide may be used to treat
CC disorders associated with decreased PI-PLC-like enzyme expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of PI-PLC-like enzymes, by expressing inactive proteins or to
CC supplement the patients own production of PI-PLC-like enzymes.
CC The polynucleotide and its complements may also be used
CC as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples. The PI-PLC-like enzymes
CC may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of PI-PLC-like enzyme
CC expression and activity. The anti-PI-PLC-like enzyme antibodies and
CC antagonists may be used to down-regulate expression and activity of
CC the enzyme and as diagnostic agents for detecting the presence of
CC PI-PLC-like enzyme in samples. The present sequence is human
CC phosphatidylinositol-specific phospholipase C-1-like enzyme.

Sequence 787 AA;

Query Match 36.7%; Score 2343; DB 23; Length 787;
Best local Similarity 61.4%; Pred. No. 6, 4e-173;
Matches 458; Conservative 107; Mismatches 145; Indels 36; Gaps 9;

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Qy 239 DLYLMLTYSNKHNDLDAISLQRLVQEQMAGVLTESCODITGEFPEPCENKSKILGI 298
Db 1 DLYLMLTYSNKHNDLDAISLQRLVQEQMAGVLTESCODITGEFPEPCENKSKILGI 60
Qy 299 DGFNTYRSPAGDIFENFHHVHDMTOPLSHYFTISNHTYVYGQOLMSQSNVDYNAV 358
Db 61 EGFNFMRSAPACIDFENLHVEYVQDMQPLCNTYTIASSNHTYVYGQOLMSQSNVDYNAV 120
Qy 359 LQAGRCVEVDCWDGPDGEFVHHGYTLTKILFKDVIETINKNAFVKNPEFVILSTENH 418
Db 121 LQEGRCVEVDCWDGPDGEFVHHGYTLTKILFRDVEETINKNAFVKNPEFVILSTENH 180
Qy 419 CSVYIOOKKMAQYLTDLIGDKLDSVSSSEDATLTPSPQMKGKILVYGGKILPANISED 478
Db 181 CSTIOOKRIAYLIGTIGDKLDSVDTGECQKLPSPQSLKGLVYGGKILPYHLGDAD 240
Qy 479 EGEVSDSDADEIDDDCKL-LNGDASTNRKRVENTAKRKIDSLIKESKIRDCEDPNNSFV 537
Db 241 EGEVSDSDADEIDDECKFKLHYNSGTTEHVESFIRKLESILKESQIDKEDPDSEFTV 300
Qy 538 STLSPSGKILGRKS--KAEDV-ESGEDAGASRRNGRLVVGFSRRKKSGSLKAASVEE 594
Db 301 RALKAKTHIEGLNAHLKQSPVKSBSG----KSHGSLMTNFGKHKKTKTTSRKSXYSTD 355
Qy 595 GDEGDS---PGQSRGATROKTKMLSRALSDLYTKTSVATHDIEMASSWQVSSFS 651
Db 356 EEDTQOSTGKEGQLYRLGRRRKTKMLCRLSDLYVTNSVAADI-VDDGTGTVLSFS 414
Qy 652 ETKAHQILQOKPAQYILRFNQOOLSRIPSSYRVSSSNYNPQFPMNAGCOMVALNTQSEGR 711
Db 415 ETKAHQVVOOKSEQFMITYNOKQLTRIPSAVYRIDSSNPNLPYMNAGCOLVALNTQSEGR 474
Qy 712 MQLNRAKFSANGCGGYVLKPGCMCGVFNPNSEDLPGQLKKQLVLRITISGQLEPKRPD 771

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Db 475 MMDLNRAKRAKANGCGYVLAKPOOMCKGTNPNSGDLPLANPKQILAKYISQOLPKPPD 534
 Qy 772 SMLGRGEIIDEPEVEIIGLPGVDSREQTRVVDNGFNPTVEETLVENMPETALVRF 831
 Db 535 SMGSGDEIIPDEVEIIGLPGVDSREQTRVVDNGFNPTVEETLVENMPETALVRF 594
 Qy 832 LVMDHDPIDGRDIFGORTLAFSSMMPYRRVYLEGMEASIFPVHVASDLSG----- 882
 Db 595 LVMDHDPIDGRDIFGORTLAFSSMMPYRRVYLEGMEASIFPVHVASDLSG----- 654
 Qy 883 -----KVKQALGKGLFLRGPCKGSLDSHAAGRPAPRPSYQRIILRTASAPTK 931
 Db 655 SYTLFLFATKTRKQGLKGLFKNKPRHSSSENN--HYVKRRTICGDLILRTASAPAK 712
 Qy 932 SQRGRGPEPELVLTGRDYGSGVAD 957
 Db 713 GRKSKMGFEQENV-EIKDSVSEATRD 737
 RESULT 7
 AAO17367
 ID AAO17367 standard; protein: 997 AA.
 XX
 XX AAO17367;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human phospholipase C epsilon.
 XX
 KW Human: endometrios; DNA chip; fibronectin; p27; reticulocalbin;
 KW aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
 KW insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
 KW transmembrane receptor PK7; collagen type XVIII alpha 1;
 KW platelet derived growth factor receptor alpha; laminin M chain;
 KW subtilisin like protein PACE4; nidogen.
 XX
 OS Homo sapiens.
 PN EP1191107-A2.
 PD 27-MAR-2002.
 XX
 XX 21-AUG-2001; 2001EP-0250300.
 XX
 XX 25-SEP-2000; 2000DE-1048633.
 XX
 PA (SCHD) SCHERING AG.
 PI Hess-stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
 PI Regidor P, Scotti S;
 XX
 DR WPI: 2002-317413/36.
 XX
 PT In vitro diagnosis and monitoring of endometrios, comprises
 PT detecting reduced expression of specific gene products, e.g. from the
 PT fibronectin gene -
 XX
 PS Claim 1; Page 20-21; 21pp; German.
 XX
 CC The present invention relates to a method for the in vitro diagnosis of
 CC endometrios by determining the amount of gene product from at least one
 CC specific gene in a patient sample and comparing this with the amount of
 CC gene product in a control sample. A reduced level is indicative of
 CC endometrios. The gene products may be fibronectin, p27, reticulocalbin,
 CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
 CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
 CC transmembrane receptor PK7, collagen type XVIII alpha 1,
 CC platelet derived growth factor receptor alpha, laminin M chain,
 CC subtilisin like protein PACE4 or nidogen. The method is useful for
 CC initial diagnosis of endometrios, and also for monitoring progress and
 CC treatment of the disease. The present sequence is human phospholipase C
 CC epsilon.

Query Match 23.9%; Score 1524.5; DB 23; Length 997;
 Best Local Similarity 36.2%; Pred. No. 4.1e-109;
 Matches 348; Conservative 156; Mismatches 279; Indels 177; Gaps 20;
 XX
 SQ Sequence 997 AA;
 Qy 41 CMGAQEGOMQVAKLNGSGKGLVRFYLDENRSCIRMRPRKN-EKAKISIDSIOGSEGR 99
 Db 13 CISFMQACEIKLKVAPNRIINRFTLDTDLQALRMESKDLKAKLIDISAKIRLGR 72
 Qy 100 OSEVFORYPDSFD---PNCPSIYHGRBSLDLVSTSSVARTWTGLRYLMAIGSIDE 156
 Db 73 NTEFTTN--NGIADQICBDAFSLIHGENYSLDLVANSADVAINIWGSLYVSRKOP 130
 Qy 157 -DSLARRORT-ROMLKOTFDEADKNGSGSLSIGEVLDTLKHVLVNP-PROHKOMFREAD 214
 Db 131 LDFMGNQNTFRFMYLKVFEADVDGNGIMLEDYSVLILQNLPTLKEAKIRLKFPEIQ 190
 Qy 215 TDDHOGT--LGFEEPCAFYKMMSTRDLYLMLTYLNHKLDAASLQRLQVQKNAV 272
 Db 191 KSEKLTTRVTEEEFCEAFCELCETRPVEYFLLVQISKNEYLDANDLMLFEAEQGYTHI 250
 Qy 273 TLESCODITTEOPPCPENKSKGLGIDGFTNTTRPADINPEHHVHODMTOPLSHYF 332
 Db 251 TEDICLDIIRRYELSEEGKQGLAIDFTQYLLSECDIDPEQKKVADPTOPLSHY 310
 Qy 333 ITSSHNTYLVGQOLMSQSRVDMYAWVLQAGRCVCEVDCDGPGEPIYHGGYTLTKILF 392
 Db 311 INASHNTYLIEDQFRPADINQIRALMKGCHSVELVSDGSDNPLCNRRNMTTHSHF 370
 Qy 393 KVIETINTKAPITKNEYPVYLSIENHGSYIQKKAQVYITLIDGLDLSVSSDATT 452
 Db 371 RSVIEYINFAFAYASEYPIITLGNHCSLPQKVAQMKKVFKNL-YTEAPLSESYL 429
 Qy 453 PPSQMLKGLIKVKKGLPLANISEDAEEGVSDESDAIEDDCXKLNGDASTNRRKVENT 512
 Db 430 PSEPKLRMIYKGRKLPD--PDVLEGEVDED----- 461
 Qy 513 AKRKLDSLIKESKRDCEPDNPNFSVTLSPSGKLKRSKAEDVESGEDAGARRNGLY 572
 Db 462 -----EQAQMSRR----- 469
 Qy 573 VGSFSSRRKKKSKLKAASYEEDGODSPGQSGRATQOKTKMLSRALSDLVYKTSV 632
 Db 470 -----MSVDYNGE-----OKOIRCRELSDVLSICKSV 497
 Qy 633 ATHDIE--MEAASSQVSSPSETKAHQIIOOKPAQYLRFNQOOLSRTPSSRYVDSNTN 690
 Db 498 QYRDFELSKSQNTYEMCSFSETEASRIANEYEDDVNTNKKFLSIYSAMRIDSNNLN 557
 Qy 691 POPFWNAGQVVALNTQSEGRMLQLNRAKFSANGCGYVLKPGCCQGV--FNPNSEDL 748
 Db 558 POFWNGCQIVAMNFOPTGPMMDLHTGWFLONGCGCYVLRPSIMDEVSYSFSAANTKGL 617
 Qy 749 PGQLKQVLRITISGOOLPKPRDSMLGDEGEIIDEPEVEIIGLPGVDSREQTRVVDNG 808
 Db 618 PGVSPALHLIKITISGOVFPKPGACA--KGVADIPVCIIEHIGIPADCEQORIKTYQNS 675
 Qy 809 FNPTVEETLVFVHMPETALVRFVMDHDPIDGRDIFGORTLAFSSMMPYRRVHYLGG--- 865
 Db 676 DIMEHVTFLFVHAIITRNSGGKAKQKRSLSYRMGKRVREYTMNLNIGLIDTIFKIAVHP 795
 Qy 866 -MEASIFVHVASDLSG-----KVKQALGKGLFLR-----GP 898
 Db 899 KPGSLD-----SHAAGRPAPRPSYQRIILRTASAPTKSQKPG-----RRGP 941
 Qy 796 LREADIRENNQNAIYISIKELGLPPL-ASLKQCLTLSSRLTTSNTPTSVSLYMDSPF 854
 Qy 942 EL 943

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PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US07994.
XX

01888885-2007-09-26

PR 15-MAR-2000; 2000US-0189693.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Hu Y, Nepomnitchy B, Donoho G, Hilbun E, Turner CA, Abulin A;
 PI Friedrich G, Zambrowicz B, Sands AT;
 XX WPI: 2001-582456/65.
 DR N-PSDB: AAD17564.
 XX
 PR New polynucleotides encoding human phospholipase protein involved in
 PT cell activation and signal transduction, useful for drug screening,
 PT diagnosis and in gene therapy of biological disorders -
 XX
 XX Claim 11: Page 41-43; 45pp; English.
 CC The present sequence is novel human protein (NHP), phospholipase
 CC protein. Phospholipases hydrolyse phospholipids and play a key
 CC role in the cell activation and signal transduction. NHPs share
 CC structural similarity with animal phospholipases, including phospho-
 CC lipase C delta-4. NHP oligonucleotides are useful in conjunction with
 CC polymerase chain reaction (PCR) to screen libraries, isolate clones,
 CC and prepare cloning and sequencing templates, and alternatively as
 CC hybridisation probes for screening libraries and assessing gene
 CC expression patterns. They are used in the identification, selection
 CC and validation of novel molecular targets for drug discovery, where
 CC identification and characterisation of human genomic clones is helpful
 CC for identifying polymorphisms, determining the genomic structure of a
 CC given locus/allele and designing diagnostic tests. The microarray
 CC comprising NHP cDNA is useful for screening collections of genetic
 CC material from patients having a particular medical condition, which
 CC is used to identify mutations associated with a particular disease and
 CC also as diagnostic or prognostic assay. NHP nucleotide sequences are
 CC useful for drug screening. Nucleotide construct encoding NHP products
 CC are used in gene therapy for modulating NHP expression and to produce
 CC genetically engineered host cells to express NHP products in vivo. The
 CC NHP sequences are useful for generating antibodies, as reagents in
 CC diagnostic assays, for identifying other cellular gene products related
 CC to NHP and as reagents in assays for screening for compounds that are
 CC useful in the treatment of mental, biological or medical disorders and
 CC diseases. They can be used to therapeutically augment the efficacy of
 CC chemotherapeutic agents used in the treatment of breast or prostate
 CC cancer.
 CC
 XX
 XX Sequence 762 AA:
 SQ
 Query Match 22.6%; Score 1441; DB 22; Length 762;
 Best Local Similarity 38.3%; Pred. No. 8.5e-103;
 Matches 330; Conservative 145; Mismatches 253; Indels 134; Gaps 20;
 QY 45 MOEGMOMVRLKRGSGKGLVRYLDEHRSCTIRW--RPSRKNNEKAKISIDSIQEVSEGRQSE 102
 DB 18 MOEGMPARKVRSKSKMKLRYFLQNDQMTV-WHAQRAGSAGKSPFSISDETIRINGHSD 76
 QY 103 VFQRYPDGSGEDPNCSESTYSGHSHESLDVSTSEVARTVGTGLRYLMAISDEDSIARR 162
 DB 77 LIRSLAELEPLEGGFTLVFHG-RRSNIDLMANVSSEAQIWMRGLLDLVLTSD----H 131
 QY 163 QRTSDOMLKOTFEADKNGSGISGEVLQILKRLNVLPRQRYKQMFREADTDHOGTL 222
 DB 132 QERIDOMLSDFQKDNQKMSFOEYORLHLNEMOEYAFSLFQAADT-SQSGTL 190
 QY 223 GFEFCAFYKMMSTRDLTYLMLTYSNHKLHLNASTLQRLQYQKMAGYVLESQDIIE 282
 DB 191 EGEEFVQFYKALTRAEVQELFESFSADGOKLTLEFLDLFOEQKSRDCTSEALALID 250
 QY 283 QEEPCPEKKSGLGIGFTWYTRSPAGDIPNPHNHVHDMOPRLSHYFTSSHNTYLV 342
 DB 251 RYEPSDSKGLNHLVSMOGLSTYLSKSDGLPNPACLPYQDMPTPLNHYFLCSSHNTYLV 310
 QY 343 GDQLMSQSRVDMYAVLQAGRCVYDCWDGPDDEPIYHNGYTLTKILFKDVIETINKY 402
 DB 311 GDQLCGSGSVGTYRALKRCRCVCEVDVWDGPDSEPVYVYHGHITLSRLFKDVAVTAQY 370

QY 403 AFIKNEYVILSIENHSCVIOQKMAQYLTIDGLDKLIDLSVSESDATLPLSPQMLKGI 462
 DB 371 AFQTSIDPVILSLTFHCSWEGQOTMARHLEILLEGOLSTLIDGLVPLTQPSPEELARKI 430
 QY 463 LVKQKLPANISDEAEEGVSEDSDEIDDOCKLNLNGDASTNRKRVENAKKRLSLIK 522
 DB 431 LVKQKLT--TLEEDL--EYEEBEAEPELEB-----SEAL 461
 QY 523 ESKTRDCEPDNNFVSVTLSPSGKLGKRSKAEDVESEGDGASRNGRLVVGSEFSRRKK 582
 DB 462 ESQFTEPEFO-----EONLQND-----KKK 484
 QY 583 GSKLKAASVEEGDEGDSPGGSGRATROKTKMLSRALSDLVKRYKVA-----THDIE 638
 DB 485 SKPI-----LCPALSLVLYLKVSFRSFTH--S 511
 QY 639 MEAASSMOWSSFSFETKAQIILQOKPAOYLRLRNOOOLSIYVSSYRVDSNNYNPQPFNNAG 698
 DB 512 KEHYFYEISFSFETKARAKRLKEAGNEFVQHNTWOLSHVPSGLRTDSNINPQELMNA 571
 QY 699 COMVALNTQSEGRMLQLRKAFSANGGCGYVLPKPCM--CGGVFNPNSEDPPLPQOLKOL 756
 DB 572 COMVAMNQTAGLEMDICDGHFRQNGCGYVLPKDFLRLDIQSSFRP--EKPISPFKQTL 629
 QY 757 VLRITISGQQLPRRDSMLDRGEIIPVEVEIIGLPVDCSREQTRVVDNGFNPTEET 816
 DB 630 LQVVISGQOLPKVDT---KEGSIVDPLVKQIFGVRLDTRAOETINVENGFNPYMGOT 686
 QY 817 LVFWHMEIALVRLVMDHDPICR-DFIGORTLAFSSMPMGYRHYVY--EG--MEBAS 870
 DB 687 LCFRLVLPPLALMRVMDYDKSKNDFTIGYTLPLWTCMOGYRHHILSLDGLSLRPAS 746
 QY 871 IFVHVAVSDISGKVRQALGLK 892
 DB 747 IFVVICIQE-----GLEG 759
 RESULT 10
 ID AAE14268 standard; Protein; 762 AA.
 AC AAE14268;
 XX
 XX 07-MAR-2002 (first entry)
 DE
 XX Human phospholipase C delta 5 (PLCD5) protein #1.
 XX Human; phospholipid C delta 5; PLCD5 protein; deep vein thrombosis;
 KW angina pectoris; percutane transluminal coronary angiography; PTCA;
 KW Thrombo embolic insult; disseminated intravascular coagulation;
 KW arteriosclerosis; epilepsy; depression; neurodegenerative disease;
 KW stroke; rheumatoid arthritis; immune disorder; chromosome localisation;
 KW vaccine; gene therapy.
 XX
 OS Homo sapiens.
 PN WO200183771-A2.
 XX 08-NOV-2001.
 PD 27-APR-2001; 2001WO-BP04784.
 XX 29-APR-2000; 2000EP-0109318.
 PF
 PR (MERE) MERCK PATENT GMBH.
 PA Brandt S, Duecker K, Gietz J;
 PI WPI: 2002-034515/04.
 DR N-PSDB: AAD23721.
 XX
 XX New phospholipase C delta 5 polypeptides, useful for treating deep vein

15/ VKRIISGQQLPKPRDSMLGDRGEIIDPFVEVEIIGLPVDCSREQTRVVDNDNGFNPTWEET 816

Best Local Similarity 3/.68;
Matches 343; Conservative 14

Query Match	22.68;	Score 1439;	DB 23;	Length 828;
Best Local Similarity	37.68;	Pred. No. 1.4e-102;		
Matches 343;	Conservative 149;	Mismatches 280;	Indels 140;	Gaps 22

QY 4 PTAGPLPGPALPDEPDGPDESRLWLSANILP-----VERCAGAGQEGMGMVKLR 55
 DB 31 PCSRALPGPAT-----LSAGYLTLPAPDLELTDDDLLOMGGMRRVVR 75
 QY 56 GSGKGLVRYVYDEHRSICIR--RPSRKNEKAKISIDSIOEVSEGESEVFORVYDGSFSD 113
 DB 76 SKSWKRLRYFLRONDGMTV-WHARQARSGAKSFSSISDVETIRNHDSLLSLAEPL 134
 QY 114 PNCFSIYHSHRESIDLVSSEVAFWVYGLRYLMAGISDESDSLARRQRTDQWMLKOT 173
 DB 135 EGGFTIVFHG-RRSNLDLMANVSEEAQIMRGLQLVLDVYSMD-----HOERLDQMLSDW 189
 QY 174 FDEADKNGGSGISIGVYDOLLKLNANLPORVYKOMFRADDDHOGTIGFEPECAFYKM 233
 DB 190 FQGDNDQNGKMSFEVORLHLNMYEMDQYAFSLFQAADT--SOSGTLEGEETVQFYKA 248
 QY 234 MSRRDLYLMLTYSNHHKHLDAASLQRFLOYEOKMAGVTLSCODIIEQFPECKNSK 293
 DB 249 LTRAEVQELFEFSADQCKLTLERLDFLOEBQKRDCTSELAELELDREYEPDSGKLR 308
 QY 294 GLLGIDFTNYTRSPAGDIFNPEHHVHODMTOPLSHYITTSNHTYLVGDOLMSQSRD 353
 DB 309 HVLMDGFLSYLCSKDGDIENFACLPYODMTOPLNHYFICSSHNTYLVGDOLCGGSVE 368
 QY 354 MYAMVLOAGRCVYVDCMOPGSEPIVHHGYTLTKLRFKDVETITNKYAFIKNEYPVLL 413
 DB 369 GYIRALKRGRCVYVDCMOPGSEPIVHHGYTLTKLRFKDVETITNKYAFIKNEYPVLL 428
 QY 414 SIENHGSVIOQKKAQYLDLIDKLDSVSESDATTLPSQMLKGLLVKGLKLPANI 473
 DB 429 SLFHCWEGQQTMARLFEIIEQLSTLTDVLPQULPSPELRKILVYKGL--TL 486
 QY 474 SEDAESEVDESDADEIDDCKLINDASTNKRKVENAKRLDLSIKESKRDCEDPN 533
 DB 487 EEDL---EYEEERPEPLE----- 503
 QY 534 NFSVSTLSPGKLGKRSKAEDEVEDSAGASRRNRLVYVSPSRKKKSLKKAASVE 593
 DB 504 -----SELALESQFTEPEPQO-----NLQNKDKKTIQAQPIIS 538
 QY 594 EGDEGODSPGOSRGATROKTKMLSNALSDLYKTTSA-----THIEEAMASMQVSS 649
 DB 539 K-----PESTLISROKSPILCPALSLVLYKVSFRSFTH--SKEHYHFEISS 587
 QY 650 FSETKAHOILOOKPAOYLRFNQOOLSRITYPSYRVDSN--YNPOFYNACCOMVALYQS 708
 DB 588 FSETRAKRLIEAGNEFYQANTWOLSKRYBSGLRTDSNNTYNPQELMAGCOMVANNMOT 647
 QY 709 EGRMLOLNRANKFSANGCGVYLKPGCM--CGGVFNPNSEDPPLPGOLKKOLVLRILISQOL 766
 DB 648 AGLEMDICDGHFRQNGCGVYLKPFDLRIDQSSFHP--EKPISPFKAOITLNOVYSVOL 705
 QY 767 PKPRDSMLGDGEITIDPRVEVEITIGLPVDCSREGTRAVDNGFMPTEETLVFVHMEI 826
 DB 706 PKVKT---KSGSLVDPLVYKQIGVRLDIAROETNVENNGENPMYQOTLCFVYLPBL 762
 QY 827 ALVRLVWDHPDPIGR-DFIGORTLAFSSMPGYRHYVL---EG--MEBASIFVHVASDI 880
 DB 763 AMLRVYVADYDKMSKNDITIGQYTLPMTCMOGYYRIHLLSDGISLRASIFVYICIE- 821
 QY 881 SGKVKQALGK 892
 DB 822 -----GLEG 825

RESULT 12
 AAU76816
 ID AAU76816 standard; Protein: 762 AA.

XX AAU76816;
 XX
 XX
 DT 21-MAY-2002 (first entry)
 XX

DE Human phospholipase C 16816 polypeptide.
 XX
 KW Human: phospholipase C, PLC; phospholipase C 16816; brain disorder;
 KW cellular proliferative disorder; differentiative disorder; prion disease;
 KW glial disorder; cerebrovascular disease; acute meningitis; cirrhosis;
 KW demyelinating disease; degenerative disease; heart disorder; rickets;
 KW ischaemic heart disease; myocardial disease; neoplastic heart disease;
 KW vascular disease; inflammatory disease; bone metabolism disorder; enzyme;
 KW chronic renal disease; haematopoietic disorder; autoimmune disease;
 KW arthritis; systemic lupus erythematosus; Sjogren's syndrome; psoriasis;
 KW Crohn's disease; uveitis; atopic allergy; balloon angioplasty;
 KW coronary artery bypass graft surgery.
 KW
 KW Homo sapiens.
 OS
 XX
 XX
 FH Key location/Qualifiers
 FT Misc-difference 254 /note= "Encoded by CCR"
 FT Misc-difference 661 /note= "Encoded by CGC"
 FT
 FT
 XX WO200206302-A2.
 XX
 XX 24-JAN-2002.
 XX
 XX 17-JUL-2001; 2001WO-US22760.
 XX
 XX 17-JUL-2000; 2000US-218675P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PI Meyers R, Rudolph-Owen L, Tsai FY;
 DR WPI: 2002-188535/24.
 XX N-PSDB: ABR10063.
 PT
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 PS
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 CC The invention relates to human phospholipase C (PLC) polypeptides 16816
 CC and 16839. The polypeptides can be used in the treatment and diagnosis of
 CC various disorders including cellular proliferative and/or differentiative
 CC disorders (e.g. carcinoma and leukaemia), brain disorders including glial
 CC disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g. acute
 CC ischaemia and hypertensive encephalopathy), infections (e.g. acute
 CC meningitis and prion diseases), demyelinating diseases (e.g. multiple
 CC sclerosis), degenerative diseases (e.g. Alzheimer's disease), heart
 CC disorders including heart failure, ischaemic heart disease (e.g.
 CC myocardial infarction), myocardial disease (e.g. myocarditis), neoplastic
 CC heart disease (e.g. angina pectoris), vascular diseases (e.g.
 CC atherosclerosis), inflammatory disease (e.g. Kawasaki syndrome), bone
 CC metabolism disorders (e.g. osteoporosis), cirrhosis, rickets, chronic
 CC renal disease, haematopoietic disorders, autoimmune diseases (e.g.
 CC diabetes mellitus), arthritis, systemic lupus erythematosus, Sjogren's
 CC syndrome, psoriasis, Crohn's disease, uveitis, atopic allergy, and
 CC pathology of therapeutic interventions in vascular disease (e.g. balloon
 CC angioplasty and related techniques) and vascular replacement (e.g.
 CC coronary artery bypass graft surgery). This sequence represents human
 CC phospholipase C 16816.
 CC
 XX
 XX Sequence 762 AA:
 SQ
 Query Match 22.4%; Score 1432; DB 23; Length 762;
 Best Local Similarity 38.2%; Pred. No. 4.2e-102; Indels 134; Gaps 20;
 Matches 329; Conservative 145; Mismatches 254;
 QY 45 MOEGMOMVKLRGSGKGLVRYVYDEHRSICIR--RPSRKNEKAKISIDSIOEVSEGESE 102
 DB 18 MOEGMOMVKLRGSGKGLVRYVYDEHRSICIR--RPSRKNEKAKISIDSIOEVSEGESE 76

GenCore version 5.1.4 ps 4578
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2003, 22:01:49 ; Search time 167 Seconds
(without alignments)
8511.657 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635
Sequence: 1 ttcggatcctcagaactagctg.....ggtacggggccagcccg 4635

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338181 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	0.5	1365	1 US-08-114-072-1	Sequence 1, Appl
C 2	21	0.5	1365	2 PCT-US94-09361-1	Sequence 1, Appl
C 3	20	0.4	1062	2 US-08-466-103A-13	Sequence 13, Appl
C 4	20	0.4	2377	4 US-09-479-195-1	Sequence 1, Appl
C 5	20	0.4	2372	3 US-09-280-420-1	Sequence 1, Appl
C 6	20	0.4	4425	2 US-08-749-169A-1	Sequence 1, Appl
C 7	20	0.4	4425	2 US-09-130-032A-1	Sequence 1, Appl
C 8	20	0.4	4488	4 US-08-406-030A-3	Sequence 3, Appl
C 9	20	0.4	62804	4 US-09-800-960-3	Sequence 3, Appl
C 10	19	0.4	703	4 US-09-276-531-31	Sequence 31, Appl
C 11	19	0.4	1420	1 US-08-358-171-1	Sequence 1, Appl
C 12	19	0.4	1420	1 US-09-090-947-1	Sequence 1, Appl
C 13	19	0.4	3870	1 US-08-138-641-1	Sequence 1, Appl
C 14	19	0.4	3870	1 US-08-138-133-1	Sequence 1, Appl
C 15	19	0.4	3893	1 US-08-138-641-3	Sequence 3, Appl
C 16	19	0.4	3893	1 US-08-138-133-3	Sequence 3, Appl
C 17	19	0.4	3955	4 US-09-214-278-4	Sequence 4, Appl
C 18	19	0.4	4464	2 US-08-400-159-7	Sequence 7, Appl
C 19	19	0.4	4483	3 US-08-611-729A-7	Sequence 7, Appl
C 20	19	0.4	5163	3 US-08-700-651-1	Sequence 1, Appl
C 21	19	0.4	5163	3 US-08-928-361B-4	Sequence 4, Appl
C 22	19	0.4	5318	3 US-08-700-651-2	Sequence 2, Appl
C 23	19	0.4	5318	3 US-08-928-361B-3	Sequence 3, Appl
C 24	19	0.4	5511	3 US-08-928-361B-2	Sequence 2, Appl
C 25	19	0.4	7334	3 US-08-928-361B-1	Sequence 1, Appl
C 26	19	0.4	7507	2 US-08-975-763-1	Sequence 1, Appl
C 27	19	0.4	7714	4 US-09-479-122-26	Sequence 26, Appl

28	19	0.4	10317	3 US-09-058-746-1	Sequence 1, Appl
29	19	0.4	10317	4 US-09-438-142-1	Sequence 1, Appl
C 30	19	0.4	80161	3 US-09-036-987A-1	Sequence 1, Appl
C 31	19	0.4	80161	4 US-09-370-700-1	Sequence 1, Appl
C 32	18	0.4	41	1 US-08-447-411-80	Sequence 80, Appl
C 33	18	0.4	43	1 US-08-049-473-23	Sequence 23, Appl
C 34	18	0.4	43	1 US-08-312-648-23	Sequence 23, Appl
C 35	18	0.4	43	5 PCT-US94-04190-23	Sequence 23, Appl
C 36	18	0.4	44	4 US-09-161-241-42	Sequence 42, Appl
C 37	18	0.4	45	4 US-09-549-770B-11	Sequence 11, Appl
C 38	18	0.4	46	4 US-09-549-770B-12	Sequence 12, Appl
C 39	18	0.4	47	4 US-09-549-770B-13	Sequence 13, Appl
C 40	18	0.4	48	4 US-09-549-770B-14	Sequence 14, Appl
C 41	18	0.4	48	4 US-09-549-770B-15	Sequence 15, Appl
C 42	18	0.4	50	1 US-08-049-473-34	Sequence 34, Appl
C 43	18	0.4	50	1 US-08-312-648-34	Sequence 34, Appl
C 44	18	0.4	50	5 PCT-US94-04190-34	Sequence 34, Appl
C 45	18	0.4	53	1 US-08-049-473-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-114-072-1/c
Sequence 1, Application US/08114072
Patent No. 5624823
GENERAL INFORMATION:
APPLICANT: Sachs, David.
APPLICANT: Leguenn, Christian.
APPLICANT: Meghan, Sykes,
APPLICANT: Biancho, Gilles
TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHVE & COCKFIELD
STREET: 60 STATE STREET Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,072
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-017
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-114-072-1

Query Match 0.5%; Score 21; DB 1; Length 1365;

Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3334 CTCGGAAGCCCGAGCCGAGG 3354
Db 1066 CTCGGAAGCCCGAGCCGAGG 1046

RESULT 2
PCT-US94-09361-1/c
Sequence 1, Application PC/TUS9409361
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09361
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-017PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-09361-1.

Query Match 0.5%; Score 21; DB 5; Length 1365;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3334 CTCGGAGAGCCCGAGCCG 3354
Db 1066 CTCGGAGAGCCCGAGCCG 1046

RESULT 3
US-08-466-103A-13/c
Sequence 13, Application US/08466103A
Patent No. 5856124
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Edisawa, Takashi
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1059
OTHER INFORMATION:
US-08-466-103A-13

Query Match 0.4%; Score 20; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 CGCCTGAGAGCTGCTGAGTG 4405
Db 52 CGCCTGAGAGCTGCTGAGTG 33

RESULT 4
US-09-479-195-1/c
Sequence 1, Application US/09479195
Patent No. 6326526
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
APPLICANT: Gilboff, Valentin K.
TITLE OF INVENTION: MELATONIN RECEPTOR-DEFICIENT MICE AND USES THEREOF
FILE REFERENCE: 10217/727002
CURRENT APPLICATION NUMBER: US/09/479,195
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/122,527
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,565
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2377
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1270)...(2328)
OTHER INFORMATION: Intron coding sequence between positions 1464 and
US-09-479-195-1

Query Match 0.4%; Score 20; DB 4; Length 2377;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 CGCCTGAGAGCTGCTGAGTG 4405
Db 1321 CGCCTGAGAGCTGCTGAGTG 1302

RESULT 5
US-09-280-420-1/c
Sequence 1, Application US/09280420
Patent No. 6037131
GENERAL INFORMATION:
APPLICANT: Reppert, Steven M.
TITLE OF INVENTION: MELATONIN 1A RECEPTOR GENE

TITLE OF INVENTION: REGULATORY REGIONS AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,420
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,701
FILING DATE:
APPLICATION NUMBER: 60/022,185
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1270...2328
OTHER INFORMATION: Intron coding sequence between positions 1464
US-09-280-420-1
Query Match 0.4%; Score 20; DB 3; Length 2772;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4386 CGCCTGAGAGCTGCTGAGTG 4405
|||
Db 1321 CGCCTGAGAGCTGCTGAGTG 1302

RESULT 6
US-08-749-169A-1
Sequence 1, Application US/08749169A
Patent No. 5846770
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-749-169A-1
Query Match 0.4%; Score 20; DB 2; Length 4425;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCCGCGCCCTCG 3183
|||
Db 73 GCCCGCGCGCCGCGCCCTCG 92

RESULT 7
US-09-130-032A-1
Sequence 1, Application US/09130032A
Patent No. 5986056
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: LAVALLIE, Edward
APPLICANT: DEROBERTIS, Edward
TITLE OF INVENTION: HUMAN CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: August 4, 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5284-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-130-032A-1
Query Match 0.4%; Score 20; DB 2; Length 4425;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCGCCCGGCGCGGCGCTCCG 3183
Db 73 GCGCCCGGCGCGGCGCTCCG 92

RESULT 8

US-08-406-030A-3/c
; Sequence 3, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Haugle, Brian M.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3
Query Match 0.4%; Score 20; DB 4; Length 4488;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCGCCCGGCGCGGCGCTCCG 3183
Db 2422 GCGCCCGGCGCGGCGCTCCG 2403

RESULT 9

US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match 0.4%; Score 20; DB 4; Length 62804;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4513 GCGCCACACACCGCGCCG 4532
Db 19561 GCGCCACACACCGCGCCG 19542

RESULT 10

US-09-276-531-31
; Sequence 31, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT01
CLONE: 713784
US-09-276-531-31

Query Match 0.4%; Score 19; DB 4; Length 703;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4126 TGGAGAGACCGCTGCTC 4144
DB 312 TGGAGAGACCGCTGCTC 330

RESULT 11
US-08-358-171-1/c
Sequence 1, Application US/08358171
Patent No. 5763578
GENERAL INFORMATION:
APPLICANT: FONG, Henry K.W.
TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,171
FILING DATE: 16-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 17..889

US-08-358-171-1

Query Match 0.4%; Score 19; DB 1; Length 1420;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3342 GCCCAGCCCGAGGAGGC 3360
DB 469 GCCCAGCCCGAGGAGGC 451

RESULT 12
US-09-090-947-1/c
Sequence 1, Application US/09090947
Patent No. 6008338
GENERAL INFORMATION:
APPLICANT: FONG, Henry K.W.
TITLE OF INVENTION: ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
TITLE OF INVENTION: ENCODING SAME, AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,171
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: FONG=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 17..889
US-09-090-947-1

Query Match 0.4%; Score 19; DB 3; Length 1420;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3342 GCCCAGCCCGAGGAGGC 3360
DB 469 GCCCAGCCCGAGGAGGC 451

RESULT 13
US-08-138-641-1
Sequence 1, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:

APPLICANT: Koblan, Kenneth S.
APPLICANT: Pompliano, David L.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-641-1
Query Match 0.4%; Score 19; DB 1; Length 3870;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1537 TGGACTGCTGGGATGGGCC 1555
DB 1097 TGGACTGCTGGGATGGGCC 1115
RESULT 14
US-08-138-133-1
Sequence 1, Application US/08138133
Patent No. 5519163
GENERAL INFORMATION:
APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MERCHANT, KEVIN J.
TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
TITLE OF INVENTION: PHOSPHOLIPASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MUTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-133-1
Query Match 0.4%; Score 19; DB 1; Length 3870;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1097 TGGACTGCTGGGATGGGCC 1115
RESULT 15
US-08-138-641-3
Sequence 3, Application US/08138641
Patent No. 5474921
GENERAL INFORMATION:
APPLICANT: Koblan, Kenneth S.
APPLICANT: Pompliano, David L.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3893 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-138-641-3
Query Match 0.4%; Score 19; DB 1; Length 3893;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Mon Mar 31 09:40:38 2003

us-09-927-112-1.oligo.rni

Page 7

Db 1097 TCGACTGCTGGAGTGGCC 1115

Search completed: March 29, 2003, 13:11:14
Job time : 575 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 07:02:54 ; Search time 360 Seconds
(without alignments)
10956.277 Million cell updates/sec

Title: US-09-927-112-1

Perfect score: 4635

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Gapop 60.0 , Gapext 60.0

Searched: 574371 seqs, 425486471 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA.*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4635	100.0	4635	10 US-09-927-112-1	Sequence 1, Appli
2	3624	78.2	3624	10 US-09-927-112-3	Sequence 3, Appli
3	20	0.4	426	10 US-09-954-456-1912	Sequence 1912, Ap
4	20	0.4	498	9 US-09-282-758-106	Sequence 106, App
5	20	0.4	1530	10 US-09-815-242-7987	Sequence 7987, Ap
6	20	0.4	1840	10 US-09-835-996A-7	Sequence 7, Appli
7	20	0.4	2289	10 US-09-804-969-14	Sequence 14, Appli
8	20	0.4	2289	10 US-09-908-664-3	Sequence 3, Appli
9	20	0.4	2573	10 US-09-917-800A-1339	Sequence 1339, Ap
10	20	0.4	2623	10 US-09-908-664-1	Sequence 1, Appli
11	20	0.4	2709	10 US-09-804-969-20	Sequence 20, Appli
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13	20	0.4	3441	9 US-09-944-403-6	Sequence 6, Appli
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24	0.4	3441	10 US-09-944-097-6	Sequence 6, Appli
25	0.4	3441	10 US-09-944-432-6	Sequence 6, Appli
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30	0.4	4235	9 US-09-926-457-317	Sequence 317, App
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33	0.4	4235	9 US-10-017-754-317	Sequence 317, App
34	0.4	62804	12 US-10-096-960-3	Sequence 3, Appli
35	0.4	273	10 US-09-878-574-8990	Sequence 8990, Ap
36	0.4	289	10 US-09-864-761-19416	Sequence 19416, A
37	0.4	290	10 US-09-864-761-25548	Sequence 25548, A
38	0.4	358	10 US-09-833-381-1154	Sequence 1154, Ap
39	0.4	537	10 US-09-864-761-8883	Sequence 8883, Ap
40	0.4	1540	10 US-09-880-107-2390	Sequence 2390, Ap
41	0.4	1540	10 US-09-880-107-2390	Sequence 2390, Ap
42	0.4	2421	10 US-09-815-242-7677	Sequence 304, App
43	0.4	3043	9 US-10-098-841-304	Sequence 304, App
44	0.4	3441	9 US-10-084-700-3	Sequence 3, Appli
45	0.4	3955	9 US-10-219-248-4	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-927-112-1
Sequence 1, Application US/09927112
Patent No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: Silos-Santiago, Immaculada
TITLE OF INVENTION: a novel human phospholipase C and
FILE REFERENCE: 38155-20048.00
CURRENT FILING DATE: 2001-08-10
PRIORITY FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/246,808
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4635
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (435) ... (4058)
US-09-927-112-1

Query Match 100.0%; Score 4635; DB 10; Length 4635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AACCTGCGGCTCTCGGCTGGAGCGGAGTGGATCAGCTCAAGCTCCAGGCGCTGAG	120
DB	61	AACCTGCGGCTCTCGGCTGGAGCGGAGTGGATCAGCTCAAGCTCCAGGCGCTGAG	120
QY	121	GCTGAGGAGGCTGAGTGTCTATTCAGCCGCTCGGGGAAACCGGGCTGGAGAACCCCATG	180
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QY	181	CTGGGGGTGAGCTCTGGAACCAAGGCGAGTGGCGGTGAGAAGCTTCGGAGAAGAGGCTGAGC	240
Db	181	CTGGGGGTGAGCTCTGGAACCAAGGCGAGTGGCGGTGAGAAGCTTCGGAGAAGAGGCTGAGC	240
QY	241	ACCACCAAGGCTTGGGTGTGTGATGCGCTGTGAGCTGAGCCCAAGCTTACACCCCGACAAGGGGAC	300
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QY	301	CGGGGGCTTGGGAGCAGAGAGACTTCAAGAGCTTCTCTGCTCTCTGTGAGCGGCC	360
Db	301	CGGGGGCTTGGGAGCAGAGAGACTTCAAGAGCTTCTCTGCTCTCTGTGAGCGGCC	360
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Db	541	CCGTGTGGAGCGGTGATGAGGTGCAATGAGGAGGAGATGCAATGTGTAACTTGCCTG	600
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QY	661	GGAGGCGCTTCAAGCAAGAACAGAAAGGCAAGACTCTCATCGACTCCATCCAGAGGTCA	720
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Db	721	GTGAGGGGCGGCAAGTCCGAGGTCTTCAAGGCTACTCTGACGGAGCTTGCACCCCACT	780
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Db	1141	CCGCGCGGAGCTTACCTGCTCATGTGCTACCAAGCAACCAAGGACCAACTGGATG	1200
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QY	1381	AGCACCAACCATGTGACACGAGGACATGACGACGCCGCTGAGCCACTATCTTATCATCCTCGT	144
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Db	1501	CTTGGGTCCTGAGGCTGAGCTGCGCTGCGCTGAGGATGAGCATCTGAGATGGGCCCGACG	156
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Db	1561	GGGAGCCCATTTGTGCACATGGCTCAACTGTGACTTCCAAAGATCTCTTCAAGAAGCTCA	162
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QY	1921	AGCTCTCAATGGGAGATGCATCCAACTGGAAGGGGTGAGAAACAATGCTTAAGAGA	198
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QY	2041	CCGTCTCCACACTGTCCCACTCTGGAAGGCTGGGAGCGCAAGAGCAAGGCTGTAAGAGAGG	210
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Qy 2581 ACCGAGCAGATTCAAGCGCCCAAGGTGGCTGCGGCTACGTACTCAAGCTTGGGTGATGT 2640
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Db 2941 ACATTCCTATCGGCGTGTGATCTTCAATTTGGCCAGAGAGCGTGGCCTTACAGCAGATGTC 3000
Qy 3001 CAGGCTACAGACAGGTGTACTTAAGGAGATGAAAGAGGCTTCCATCTTCTGATGTGG 3060
Db 3001 CAGGCTACAGACAGGTGTACTTAAGGAGATGAAAGAGGCTTCCATCTTCTGATGTGG 3060
Qy 3061 CTGTCACTGATCATGACGCTTAAGTCAAGAGGCTTGGGCTTAAAGGCTTCTTCTCC 3120
Db 3061 CTGTCACTGATCATGACGCTTAAGTCAAGAGGCTTGGGCTTAAAGGCTTCTTCTCC 3120
Qy 3121 GAGGCCCCAAGCCCGGCTCGCTGACATGCTGCTGGGCGGCCCGGCGCCCT 3180
Db 3121 GAGGCCCCAAGCCCGGCTCGCTGACATGCTGCTGGGCGGCCCGGCGCCCT 3180
Qy 3181 CCGTATGACAGGATCTCTGCGGCGCACAGGCGCCCGACCAAGAGCCGAGCCGG 3240
Db 3181 CCGTATGACAGGATCTCTGCGGCGCACAGGCGCCCGACCAAGAGCCGAGCCGG 3240
Qy 3241 GCGGAGGGGCTTCCCGAGCTGTCTGTGGATCAACGAGGACCAAGGCTTCAAGGGGGTGG 3300
Db 3241 GCGGAGGGGCTTCCCGAGCTGTCTGTGGATCAACGAGGACCAAGGCTTCAAGGGGGTGG 3300
Qy 3301 CAGAGCATGTGTGCCCCCGGGCCCGGACCTGCTCCGAAAGCCCAAGCAGAGGGGC 3360
Db 3301 CAGAGCATGTGTGCCCCCGGGCCCGGACCTGCTCCGAAAGCCCAAGCAGAGGGGC 3360
Qy 3361 CCGGAGCGGAGCCCTCCGAGGTAAAGCGCCAGCTGGGTGGCAAGAAAGCCCTGTGGC 3420
Db 3361 CCGGAGCGGAGCCCTCCGAGGTAAAGCGCCAGCTGGGTGGCAAGAAAGCCCTGTGGC 3420
Qy 3421 GAGTGTGCGCCCGGCTGTCTGAGCAGGCGCGGGCTGTGGATGGCGGCATGCA 3480
Db 3421 GAGTGTGCGCCCGGCTGTCTGAGCAGGCGCGGGCTGTGGATGGCGGCATGCA 3480

Qy 3481 TGAAGTGTGTGGGATCTTGCGCCGCGGTGAACACCGGGGGCTTGCAGAGGAGCGGC 3540
Db 3481 TGAAGTGTGTGGGATCTTGCGCCGCGGTGAACACCGGGGGCTTGCAGAGGAGCGGC 3540
Qy 3541 CACCCAGCCCGGGGCTTGCAGAGCAGGAGCGCATTTCCGACAGACCCCGGGCCCGG 3600
Db 3541 CACCCAGCCCGGGGCTTGCAGAGCAGGAGCGCATTTCCGACAGACCCCGGGCCCGG 3600
Qy 3601 CTGATCTACTGGGGGCCCCCTGTGTGGCTTGAACCCCTCAAGCATCCCGGGAGAAACA 3660
Db 3601 CTGATCTACTGGGGGCCCCCTGTGTGGCTTGAACCCCTCAAGCATCCCGGGAGAAACA 3660
Qy 3661 GAGAGGCCCCCAAGGGGTCTGGGGCTTGAAGCAGGGCTCAGGGGTAGCGGCTCAATGT 3720
Db 3661 GAGAGGCCCCCAAGGGGTCTGGGGCTTGAAGCAGGGCTCAGGGGTAGCGGCTCAATGT 3720
Qy 3721 CCTCGACTCCAGCAGCCCAAGCAGCCCGGCAATCCCGAAAGTCCCCCGCTGGCTG 3780
Db 3721 CCTCGACTCCAGCAGCCCAAGCAGCCCGGCAATCCCGAAAGTCCCCCGCTGGCTG 3780
Qy 3781 AGGTTGCTGCAAGCAGACCCGGGGCTTGCAGAGGAGATAGTGGCTTGTGCTCAA 3840
Db 3781 AGGTTGCTGCAAGCAGACCCGGGGCTTGCAGAGGAGATAGTGGCTTGTGCTCAA 3840
Qy 3841 AGCTGAGGAGATCAAGAGTAAATCCCAATGTTCTCCGCGGTAAAGCCCTTGGCCCT 3900
Db 3841 AGCTGAGGAGATCAAGAGTAAATCCCAATGTTCTCCGCGGTAAAGCCCTTGGCCCT 3900
Qy 3901 GCGTGTCTCTCCGAGCAGCCCTTGGCATGAGCTGGGCTTGGCTGCTGTGCTTCTG 3960
Db 3901 GCGTGTCTCTCCGAGCAGCCCTTGGCATGAGCTGGGCTTGGCTGCTGTGCTTCTG 3960
Qy 3961 CGTGACGATGTGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 4020
Db 3961 CGTGACGATGTGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 4020
Qy 4021 GTGGACCTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 4080
Db 4021 GTGGACCTGCTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 4080
Qy 4081 TGAAGCCCTGAGCATTTGGGTGAGTGTGTTGAGGCGCCGACAGGCTTGGAGAACCAAGCT 4140
Db 4081 TGAAGCCCTGAGCATTTGGGTGAGTGTGTTGAGGCGCCGACAGGCTTGGAGAACCAAGCT 4140
Qy 4141 GCTTGTGCTGAGGCTTGGGGCGGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 4200
Db 4141 GCTTGTGCTGAGGCTTGGGGCGGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 4200
Qy 4201 GCGCTTCCCAAACTGACCTTGGGCGGCTTGGCGACCTGACATGAGCCCTGATGCTTTC 4260
Db 4201 GCGCTTCCCAAACTGACCTTGGGCGGCTTGGCGACCTGACATGAGCCCTGATGCTTTC 4260
Qy 4261 CTGGGACTGGGGGCAATGATCAATCCATTCCTTCCAGGGCAGGCTTCCAGGGG 4320
Db 4261 CTGGGACTGGGGGCAATGATCAATCCATTCCTTCCAGGGCAGGCTTCCAGGGG 4320
Qy 4321 TCCCTACTGGAAGTGTGATGTGGGAGATGTGAGCTGTGGGCTTCTGGGCGCC 4380
Db 4321 TCCCTACTGGAAGTGTGATGTGGGAGATGTGAGCTGTGGGCTTCTGGGCGCC 4380
Qy 4381 TGGAGCGCTTGGAGCCTGCTGAGTGTGGGTGGAGTGAATTCCTTGGGCGCCAGGCTTTC 4440
Db 4381 TGGAGCGCTTGGAGCCTGCTGAGTGTGGGTGGAGTGAATTCCTTGGGCGCCAGGCTTTC 4440
Qy 4441 GCTGCTTTGGGCTGAGGACCCCACTAGAAAGGTGTCTCTTAGCTGAGGGAGGAGACA 4500
Db 4441 GCTGCTTTGGGCTGAGGACCCCACTAGAAAGGTGTCTCTTAGCTGAGGGAGGAGACA 4500
Qy 4501 TACAGGAGCCCGCCCAACACCTGCTTCCAGATCCCTTCCAGATCCCTTCCAGATCCCTT 4560
Db 4501 TACAGGAGCCCGCCCAACACCTGCTTCCAGATCCCTTCCAGATCCCTTCCAGATCCCTT 4560

QY 4561 TCTGCCCCCAGCCAGCTTGGCTCCGAGTTAGAACTGAGAGCGGCGAGTACAGCTAA 4620
Db 4561 TCTGCCCCCAGCCAGCTTGGCTCCGAGTTAGAACTGAGAGCGGCGAGTACAGCTAA 4620
QY 4621 CGGGGCCCCAGCCCG 4635
Db 4621 CGGGGCCCCAGCCCG 4635

RESULT 2

US-09-927-112-3
/ Sequence 3, Application US/09927112
/ Patent No. US2002010674A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Meyers, Rachel
/ APPLICANT: Silos-Santiago, Immaculada
/ TITLE OF INVENTION: 3254, a novel human phospholipase C and
/ FILE REFERENCE: 38155-20048.00
/ CURRENT APPLICATION NUMBER: US/09/927,112
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: US 60/246,808
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 3624
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-927-112-3

Query Match 78.2%; Score 3624; DB 10; Length 3624;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 435 ATGCTCTCCCGCAGCGGCGCCCTTCTGCGCCAGCTTTCCGCTAGAGAGCCAGAG 494
Db 1 ATGGCTCTCCCGCAGCGGCGCCCTTCTGCGCCAGCTTTCCGCTAGAGAGCCAGAG 60
QY 495 CCGAGTCCGAGAGAGAGGCTTTCTTGAAGCGGCAATTCCGCGCGTGGTGAAGG 554
Db 61 CCGAGTCCGAGAGAGAGGCTTTCTTGAAGCGGCAATTCCGCGCGTGGTGAAGG 120
QY 555 TGCATGGGTGCGCATCAAGAGGAGTGAAGTGTGAAGCTTGGCGGCTCCAAAGGC 614
Db 121 TGCATGGGTGCGCATCAAGAGGAGTGAAGTGTGAAGCTTGGCGGCTCCAAAGGC 180
QY 615 CTGCTCCGCTTTACTACTGAGCAGACCGGCTTCTGATCCGCTGAGGCGCTTCAAGC 674
Db 181 CTGCTCCGCTTTACTACTGAGCAGACCGGCTTCTGATCCGCTGAGGCGCTTCAAGC 240
QY 675 AAGAAGAGAGAGCCAGATCTCCATCGACTCCATCCAGAGGTGAGTGAAGGCGGAG 734
Db 241 AAGAAGAGAGAGCCAGATCTCCATCGACTCCATCCAGAGGTGAGTGAAGGCGGAG 300
QY 735 TCGAGGTCTTTCAGCGCTTACTGACGCGAGCTTGAAGCTTGAAGCTTTCAGGATC 794
Db 301 TCGAGGTCTTTCAGCGCTTACTGACGCGAGCTTGAAGCTTGAAGCTTTCAGGATC 360
QY 795 TACACGCGCAGCAGCCGAGTCCGCTGAGCCTGCTTCCACAGACAGAGTGGCGGC 854
Db 361 TACACGCGCAGCAGCCGAGTCCGCTGAGCCTGCTTCCACAGACAGAGTGGCGGC 420
QY 855 ACCTGGGTCACTGAGCTGCGCTTACTGAGCAGGATCAAGCGAGCAGAGAGCTGCT 914
Db 421 ACCTGGGTCACTGAGCTGCGCTTACTGAGCAGGATCAAGCGAGCAGAGAGCTGCT 480
QY 915 CGCCGCGCAGCAGCAGGAGCAGTGGTGAAGAGAGCTTTGAGAGGCGCGAAGAAC 974
Db 481 CGCCGCGCAGCAGCAGGAGCAGTGGTGAAGAGAGCTTTGAGAGGCGCGAAGAAC 540
QY 975 GGGAGTGAAGCTGAGGATGAGGAGTCTGAGGCTGAGCAAGCTCAAGCTCAAGTGAAC 1034

Db 541 GGGAGTGAAGCTGAGGATGAGGAGTCTGAGGCTGAGCAAGCTCAAGCTCAAGTGAAC 600
QY 1035 CTGCCCCGCGAGAGGAGTGAAGAGTGTTCAGAGGAGCGGACAGAGTGAACCAAGG 1094
Db 601 CTGCCCCGCGAGAGGAGTGAAGAGTGTTCAGAGGAGCGGACAGAGTGAACCAAGG 660
QY 1095 ACCTGGGTCTTGAAGAGTCTGAGCTTCTTCAAGATGATGCAAGCCGCGGAGCTTC 1154
Db 661 ACCTGGGTCTTGAAGAGTCTGAGCTTCTTCAAGATGATGCAAGCCGCGGAGCTTC 720
QY 1155 TACCTGCTCATGCTGAGCCTTACAGCAACCAAGAGCAGCTGATCCGCAAGCTGAG 1214
Db 721 TACCTGCTCATGCTGAGCCTTACAGCAACCAAGAGCAGCTGATCCGCAAGCTGAG 780
QY 1215 CGCTTCTGAGAGTGAAGAGATGAGCGAGGAGTGAAGCTTGAAGAGCTGAGAGCATC 1274
Db 781 CGCTTCTGAGAGTGAAGAGATGAGCGAGGAGTGAAGCTTGAAGAGCTGAGAGCATC 840
QY 1275 ATGAGCAGTTTGAAGCAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1334
Db 841 ATGAGCAGTTTGAAGCAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1335 TTACCAACTTACACAG 1394
Db 901 TTACCAACTTACACAG 960
QY 1395 CACCAAGACATGACAGAGCGGCTGAGCCACTTCTTCAATGATGATGATGATGATG 1454
Db 961 CACCAAGACATGACAGAGCGGCTGAGCCACTTCTTCAATGATGATGATGATGATG 1020
QY 1455 CTGCTGGGTGAGCAGAGTCTTCCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1514
Db 1021 CTGCTGGGTGAGCAGAGTCTTCCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1080
QY 1515 GCTGGGTGAGCAGAGTCTTCCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1574
Db 1081 GCTGGGTGAGCAGAGTCTTCCAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1140
QY 1575 CACCAAGACATGACAGAGCGGCTGAGCCACTTCTTCAATGATGATGATGATGATG 1634
Db 1141 CACCAAGACATGACAGAGCGGCTGAGCCACTTCTTCAATGATGATGATGATGATG 1200
QY 1635 AATATGCTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1694
Db 1201 AATATGCTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1695 GTGATCAGCAG 1754
Db 1261 GTGATCAGCAG 1320
QY 1755 CTGCTATGAGTGAAG 1814
Db 1321 CTGCTATGAGTGAAG 1380
QY 1815 AAGATCTGCTGAAG 1874
Db 1381 AAGATCTGCTGAAG 1440
QY 1875 GAGGTGTCTGATGAG 1934
Db 1441 GAGGTGTCTGATGAG 1500
QY 1935 GATGATCAGCAG 1994
Db 1501 GATGATCAGCAG 1560
QY 1995 ATCAAGAGTGAAG 2054
Db 1561 ATCAAGAGTGAAG 1620
QY 2055 TCCCATCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2114

Db 1621 TCCCATCTGAAAAGCTCGGAGCGCAAGCAAGGCTGAAAGAGACGTGAGTCTGGGAG 1680
 Qy 2115 GATGCCGGGGCCAGCAGACGCAATGGCCGCTGTGTGGAAAGCTTTCAGGGCCAG 2174
 Db 1681 GATGCCGGGGCCAGCAGACGCAATGGCCGCTGTGTGGAAAGCTTTCAGGGCCAG 1740
 Qy 2175 AAGAAAGGCGCAGAGCTGAAAGAGGGCGGCGAGCTGAGAGGAGATGAGGGTACAGAC 2234
 Db 1741 AAGAAAGGCGCAGAGCTGAAAGAGGGCGGCGAGCTGAGAGGAGATGAGGGTACAGAC 1800
 Qy 2235 TCCCGGAGAGCCAGAGCCGAGGGGCGACCCGCGAGAAAGACATGAAGCTTCCG 2294
 Db 1801 TCCCGGAGAGCCAGAGCCGAGGGGCGACCCGCGAGAAAGACATGAAGCTTCCG 1860
 Qy 2295 GCCCTCTCTGACTGCTGAAATCAACCAATCCGTGGCCACCAACCACTAGAGATGAG 2354
 Db 1861 GCCCTCTCTGACTGCTGAAATCAACCAATCCGTGGCCACCAACCACTAGAGATGAG 1920
 Qy 2355 GCGGCGCTCAGCTGGAGAGTGTCTCTTCAAGCAGACCAAGGCCACAGATTCTGAG 2414
 Db 1921 GCGGCGCTCAGCTGGAGAGTGTCTCTTCAAGCAGACCAAGGCCACAGATTCTGAG 1980
 Qy 2415 CAGAAAGCCGCGAGATCACTACGCTTCAACCAAGACAGCTTCCGCACTACCTCC 2474
 Db 1981 CAGAAAGCCGCGAGATCACTACGCTTCAACCAAGACAGCTTCCGCACTACCTCC 2040
 Qy 2475 TCTCACTGTGTGACTCAGACCACTACAACCCGAGCCCTTCTGAAAGCGCGGCTGCA 2534
 Db 2041 TCTCACTGTGTGACTCAGACCACTACAACCCGAGCCCTTCTGAAAGCGCGGCTGCA 2100
 Qy 2535 ATGGTTCCCTGAACTACAGTCAAGAGGGCGAGTGTGAGCTGAAACCGAGCAATTC 2594
 Db 2101 ATGGTTCCCTGAACTACAGTCAAGAGGGCGAGTGTGAGCTGAAACCGAGCAATTC 2160
 Qy 2595 AGCGCAACGGTGTGCTGCGCTACCTAAGCTGTGCTGCAAGCTGTGCTGCAAGCTGTGCT 2654
 Db 2161 AGCGCAACGGTGTGCTGCGCTACCTAAGCTGTGCTGCAAGCTGTGCTGCAAGCTGTGCT 2220
 Qy 2655 AACCCCACTGTGAGAGAGCCCTGCGCGGAGCTCAAGAAAGAGCTGTGCTGCGGATC 2714
 Db 2221 AACCCCACTGTGAGAGAGCCCTGCGCGGAGCTCAAGAAAGAGCTGTGCTGCGGATC 2280
 Qy 2715 ATCAGTGGCCAGAGCTTCCCAAGCCGCGAGCTCAATGTGCTGCGGAGATC 2774
 Db 2281 ATCAGTGGCCAGAGCTTCCCAAGCCGCGAGCTCAATGTGCTGCGGAGATC 2340
 Qy 2775 ATCGAAGCTTGTGTGAGTGTGAGATCAATTTGGCTCCCTGTGAGCTGAGAGGAGAC 2834
 Db 2341 ATCGAAGCTTGTGTGAGTGTGAGATCAATTTGGCTCCCTGTGAGCTGAGAGGAGAC 2400
 Qy 2835 ACCGCGGTGTGAGAGCAAGGGTTCAACCCCACTGTGAGAGAGACCTGTGTTTCTATG 2894
 Db 2401 ACCGCGGTGTGAGAGCAAGGGTTCAACCCCACTGTGAGAGAGACCTGTGTTTCTATG 2460
 Qy 2895 GTGCAATGCGGAGATGCGCTGCTGCTTCTGCTGTGAGACCAAGATCCCATGCGG 2954
 Db 2461 GTGCAATGCGGAGATGCGCTGCTGCTTCTGCTGTGAGACCAAGATCCCATGCGG 2520
 Qy 2955 CGTGAATCTTGTGCGCAAGAGACGCTGCGCTTCCAGCAGACAGATGAGGAGTACAGAC 3014
 Db 2521 CGTGAATCTTGTGCGCAAGAGACGCTGCGCTTCCAGCAGACAGATGAGGAGTACAGAC 2580
 Qy 3015 GTGTACTTGAAGGAGTGAAGAGGCTCCATCTTGTGAGATGTGTGAGTGTGAGTGTG 3074
 Db 2581 GTGTACTTGAAGGAGTGAAGAGGCTCCATCTTGTGAGATGTGTGAGTGTGAGTGTG 2640
 Qy 3075 AGCGGTAAAGTCAAGCAGAGCTTGTGCTTAAAGGCTTCTTCCAGAGCCCAAAGCCC 3134
 Db 2641 AGCGGTAAAGTCAAGCAGAGCTTGTGCTTAAAGGCTTCTTCCAGAGCCCAAAGCCC 2700
 Qy 3135 GCGTGTGTGAGACATCAAGCTGTGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 3194
 Db 2701 GCGTGTGTGAGACATCAAGCTGTGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 2760

Qy 3195 ATCTGCGGCGCAGCGGCGAGCGCCCGACCAAGAGCCGAAGAGCCGCGCGCGCGCTTC 3254
 Db 2761 ATCTGCGGCGCAGCGGCGAGCGCCCGACCAAGAGCCGAAGAGCCGCGCGCGCGCTTC 2820
 Qy 3255 CCGAGCTGTCTGTGGTCAACCGGAGCAAGGCTTCAAGGGGGTGTGAGACATGTGTG 3314
 Db 2821 CCGAGCTGTCTGTGGTCAACCGGAGCAAGGCTTCAAGGGGGTGTGAGACATGTGTG 2880
 Qy 3315 CCCCCCGGCGCGACCTGTCCGGAAGCCCGACCGAGAGGGGCGCGGCGAGC 3374
 Db 2881 CCCCCCGGCGCGACCTGTCCGGAAGCCCGACCGAGAGGGGCGCGGCGAGC 2940
 Qy 3375 CCGGAGTGAAGGCGCGACCTGTGCGTGTGAGAGAGCCCTGTGAGATGTGCGGCCCCG 3434
 Db 2941 CCGGAGTGAAGGCGCGACCTGTGCGTGTGAGAGAGCCCTGTGAGATGTGCGGCCCCG 3000
 Qy 3435 CGTGTCTGTGAGAGCGCCCGGCGCTGTGTGAGATGTGCGCGCAATGAATGTGTG 3494
 Db 3001 CGTGTCTGTGAGAGCGCCCGGCGCTGTGTGAGATGTGCGCGCAATGAATGTGTG 3060
 Qy 3495 GGAATCTGTGCGCGGCGTGAACACCGGGGGCTGTGAGAGAGCGGCGACCCAGCCGGGG 3554
 Db 3061 GGAATCTGTGCGCGGCGTGAACACCGGGGGCTGTGAGAGAGCGGCGACCCAGCCGGGG 3120
 Qy 3555 CCGTGAAGAGCGAGCAGACCAATTCGAGAGAGCCCGGCGCTGAGTCACTGTGGG 3614
 Db 3121 CCGTGAAGAGCGAGCAGACCAATTCGAGAGAGCCCGGCGCTGAGTCACTGTGGG 3180
 Qy 3615 GCGCCCTGTGTGTGAGACCTTCAAGCTTACCGGGGAGAGAGCAGAGAGCCCGCAAG 3674
 Db 3181 GCGCCCTGTGTGTGAGACCTTCAAGCTTACCGGGGAGAGAGCAGAGAGCCCGCAAG 3240
 Qy 3675 GGTCTGTGGGCGCTGTGAGAGCGAGGTCAGGCGGTAGCGGCTCATGTCTCTGAGTCCAGC 3734
 Db 3241 GGTCTGTGGGCGCTGTGAGAGCGAGGTCAGGCGGTAGCGGCTCATGTCTCTGAGTCCAGC 3300
 Qy 3735 AGCCAGACAGCCCGGCGATCCCGAAGAGTCCCGCGTGTGAGAGGTCCTGTGAG 3794
 Db 3301 AGCCAGACAGCCCGGCGATCCCGAAGAGTCCCGCGTGTGAGAGGTCCTGTGAG 3360
 Qy 3795 CAACCGGGGCGCTGTGAGAGAGATGAGTGTCTGTTTGTCTCAAAAGCTGAGAGATC 3854
 Db 3361 CAACCGGGGCGCTGTGAGAGAGATGAGTGTCTGTTTGTCTCAAAAGCTGAGAGATC 3420
 Qy 3855 AGAGTAAATCCCATGTCTCCGCGGTAAAGCCCTTGTGCTGTGCTGTCTCCG 3914
 Db 3421 AGAGTAAATCCCATGTCTCCGCGGTAAAGCCCTTGTGCTGTGCTGTCTCCG 3480
 Qy 3915 CACGCGCTGTGAGATGTGAGGCTGTGAGTCACTGTGCTGTCTGTGAGAGGTCG 3974
 Db 3481 CACGCGCTGTGAGATGTGAGGCTGTGAGTCACTGTGCTGTGAGAGGTCG 3540
 Qy 3975 CCGT 4034
 Db 3541 CCGT 3600
 Qy 4035 CTTGTGCTGTGCTGTGAGCCATAG 4058
 Db 3601 CTTGTGCTGTGCTGTGAGCCATAG 3624

RESULT 3
 US-09-954-456-1912/c
 ; Sequence 1912, Application US/09954456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
 ; FILE REFERENCE: 689290-76
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1912
LENGTH: 426
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1912

Query Match 0.4%; Score 20; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3044 CATCTTCGTCATGTCGCTG 3063
DB 234 CATCTTCGTCATGTCGCTG 215

RESULT 4
US-09-292-758-106
Sequence 106, Application US/09292758
Publication No. US20020197602A1
GENERAL INFORMATION:
APPLICANT: Burner, Glenna C.
APPLICANT: Brown, Joseph P.
TITLE OF INVENTION: Nucleic Acid Sequences and Proteins
TITLE OF INVENTION: Associated With Aging
FILE REFERENCE: 017473-001110US
CURRENT APPLICATION NUMBER: US/09/292,758
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: US 60/081,887
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 106
LENGTH: 498
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(498)
OTHER INFORMATION: n = a,t,c or g
US-09-292-758-106

Query Match 0.4%; Score 20; DB 9; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3044 CATCTTCGTCATGTCGCTG 3063
DB 200 CATCTTCGTCATGTCGCTG 219

RESULT 5
US-09-815-242-7987
Sequence 7987, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7987
LENGTH: 1530
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1530)
US-09-815-242-7987

Query Match 0.4%; Score 20; DB 10; Length 1530;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 CCAGCAGCGAGTGCGCGC 854
DB 785 CCAGCAGCGAGTGCGCGC 804

RESULT 6
US-09-835-996A-7
Sequence 7, Application US/0983596A
Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Dumanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A

;; CURRENT APPLICATION NUMBER: US/09/835,996A
;; CURRENT FILING DATE: 2001-04-16
;; PRIOR APPLICATION NUMBER: US 60/197,137
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/714,936
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: US 09/667,298
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 09/631,451
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 09/598,042
;; PRIOR FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 7
;; LENGTH: 1840
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (140)..(1840)
;; US-09-835-996A-7

Query Match 0.4%; Score 20; DB 10; Length 1840;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 1130 TGCCGCTGCTGAGGTGA 1149

RESULT 7
US-09-804-969-14
;; Sequence 14, Application US/09804969
;; Patent No. US20020081595A1
;; GENERAL INFORMATION:
;; APPLICANT: Hu Yi
;; APPLICANT: Nepomichy, Boris
;; APPLICANT: Donoho, Gregory
;; APPLICANT: Halbun, Erin
;; APPLICANT: Turner, C. Alexander Jr.
;; APPLICANT: Abuin, Alejandro
;; APPLICANT: Friedrich, Glenn
;; APPLICANT: Zambrowicz, Brian
;; APPLICANT: Sands, Arthur T.
;; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides Et
;; FILE REFERENCE: LEX-0148-USA
;; CURRENT APPLICATION NUMBER: US/09/804,969
;; CURRENT FILING DATE: 2001-03-13
;; PRIOR APPLICATION NUMBER: US 60/188,885
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: US 60/189,693
;; PRIOR FILING DATE: 2000-03-15
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14
;; LENGTH: 2289
;; TYPE: DNA
;; ORGANISM: homo sapiens
;; US-09-804-969-14

Query Match 0.4%; Score 20; DB 10; Length 2289;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 991 TGCCGCTGCTGAGGTGA 1010

RESULT 8
US-09-908-664-3

;; Sequence 3, Application US/09908664
;; Patent No. US20020115178A1
;; GENERAL INFORMATION:
;; APPLICANT: Millennium Pharmaceuticals, Inc.
;; APPLICANT: Meyers, Rachel
;; APPLICANT: Rudolph-Owen, Laura
;; APPLICANT: Tsai, Fong Yin
;; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
;; FILE REFERENCE: 38155-20022.00
;; CURRENT APPLICATION NUMBER: US/09/908,664
;; CURRENT FILING DATE: 2001-07-17
;; PRIOR APPLICATION NUMBER: US 60/218,675
;; PRIOR FILING DATE: 2000-07-17
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 2289
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; US-09-908-664-3

Query Match 0.4%; Score 20; DB 10; Length 2289;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1521 TGCCGCTGCTGAGGTGA 1540
DB 991 TGCCGCTGCTGAGGTGA 1010

RESULT 9
US-09-917-800A-1339
;; Sequence 1339, Application US/09917800A
;; Patent No. US20020119462A1
;; GENERAL INFORMATION:
;; APPLICANT: Mendrick, Donna
;; APPLICANT: Porter, Mark
;; APPLICANT: Johnson, Kory
;; APPLICANT: Castle, Arthur
;; APPLICANT: Elashoff, Michael
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Molecular Toxicology Modeling
;; FILE REFERENCE: 44921-5038-US
;; CURRENT APPLICATION NUMBER: US/09/917,800A
;; CURRENT FILING DATE: 2001-07-31
;; PRIOR APPLICATION NUMBER: US 60/222,040
;; PRIOR FILING DATE: 2000-07-31
;; PRIOR APPLICATION NUMBER: US 60/222,880
;; PRIOR FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: US 60/290,029
;; PRIOR FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US 60/290,645
;; PRIOR FILING DATE: 2001-05-15
;; PRIOR APPLICATION NUMBER: US 60/292,336
;; PRIOR FILING DATE: 2001-05-22
;; PRIOR APPLICATION NUMBER: US 60/295,798
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: US 60/297,457
;; PRIOR FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/298,884
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: US 60/303,459
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 1740
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1339
;; LENGTH: 2573
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D42148
;; US-09-917-800A-1339

Query Match 0.4%; Score 20; DB 10; Length 2573;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2686 AGCTCAAGAGAGCTGTG 2705
1653 AGCTCAAGAGAGCTGTG 1672

RESULT 10
US-09-908-664-1
Sequence 1, Application US/09908664
Patent No. US20020115178A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Tsai, Fong Yin
TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
FILE REFERENCE: 38155-20022.00
CURRENT APPLICATION NUMBER: US/09/908,664
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/218,675
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2629
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (257)...(2545)
US-09-908-664-1

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Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 TGCCGCTGCTGTGAGGTGA 1540
Db 1247 TGCCGCTGCTGTGAGGTGA 1266

RESULT 11
US-09-804-969-20
Sequence 20, Application US/09804969
Patent No. US20020081595A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomichy, Boris
APPLICANT: Donoho, Gregory
APPLICANT: Hilburn, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuin, Alejandro
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides En
FILE REFERENCE: LEX-0148-USA
CURRENT APPLICATION NUMBER: US/09/804,969
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/188,885
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 60/189,693
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 2709
TYPE: DNA

ORGANISM: homo sapiens
US-09-804-969-20

Query Match 0.4%; Score 20; DB 10; Length 2709;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 TGCCGCTGCTGTGAGGTGA 1540
Db 1248 TGCCGCTGCTGTGAGGTGA 1267

RESULT 12
US-09-944-413-6
Sequence 6, Application US/09944413
Patent No. US20020156004A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guiney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tomas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,413
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296

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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US200201560041ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US200201560041ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 6
; LENGTH: 3441
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-413-6
Query March 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3164 GCCCGCGCGCGCGCGCTCG 3183
Db 36 GCCCGCGCGCGCGCGCTCG 55
RESULT 13
US-09-944-403-6
; Sequence 6, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austlin
; APPLICANT: Hillan, Kenneth
```

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; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tamas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,403
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 15, 1997
; PRIOR APPLICATION NUMBER: 60/069,684
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 6
;; LENGTH: 3441
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-944-403-6

Query Match 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCG 3183
DB 36 GCCCGCGCGCGCGCGCTCG 55

RESULT 14
US-09-944-896-6
; Sequence 6, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 896
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
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; PRIOR FILING DATE: December 12, 1997
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;; PRIOR APPLICATION NUMBER: 60/069, 873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068, 017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070, 440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074, 086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074, 092
;; PRIOR FILING DATE: February 9, 1998
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;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112, 850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113, 296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146, 222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216, 021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218, 517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254, 311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 6
;; LENGTH: 3441
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-944-896-6

Query Match 0.4%; Score 20; DB 9; Length 3441;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3164 GCCCGCGCGCGCGCGCTCG 3183
DB 36 GCCCGCGCGCGCGCGCTCG 55

RESULT 15

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:52:40 ; Search time 81 Seconds
(without alignments)
1985.599 Million cell updates/sec

Title: US-09-927-112-2

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Searched: 908470 seqs, 133250620 residues

Word size: 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	613	50.8	621	23	ABB07493 Human lipid metabo
3	371	30.7	1619	23	AAU77498 Human lipid metabo
4	83	6.9	178	23	ABG59980 Human DITHP polype
5	23	1.9	466	22	AAU95125 Human protein sequ
6	23	1.9	787	22	ABG13659 Novel human diago
7	23	1.9	787	22	AAE14673 Human phosphatidyl
8	23	1.9	1014	23	ABB08001 Human lipid metabo
9	22	1.8	682	22	ABG13670 Novel human diago
10	14	1.2	1054	23	AAU11619 P. patens signal t

11	13	1.1	119	22	AAU87634 Novel central nerv
12	13	1.1	119	22	ABU17239 Human nervous syst
13	13	1.1	119	22	AAU17072 Novel signal trans
14	13	1.1	119	22	AAU43643 Human polypeptide
15	13	1.1	214	22	AAU87352 Novel central nerv
16	13	1.1	214	22	AAU43569 Human polypeptide
17	12	1.0	102	22	ABE13105 Human PLC 1636 pr
18	12	1.0	306	22	AAU94419 Human protein sequ
19	12	1.0	340	22	AAE11930 Human CG121 (or C5
20	12	1.0	567	22	AAE11925 Human protein sequ
21	12	1.0	639	22	AAU94695 Novel human diago
22	12	1.0	666	22	ABG12052 Human lipid metabo
23	12	1.0	731	23	ABU07492 Human phospholipas
24	12	1.0	759	23	AAE14270 Human human phosph
25	12	1.0	762	23	AAU10440 Human phospholipas
26	12	1.0	762	23	AAU76816 Human phospholipas
27	12	1.0	762	23	AAE14268 Human phospholipas
28	12	1.0	785	23	AAE14269 Human lipid metabo
29	12	1.0	828	23	ABB08008 Human lipid metabo
30	12	1.0	1058	22	AAU80177 Human protein sequ
31	12	1.0	1216	22	AAU79193 Human protein sequ
32	12	1.0	1216	22	ABB08204 Human lipid metabo
33	11	0.9	237	22	AAU87515 Novel central nerv
34	11	0.9	237	22	AAU23567 Novel human enzyme
35	11	0.9	254	22	ABU11181 Human pancreas pho
36	11	0.9	541	22	AAU67205 Novel central nerv
37	11	0.9	541	22	AAU22936 Novel human enzyme
38	11	0.9	595	23	ABB04337 Human phosphoester
39	11	0.9	806	22	AAU94052 Human protein sequ
40	11	0.9	1579	23	ABG6735 Human novel polype
41	11	0.9	1809	22	AAE13101 Human phospholipas
42	11	0.9	1898	23	ABU07352 Amino acid sequenc
43	10	0.8	156	22	AAE05974 Rat phospholipasti
44	10	0.8	229	23	ABG6716 Human novel polype
45	10	0.8	332	22	ABU11342 Human phospholipas

ALIGNMENTS

RESULT 1	ABB08205	1239 AA.
ID	ABB08205	standard; Protein: 1239 AA.
XX	ABB08205;	
AC	04-MAR-2002 (first entry)	
XX		
DT		
XX		
DE	Human lipid metabolism enzyme-5 (LME-5).	
XX		
KW	Human; LME-5; lipid metabolism enzyme-5; cytosolic; neuroprotective;	
KW	immunosuppressive; anti-inflammatory; cardiovascular; gene therapy;	
KW	enzyme therapy; cancer; neurological disorder; autoimmune disorder;	
KW	inflammatory disorder; cardiovascular disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200185956-A2.	
XX		
PD	15-NOV-2001.	
XX		
PF	11-MAY-2001; 2001WO-US15210.	
XX		
PR	11-MAY-2000; 2000US-203511P.	
PR	25-MAY-2000; 2000US-207903P.	
PR	07-JUN-2000; 2000US-210150P.	
PR	23-JUN-2000; 2000US-213392P.	
XX		
PA	(INCYT) INCYTE GENOMICS INC.	
XX		
PI	Das D, Reddy R, Yao MG, Nguyen DB, Lu Y, Tribouley CM, Yue H;	
PI	Khan FA, Gandhi AR, Au-young J, Lal P, Kearney L, Elliott VS;	
PI	Ding L, Thornton M;	

XX WPI: 2002-089794/12.
 DR N-PSDB: ABA96005.
 XX
 PT New lipid metabolism enzymes useful for diagnosing, treating and
 XX preventing cancer, neurological disorders, autoimmune/inflammatory
 XX disorders, and cardiovascular disorders.
 PS Claim 1; Page 114-116; 122pp; English.
 XX
 CC The sequence represents a novel human lipid metabolism enzyme (LME-5) of
 CC the invention. The invention relates to novel human LME's, and the
 CC polynucleotides which identify and encode them. The enzymes of the
 CC invention have cytosolic, neuroprotective, immunosuppressive,
 CC anti-inflammatory, and cardiovascular activity. The polypeptides and
 CC polynucleotides have a use in gene therapy and enzyme therapy. The lipid
 CC metabolism enzymes are useful in the diagnosis, treatment and prevention
 CC of cancer, neurological disorders, autoimmune/inflammatory disorders, and
 CC cardiovascular disorders, and in the assessment of the effects of
 CC exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of lipid metabolism enzymes. LMEs may also be used to screen
 CC for compounds that modulate the activity of LME. Polynucleotides encoding
 CC LME may be used for somatic or germline gene therapy, to detect and
 CC quantify gene expression in biopsied tissues in which expression of LME
 CC may be correlated with disease, to generate a transcript image of a
 CC tissue or cell type, to generate hybridization probes useful in mapping
 CC the naturally occurring genomic sequence, and for screening libraries of
 CC compounds in drug screening techniques. The polypeptide sequences may be
 CC used to analyse the proteome of a tissue or cell type. Oligonucleotide
 CC primers derived from polynucleotide sequences encoding LME may be used to
 CC detect single nucleotide polymorphisms.
 XX
 SQ Sequence 1239 AA:
 Query Match 82.5%; Score 96; DB 23; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 LKKOLVLRITISGOQLPKPRDSMLGDRGETIDPFVEVEITIGLPVDCSRQRTFVVDNGFNP 811
 DB 784 LKKOLVLRITISGOQLPKPRDSMLGDRGETIDPFVEVEITIGLPVDCSRQRTFVVDNGFNP 843
 QY 812 TWEETLVFVWHPHPELALVFLVMDHPDPIGRDPIGORTAFSSMPGYPHYVLEGEAEASI 871
 DB 844 TWEETLVFVWHPHPELALVFLVMDHPDPIGRDPIGORTAFSSMPGYPHYVLEGEAEASI 903
 QY 872 FVHVAVSDISGKVKQALGLKFLRGPFGSIDSHAARPPAPPSVQRILRTASAPTK 931
 DB 904 FVHVAVSDISGKVKQALGLKFLRGPFGSIDSHAARPPAPPSVQRILRTASAPTK 963
 QY 932 SOKPGRGPELVLTGRDTSKGVADVVPDPGPAPAPAPPOEGSGSSPRGKAPAAVAE 991
 DB 964 SOKPGRGPELVLTGRDTSKGVADVVPDPGPAPAPAPPOEGSGSSPRGKAPAAVAE 1033
 QY 992 KSPVRRPVRVLDGPGPAGMATCKKCVGSCAGVNTGTLRERPPSPGPASQAATIRQ 1051
 DB 1024 KSPVRRPVRVLDGPGPAGMATCKKCVGSCAGVNTGTLRERPPSPGPASQAATIRQ 1083
 QY 1052 PARADSLGAPCCGLDPHAIPIRSREAPKPGAMRQPGSGSSMSDSSSPDSFGTEPERS 1111
 DB 1084 PARADSLGAPCCGLDPHAIPIRSREAPKPGAMRQPGSGSGMSDSSSPDSFGTEPERS 1143
 QY 1112 PMPWPGACROPALGEMSALEFAOKLEETRSKSPWFSAGKFLPLCCVYLPHAPGAGPSP 1171
 DB 1144 PMPWPGACROPALGEMSALEFAOKLEETRSKSPWFSAGKFLPLCCVYLPHAPGAGPSP 1203
 QY 1172 AAASMTVSPRVLYVALYPWHCLRGTLPLWLAGCP 1207
 DB 1204 AAASMTVSPRVLYVALYPWHCLRGTLPLWLAGCP 1239

RESULT 2
 ABB07493
 ID ABB07493 standard; Protein; 621 AA.
 XX
 AC ABB07493;
 DT 23-APR-2002 (first entry)
 XX
 DE Human lipid metabolism molecule (LMM) polypeptide (ID: 2965233CD1).
 XX
 KW Lipid metabolism molecule; LMM; cytosolic; neurotropic; neuroprotective;
 KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;
 KW cardiovascular; anti-HIV; antileptic; antiallergic; hypertensive; human;
 KW cancer; gene therapy; protein therapy.
 XX
 OS Homo sapiens.
 OS
 FN WC020024490-A2.
 PD 17-JAN-2002.
 XX
 PE 06-JUL-2001; 2001WO-US21432.
 XX
 PR 07-JUL-2000; 2000US-216801P.
 PR 07-JUL-2000; 2000US-216803P.
 PR 14-JUL-2000; 2000US-218233P.
 PR 21-JUL-2000; 2000US-220046P.
 PR 26-JUL-2000; 2000US-220739P.
 PR 04-AUG-2000; 2000US-222824P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Tang YT, Azimzai Y, Das D, Thornton M, Lu DM, Tribouley CM,
 PI Yue H, Gandhi AR, Wala NK, Khan FA, Lu Y, Yao MG, Hafalia AJA,
 PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugh KR;
 XX
 DR WPI: 2002-164631/21.
 DR N-PSDB: ABA94696.
 XX

PT Lipid metabolism molecules useful in diagnosing, treating or preventing
 CC cancers, and neurological, autoimmune/inflammatory, gastrointestinal,
 PT skin and cardiovascular disorders -

PS Claim 1; Page 112-113; 128pp; English.

CC The invention provides human lipid metabolism molecule (LMW) polypeptides
 CC and polynucleotides. The LMW polypeptides can be expressed by standard
 CC recombinant methodology. The LMW polypeptides are useful for diagnosing
 CC or treating a condition or disease associated with the expression of LMW,
 CC or screening for compounds that specifically bind to or modulate the
 CC activity or expression of LMW. They are also used to generate antibodies
 CC and assess the toxicity of test compounds. The LMW polypeptides,
 CC modulators and antibodies are specifically useful for diagnosing,
 CC treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,
 CC melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,
 CC cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/
 CC inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,
 CC or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide
 CC esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin
 CC disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular
 CC disorders (e.g. hypertension, arterial dissections, vascular tumours, or
 CC thrombolysis). The present sequence represents a human LMW polypeptide
 CC sequence.

XX Sequence 621 AA;

Query Match 50.8%; Score 613; DB 23; Length 621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPTAGPLPGLPPEDEGPPPESSWLELSANILPYVERCGAMOGMVKLGSGSKG 60
 DB 2 MAPPTAGPLPGLPPEDEGPPPESSWLELSANILPYVERCGAMOGMVKLGSGSKG 61
 QY 61 LVFEVYLDHRSCTIRWPRSKNEKAKISIDISOEVSEGSQSEVFORPPGSGFDPNCCFSI 120
 DB 62 LVFEVYLDHRSCTIRWPRSKNEKAKISIDISOEVSEGSQSEVFORPPGSGFDPNCCFSI 121
 QY 121 YHGSRESLIDVSTSESVARTWYGLRYLMAGISDEDSIARRORTRDOLAKOTFEADKN 180
 DB 122 YHGSRESLIDVSTSESVARTWYGLRYLMAGISDEDSIARRORTRDOLAKOTFEADKN 181
 QY 181 GDGSLSTGEVLDLHKLNLNLPORRYKOMFREADTDHOGTLGFEFCAFYKMKSTRDL 240
 DB 182 GDGSLSTGEVLDLHKLNLNLPORRYKOMFREADTDHOGTLGFEFCAFYKMKSTRDL 241
 QY 241 YILMLTYSNHKKHIDLAASLQRFQVPOKMAVYLESODIIEFEPCKENSKGLIGIDG 300
 DB 242 YILMLTYSNHKKHIDLAASLQRFQVPOKMAVYLESODIIEFEPCKENSKGLIGIDG 301
 QY 301 FTNYTSPADIDFNEHHVHODMTPLSHYFTTSSHNNTYLVGDOLMSQSRDVMYVQ 360
 DB 302 FTNYTSPADIDFNEHHVHODMTPLSHYFTTSSHNNTYLVGDOLMSQSRDVMYVQ 361
 QY 361 AGRCVAVDQWDPDGPVYHNGYTLTSKLFVDVETIKKVFYKNEPVLIISINHC 420
 DB 362 AGRCVAVDQWDPDGPVYHNGYTLTSKLFVDVETIKKVFYKNEPVLIISINHC 421
 QY 421 VIOOKKMAQVLTPLIGDKLIDLSVSSSEDATTLPSQMLKGLIYVKKPLPANTISEDABEG 480
 DB 422 VIOOKKMAQVLTPLIGDKLIDLSVSSSEDATTLPSQMLKGLIYVKKPLPANTISEDABEG 481
 QY 481 EVSDSDADETIDDDCKLLNDASTNKRKVENTAKRKIDSLIKSKTRDCDPPNFSYSTL 540
 DB 482 EVSDSDADETIDDDCKLLNDASTNKRKVENTAKRKIDSLIKSKTRDCDPPNFSYSTL 541
 QY 541 SPSPKLGKKAEDVSGSDAGASRRNGRLVYGSFRRKKKSKLKAASVEGDEGDD 600
 DB 542 SPSPKLGKKAEDVSGSDAGASRRNGRLVYGSFRRKKKSKLKAASVEGDEGDD 601
 QY 601 SPGGSRGATROK 613
 ||||||||||||

DB 602 SPGGSRGATROK 614

RESULT 3

AAU77498 standard; Protein; 1619 AA.

AAU77498;

05-JUN-2002 (first entry)

Human lipid metabolism enzyme, LMW-6.

Human lipid metabolism enzyme; LMW-6; immune system disorder;

cell proliferative disorder; immunomodulator; neuroprotective;

cytostatic; enzyme.

Homo sapiens.

WO200216597-A2.

28-FEB-2002.

22-AUG-2001; 2001WO-US26365.

23-AUG-2000; 2000US-227429P.

08-SEP-2000; 2000US-231370P.

15-SEP-2000; 2000US-231212P.

29-SEP-2000; 2000US-236885P.

(INCY-) INCYTE GENOMICS INC.

Griffin JR, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;

Walla NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M;

Lal P;

WPI: 2002-280936/32.

N-PSDB: ABK12390.

Claim 50; Page 113-117; 122pp; English.

CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LMW) designated LMW-1 to LMW-6, and the
 CC polynucleotide sequences encoding them. The LMW polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LMW, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LMW-6.

XX Sequence 1619 AA;

Query Match 30.7%; Score 371; DB 23; Length 1619;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 550 SRAEDVESGSDAGASRRNGRLVYGSFRRKKKSKLKAASVEGDEGDDSPGQSGCA 609
 DB 1154 SRAEDVESGSDAGASRRNGRLVYGSFRRKKKSKLKAASVEGDEGDDSPGQSGCA 1213
 QY 610 TROKKTMTLSRLSDLVYKTKSVATHDIMEAASNOVSSFEETAHOLIOOKPAQYLR 669
 DB 1214 TROKKTMTLSRLSDLVYKTKSVATHDIMEAASNOVSSFEETAHOLIOOKPAQYLR 1273
 ||||||||||||

QY 670 NQOOLSRIPSSRYDSSNYPQPFNNAGCOMVALNTOSEGRMTOLNRAKFSANGGGYV 729
 DQ 1274 NQOOLSRIPSSRYDSSNYPQPFNNAGCOMVALNTOSEGRMTOLNRAKFSANGGGYV 1333
 QY 730 LKPGCMCGYFNPNSDPLPGOLKQOLVLRISGQOLPKPRDSMLGDRGELIDPEVEVEI 789
 DQ 1334 LKPGCMCGYFNPNSDPLPGOLKQOLVLRISGQOLPKPRDSMLGDRGELIDPEVEVEI 1393
 QY 790 IGLPVDCSREQTRVVDNGFNPWEELVPMVHMPETALRFLVMDHDPICGRDFIGQRTL 849
 DQ 1394 IGLPVDCSREQTRVVDNGFNPWEELVPMVHMPETALRFLVMDHDPICGRDFIGQRTL 1453
 QY 850 AFSSMMPGCRYHYLLEGEASIFVHVAVSDISGRVKQALGLKGLFLRPGKSIDSHAG 909
 DQ 1454 AFSSMMPGCRYHYLLEGEASIFVHVAVSDISGRVKQALGLKGLFLRPGKSIDSHAG 1513
 QY 910 RPPARPSVSQR 920
 DQ 1514 RPPARPSVSQR 1524

RESULT 4

ABG59980 standard; Protein; 178 AA.

AC ABG59980;

DT 30-JUL-2002 (first entry)

DE Human DITHP polypeptide #38.

Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
 cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 inflammatory disorder; viral infection; bacterial infection; seizure;
 fungal infection; parasitic infections; developmental disorder; breast;
 endocrine disorder; metabolic disorder; neurological disorder; cervix;
 gastrointestinal disorder; transport disorder; gene therapy; kidney;
 adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
 thymus.

OS Homo sapiens.

PN WO200220754-A2.

PD 14-MAR-2002.

PF 29-AUG-2001; 2001WO-US27127.

PR 05-SEP-2000; 2000US-229747P.
 PR 05-SEP-2000; 2000US-229748P.
 PR 05-SEP-2000; 2000US-229749P.
 PR 05-SEP-2000; 2000US-229750P.
 PR 05-SEP-2000; 2000US-229751P.
 PR 06-SEP-2000; 2000US-230583P.
 PR 06-SEP-2000; 2000US-230585P.
 PR 06-SEP-2000; 2000US-230514P.
 PR 06-SEP-2000; 2000US-230515P.
 PR 06-SEP-2000; 2000US-230517P.
 PR 06-SEP-2000; 2000US-230518P.
 PR 06-SEP-2000; 2000US-230519P.
 PR 06-SEP-2000; 2000US-230597P.
 PR 06-SEP-2000; 2000US-230598P.
 PR 06-SEP-2000; 2000US-230599P.
 PR 06-SEP-2000; 2000US-230610P.
 PR 06-SEP-2000; 2000US-230656P.
 PR 06-SEP-2000; 2000US-230988P.
 PR 07-SEP-2000; 2000US-230951P.
 PR 07-SEP-2000; 2000US-231163P.
 PR 07-SEP-2000; 2000US-231167P.
 PR XX
 PA (INCY-) INCYTE GENOMICS INC.

XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
 PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 DR WPI: 2002-383054/41.
 N-PSDB: ABR71572.

An isolated polynucleotide useful in diagnostics and therapeutics -

Claim 29; Page 554; 686pp; English.

CC The invention relates to human diagnostic and therapeutic (dithp)
 CC polynucleotides and their associated polypeptides (DITHP polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
 CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
 CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
 CC XX

Sequence 178 AA:

Query Match 6.9%; Score 83; DB 23; Length 178;
 Best Local Similarity 100.0%; Pred. No. 4.5e-76;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 VHQDMTOPLSHYFTSSNITVLDOLMSOSRYVMYVLAQAGRCYVCMGPDGEPT 379
 DB 96 VHQDMTOPLSHYFTSSNITVLDOLMSOSRYVMYVLAQAGRCYVCMGPDGEPT 155
 QY 380 VHGTYLTSKILFKDYIETINKY 402
 DB 156 VHGTYLTSKILFKDYIETINKY 178

RESULT 5

AAB95125 standard; Protein; 466 AA.

AC AAB95125;

DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:17124.

Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 27-AUG-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 PR XX
 PA (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 DR
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 17124; 2537bp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 466 AA:
 XX
 Query Match 1.9%; Score 23; DB 22; Length 466;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 821 VHMPEIALVRLVMDHPDPIGRDF 843
 DB 251 VHMPEIALVRLVMDHPDPIGRDF 273
 RESULT 6
 ABG13669 standard; Protein; 787 AA.
 XX
 AC ABG13669;
 XX
 DT 18-FEB-2002 (first entry)
 DE
 XX Novel human diagnostic protein #13660.
 XX
 KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS77856.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 44028; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 787 AA:
 XX
 Query Match 1.9%; Score 23; DB 22; Length 787;
 Best Local Similarity 100.0%; Pred. No. 6.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 821 VHMPEIALVRLVMDHPDPIGRDF 843
 DB 584 VHMPEIALVRLVMDHPDPIGRDF 606
 RESULT 7
 AAEL14673
 ID AAEL14673 standard; Protein; 787 AA.
 XX
 AC AAEL14673;
 XX
 DT 26-JUL-2002 (first entry)
 DE
 XX Human phosphatidylinositol-specific phospholipase C-11k enzyme.
 XX
 KM Human: phosphatidylinositol-specific phospholipase C-like enzyme;
 KM PI-PKC-like enzyme; chromosome 3; asthma; cancer; central nervous system;
 KM CNS disorder; Parkinson's disease; dementia; COPD; protein therapy;
 KM chronic obstructive pulmonary disease; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200226996-A2.
 PD 04-APR-2002.
 XX
 PF 24-SEP-2001; 2001WO-EP11012.
 XX
 PR 27-SEP-2000; 2000US-235552P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Zhu Z;

XX WPI: 2002-372128/40.
 DR N-PSDB: AAD31081.
 XX
 PT Isolated polynucleotides encoding human phosphatidylinositol-specific
 phospholipase C-like enzymes, useful for preventing, diagnosing and
 treating e.g. asthma, cancer, a CNS disorder or chronic obstructive
 PT pulmonary disease -
 XX
 PS Claim 25; Fig 2; 125pp; English.
 XX
 CC The invention relates to polynucleotide encoding human
 CC phosphatidylinositol-specific phospholipase C-like enzyme
 CC (PI-PLC-like enzyme). Human PI-PLC-like enzyme gene is located on
 CC chromosome 3. The PI-PLC-like enzyme polypeptide and
 CC polynucleotide may be used in the prevention, diagnosis and
 CC treatment of diseases associated with enzyme dysfunction,
 CC e.g. asthma, cancer, central nervous system (CNS) disorder (e.g.
 CC Parkinson's disease, dementia) and chronic obstructive pulmonary disease
 CC (COPD). The polynucleotide and polypeptide may be used to treat
 CC disorders associated with decreased PI-PLC-like enzyme expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of PI-PLC-like enzymes, by expressing inactive proteins or to
 CC supplement the patient's own production of PI-PLC-like enzymes.
 CC The polynucleotide and its complements may also be used
 CC as DNA probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acids in samples. The PI-PLC-like enzymes
 CC may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of PI-PLC-like enzyme
 CC expression and activity. The anti-PI-PLC-like enzyme antibodies and
 CC antagonists may be used to down-regulate expression and activity of
 CC the enzyme and as diagnostic agents for detecting the presence of
 CC PI-PLC-like enzyme in samples. The present sequence is human
 CC phosphatidylinositol-specific phospholipase C-like enzyme.
 XX
 SQ Sequence 787 AA;

Query Match 1.9%; Score 23; DB 23; Length 787;
 Best Local Similarity 100.0%; Pred. No. 6.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VHMPEIALVRLVMDHDPGRDF 843
 ||||||||||||||||||
 DB 584 VHMPEIALVRLVMDHDPGRDF 606

RESULT 8
 ABB08001
 ID ABB08001 standard; Protein: 1014 AA.
 XX
 AC ABB08001;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme (LME)-1 (Id: 7472210CD1).
 XX
 KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective;
 KW noctropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;
 KW antileptotic; antimicrobial; anti-AIDS; cardiovascular; antianginal;
 KW gene therapy; protein therapy; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200229036-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31302.
 XX
 PR 06-OCT-2000; 2000US-238388P.
 PR 13-OCT-2000; 2000US-240616P.
 PR 02-NOV-2000; 2000US-245719P.
 PR 08-NOV-2000; 2000US-247503P.
 PT

PR 17-NOV-2000; 2000US-249503P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Harald L, Arviu C, Das D, Griffin JA, Baughn MR, Ding L,
 PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J,
 PI Lal PG, Tribouley CM;
 XX
 DR WPI: 2002-315862/35.
 DR N-PSDB: ABL60537.
 XX
 PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and
 PT Creutzfeldt-Jakob disease -
 XX
 PS Claim 1; Page 110-113; 127pp; English.
 XX
 CC The invention relates to human lipid metabolism enzymes (LMEs) and
 CC encoding polynucleotides. The LMEs can be expressed by standard
 CC recombinant technology. The LME polypeptides, polynucleotides and
 CC modulators may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate LME expression such as cancer
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections
 CC (e.g. Creutzfeldt-Jakob disease and Acquired Immune deficiency syndrome
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina
 CC pectoris and mitral valve prolapse). The present sequence represents
 CC the human LME-1 polypeptide.
 XX
 SQ Sequence 1014 AA;

Query Match 1.9%; Score 23; DB 23; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 7.7e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VHMPEIALVRLVMDHDPGRDF 843
 ||||||||||||||||||
 DB 811 VHMPEIALVRLVMDHDPGRDF 833

RESULT 9
 ABG13670
 ID ABG13670 standard; Protein: 682 AA.
 XX
 AC ABG13670;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13661.
 XX
 KW Human; Chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS77857.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20; SEQ ID No 44029; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful for treating
 CC imaging or sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological actions in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. Abg00010-Abg30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 682 AA:
 SO
 Query Match 1.8%; Score 22; DB 22; Length 682;
 Best Local Similarity 100.0%; Pred. No. 5.6e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 775 GDRGEITDPVEVEIIGLPVDC 796
 DB 64 GDRGEITDPVEVEIIGLPVDC 85
 ||||||||||||||||||||
 RESULT 10
 ID AAU11619 standard; Protein: 1054 AA.
 AC AAU11619;
 XX
 XX 12-MAR-2002 (first entry)
 DE P. patens signal transduction stress-related protein PLC-1.
 KW Signal transduction stress-related protein; STSRP; PLC-1; PLC-2;
 KW 14-3-3p-1; 14-3-3p-2; CBP-1; Phospholipase C; Ca2+ binding protein;
 KW transgenic plant; environmental stress; salinity; drought;
 KW low temperature.
 XX
 OS Physcomitrella patens.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 126 /note= "Encoded by CAG"
 FT MISC-difference 420..1054 /note= "Region not encoded by the cDNA sequence
 FT /note= "Region not encoded by the cDNA sequence
 FT appearing as AAS17965"
 FT
 XX
 PN WO200177355-A2.
 XX
 PD 18-OCT-2001.
 XX
 PE 06-APR-2001; 2001WO-US11398.
 XX
 PR 07-APR-2000; 2000US-196001P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Costa Silva EO, Bohnert HJ, Van Thieleen N, Chen R, Ishitani M;

XX
 DR WPI; 2002-049152/06.
 DR N-PSDB; AAS17965.
 XX
 XX New polypeptide, useful for increasing tolerance to environmental
 PT stress, comprises a Signal Transduction Stress-Related Protein selected
 PT from phospholipases, 14-3-3 proteins and calcium binding proteins -
 PS Claim 3; Fig 3A; 101pp; English.
 CC The invention relates to a Signal Transduction Stress-Related Protein
 CC (STSRP) isolated from Physcomitrella patens, and selected from
 CC phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein
 CC (14-3-3p-1, 14-3-3p-2 and Ca2+-Binding Protein (CBP)-1, or their
 CC orthologues. Also include are a transgenic plant transformed with
 CC an STSRP coding nucleic acid, where the expression of the nucleic acid in
 CC the plant cell results in increased tolerance to an environmental stress
 CC as compared to a wild type variety of the plant cell, a nucleic
 CC acid encoding an STSRP, and an expression vector comprising the nucleic
 CC acid. The STSRP and nucleic acids are useful for increasing tolerance to
 CC environmental stress selected from salinity, drought and low temperature,
 CC in transgenic plants including monocot and dicot selected from maize,
 CC wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
 CC rapeseed, canola, manihot, pepper, tagetes, solanaceous
 CC plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa,
 CC coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and
 CC forage crops. The nucleic acid is also useful for identifying organisms
 CC e.g. Physcomitrella patens in a mixed population of microorganisms,
 CC for evolutionary and protein structural studies and are useful as markers
 CC for specific regions of the genome. The present sequence represents
 CC PLC-1.
 CC
 CC Sequence 1054 AA:
 SO
 Query Match 1.2%; Score 14; DB 23; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 320 VHODMTOPLSHYFI 333
 DB 104 VHODMTOPLSHYFI 117
 ||||||||||||||||
 RESULT 11
 ID AAU87634 standard; Protein: 119 AA.
 AC AAU87634;
 XX
 XX 05-JUN-2002 (first entry)
 DE Novel central nervous system protein #544.
 KW Central nervous system protein #544.
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155318-A2.
 XX
 PD 02-AUG-2001.
 XX
 PE 17-JAN-2001; 2001WO-US01332.
 XX
 PF 31-JAN-2000; 2000US-0179065.
 XX
 PR

PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	13-OCT-2000	2000US-0239935
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241221
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	01-NOV-2000	2000US-0244816
PR	08-NOV-2000	2000US-0244674
PR	08-NOV-2000	2000US-0244475
PR	08-NOV-2000	2000US-0244476
PR	08-NOV-2000	2000US-0244477
PR	08-NOV-2000	2000US-0244478
PR	08-NOV-2000	2000US-0244524
PR	08-NOV-2000	2000US-0244525
PR	08-NOV-2000	2000US-0244526
PR	08-NOV-2000	2000US-0244527
PR	08-NOV-2000	2000US-0246528
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610
PR	08-NOV-2000	2000US-0246611
PR	17-NOV-2000	2000US-0249212
PR	17-NOV-2000	2000US-0249213
PR	17-NOV-2000	2000US-0249214
PR	17-NOV-2000	2000US-0249215
PR	17-NOV-2000	2000US-0249216
PR	17-NOV-2000	2000US-0249217
PR	17-NOV-2000	2000US-0249218
PR	17-NOV-2000	2000US-0249244
PR	17-NOV-2000	2000US-0249245
PR	17-NOV-2000	2000US-0249246
PR	17-NOV-2000	2000US-0249255
PR	17-NOV-2000	2000US-0249297
PR	17-NOV-2000	2000US-0249300
PR	01-DEC-2000	2000US-0249329
PR	01-DEC-2000	2000US-0250160
PR	03-DEC-2000	2000US-0250391
PR	03-DEC-2000	2000US-0250391
PR	05-DEC-2000	2000US-0251088
PR	05-DEC-2000	2000US-0251479
PR	06-DEC-2000	2000US-0251479
PR	08-DEC-2000	2000US-0251856
PR	08-DEC-2000	2000US-0251868
PR	08-DEC-2000	2000US-0251869
PR	08-DEC-2000	2000US-0251899
PR	11-DEC-2000	2000US-0254097
PR	05-JAN-2001	2000US-0259678
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM,	
XX	WPI: 2001-581633/65.	
XX	N-PSDB; ABRK3964.	
PT	New isolated nucleic acid encodinf	
PT	Preventing, treating or ameliorat	
PT	Food additives or preservatives	

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

XX Claim 9; SEQ ID NO 1152; 837pp; English.

PS The invention describes an isolated nucleic acid molecule (I) encoding a
XX novel nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiodysplasia, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 1.1%; Score 13; DB 22; Length 119;

Best Local Similarity 100.0%; Pred. NO. 0.00017;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 YIMAGISDEDSIA 160

DB 53 YIMAGISDEDSIA 65

RESULT 12

ABBI7239 standard; Protein: 119 AA.

AC ABBI7239;

DT 23-JAN-2002 (first entry)

DE Human nervous system related polypeptide SEQ ID NO 5896.

XX Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antischistosomal; antianemic; antiarthritic; cancer;
KW antineuritic; hepatotropic; neuroprotective; anti-inflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX Homo sapiens.

OS WO200159063-A2.

PN 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0188874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.

PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.

PR 27-SEP-2000; 2000US-0235836.

PR 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.

PR 29-SEP-2000; 2000US-0236369.

PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.

PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239335.

PR 13-OCT-2000; 2000US-0239337.

PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244221.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0251989.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR N-PSDB; ABA13565.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Claim 11: SEQ ID NO 5896; 1701pp + Sequence Listing; English.
 CC
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone

CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 119 AA:
 QY Query Match 1.18; Score 13; DB 22; Length 119;
 Db Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 148 YLMAGISDEDSLA 160
 53 YLMAGISDEDSLA 65
 RESULT 13
 AAU17072
 ID AAU17072 standard; Protein: 119 AA.
 AC
 XX AAU17072;
 DT 07-NOV-2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, Seq ID 637.
 XX
 KW Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;
 KW organ transplant rejection; infection; hepatitis C; blood disorder;
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KW reproductive system; gastrointestinal; liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens.
 OS
 PN MO200154733-A1.
 XX
 PD 02-AUG-2001.
 XX
 PE 17-JAN-2001; 2001WO-US01312.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216880.
 PR 07-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
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 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
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 PR 11-JAN-2001; 2001US-0259678.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-465460/50.
 DR N-PSDB; AAS26989.
 XX Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders
 XX
 PS Claim 1; SEQ ID No 637; 880pp; English.
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), Chromosomal
 CC abnormalities (Down syndrome), Ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),

CC as stimulators of B-cell responsiveness to pathogens, activators of
CC T-cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AA017059-AA017063 represent novel signal transduction
CC pathway protein, amino acid sequences of the invention.
XX

Query Match 1.1%; Score 13; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 0 00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YLMAGISDESLA 160
Db 53 YLMAGISDESLA 65

RESULT 14
AAM43643
ID AAM43643 standard; Protein; 119 AA.
XX
AC AAM43643;
XX
DT 22-OCT-2001 (first entry)
XX

Human polypeptide SEQ ID NO 321.

Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antiatherogenic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; anticonvulsant; antibacterial;
KW antiparasitic; cardiatic; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN MO200155308-A2.
XX
PD 02-AUG-2001.
XX

17-JAN-2001; 2001MO-US01309.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 04-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0225757.
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PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 08-NOV-2000; 2000US-0246613.

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 14:00:21 ; Search time 54 Seconds
(without alignments)
2148.782 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 1207

Sequence: 1 MAPPTAGLPGLPGLPDPG.....ALYPMHCLRTLLPLACGP 1207

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	12	1.0	764	1	1-phosphatidylinos
2	12	1.0	764	1	1-phosphatidylinos
3	12	1.0	764	1	1-phosphatidylinos
4	12	1.0	764	1	1-phosphatidylinos
5	12	1.0	764	1	1-phosphatidylinos
6	12	1.0	764	1	1-phosphatidylinos
7	12	1.0	764	1	1-phosphatidylinos
8	12	1.0	764	1	1-phosphatidylinos
9	12	1.0	764	1	1-phosphatidylinos
10	12	1.0	764	1	1-phosphatidylinos
11	12	1.0	764	1	1-phosphatidylinos
12	12	1.0	764	1	1-phosphatidylinos
13	12	1.0	764	1	1-phosphatidylinos
14	12	1.0	764	1	1-phosphatidylinos
15	12	1.0	764	1	1-phosphatidylinos
16	12	1.0	764	1	1-phosphatidylinos
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18	12	1.0	764	1	1-phosphatidylinos
19	12	1.0	764	1	1-phosphatidylinos
20	12	1.0	764	1	1-phosphatidylinos
21	12	1.0	764	1	1-phosphatidylinos
22	12	1.0	764	1	1-phosphatidylinos
23	12	1.0	764	1	1-phosphatidylinos
24	12	1.0	764	1	1-phosphatidylinos
25	12	1.0	764	1	1-phosphatidylinos
26	12	1.0	764	1	1-phosphatidylinos
27	12	1.0	764	1	1-phosphatidylinos
28	12	1.0	764	1	1-phosphatidylinos
29	12	1.0	764	1	1-phosphatidylinos

spec-related prote
hypothetical prote
Spec-related prote
TIM-barrel protein
octaprenyl-diphosp
conserved hypothet
probable membrane
conserved transcript
probable transcrip
hypothetical prote
probable UDP-galac
hypothetical prote
IMF dehydrogenase
1-phosphatidylinos
1-phosphatidylinos
ubiquinone biosynt

ALIGNMENTS

RESULT 1

514113

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-2 - bov

N:Alternative names: phosphoinositidase C; phospholipase C-delta-2; triphosphoinositide

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Jun-2000

C:Accession: S14113; S04944

R:Meldrum, E.; Kriz, R.W.; Totty, N.; Parker, P.J.

Eur. J. Biochem. 196, 159-165, 1991

A:Title: A second gene product of the inositol-phospholipid-specific phospholipase C-

A:Reference number: S14113; MUID:91160548; PMID:1848183

A:Accession: S14113

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1764 <ME2>

A:Experimental source: brain

R:Meldrum, E.; Katan, M.; Parker, P.

Eur. J. Biochem. 182, 673-677, 1989

A:Title: A novel inositol-phospholipid-specific phospholipase C. Rapid purification a

A:Reference number: S04944; MUID:89325315; PMID:2753038

A:Accession: S04944

A>Status: preliminary

A:Molecule type: protein

A:Residues: 528-541, 'X', '543-553; 659-669 <ME2>

A:Experimental source: brain

C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-triphos

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-p

C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; st

F:115-122/Domain: pleckstrin repeat homology <PLK>

F:134-166/Domain: calmodulin repeat homology <EF1>

F:170-202/Domain: calmodulin repeat homology <EF2>

F:292-435/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

F:489-609/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

F:611-723/Domain: protein kinase C C2 region homology <KC2>

Query Match 1.0%; Score 12; DB 1; Length 764;

Best local similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346

DB 303 SSHNTYLVGDQL 314

RESULT 2

T46339

hypothetical protein DKFZp434A0814.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000

C:Accession: T46339

R:Koenrter, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wleemann, S.

Submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23037

A:Accession: T46339

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-913 <AAA>

A:Cross-references: EMBL:AL137267

A:Experimental source: adult testis; clone DKFZp434A0814

C:Genetics:

A:Note: DKFZp434A0814.1

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology

F:58-207/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 1.0%; Score 12; DB 2; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

DB 354 FNNAGCOMVALN 365

RESULT 3

A43346

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) beta-2 - human

N:Alternate names: phospholipase C beta-2; triphosphoinositide phosphodiesterase

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999

A:Accession: A43346

R:Park, D.; Jhon, D.Y.; Kriz, R.; Knopf, J.; Rhee, S.G.

J. Biol. Chem. 267, 16048-16055, 1992

A:Title: Cloning, sequencing, expression, and Gq-independent activation of phospholipase

A:Reference number: A43346; MUID:9235553; PMID:1644792

A:Accession: A43346

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1181 <PAR>

A:Cross-references: GB:M95678; NID:q190039; PIDN:AAA36453.1; PID:q190040

A:Note: sequence extracted from NCBI backbone (NCBI:110494)

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology

C:Keywords: phosphoric diester hydrolase

F:314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

F:541-661/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom

Query Match 1.0%; Score 12; DB 2; Length 1181;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

DB 616 FNNAGCOMVALN 627

RESULT 4

A48001

phospholipase C (EC 3.1.4.3) beta, oocyte - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 22-Jun-1999

A:Accession: A48001

R:Ma, H.W.; Blitzer, R.D.; Healy, E.C.; Premont, R.T.; Landau, E.M.; Iyengar, R.

J. Biol. Chem. 268, 19915-19918, 1993

A:Title: Receptor-evoked Cl(-) current in Xenopus oocytes is mediated through a beta-tyr

A:Reference number: A48001; MUID:9338545; PMID:8397190

A:Accession: A48001

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1210 <MAA>

A:Cross-references: GB:L20815; NID:q405589; PIDN:AAA03065.1; PID:q405590

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology

C:Keywords: phosphoric diester hydrolase

F:319-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

F:575-695/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match 1.0%; Score 12; DB 2; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCOMVALN 705

DB 650 FNNAGCOMVALN 661

RESULT 5

S68251

phospholipase C, inositol-lipid specific (EC 3.1.4.-) isoform beta - turkey

C:Species: Meleagris gallopavo (common turkey)

C>Date: 05-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 22-Jun-1999

A:Accession: S68251; S72374; A61270

R:Waldo, G.L.; Paterson, A.; Boyer, J.L.; Nicholas, R.A.; Harden, T.K.

Biochem. J. 316, 559-568, 1996

A:Title: Molecular cloning, expression and regulatory activity of G-alpha(11) - and be

A:Reference number: S68251; MUID:96257751; PMID:8667401

A:Accession: S68251

A:Molecule type: mRNA

A:Residues: 1-1211 <MALI>

A:Cross-references: GB:049431; NID:q123919; PIDN:AAC60011.1; PID:q123920

A:Experimental source: erythrocyte

A:Accession: S72374

A:Molecule type: protein

A:Residues: 210-216, 'M', 218-231, 244-248; 284-291, 345-353, 'S', 355-360, 453-461; 661-679 <

A:Experimental source: erythrocyte

R:Waldo, G.L.; Morris, A.J.; Klapper, D.G.; Harden, T.K.

Mol. Pharmacol. 40, 480-489, 1991

A:Title: Receptor- and G-protein-regulated 150-kDa avian phospholipase C: inhibition

ished by immunoreactivity and peptide sequence.

A:Reference number: A61270; MUID:9201673; PMID:1656188

A:Accession: A61270

A>Status: preliminary

A:Molecule type: protein

A:Residues: 284-292, 'X', 294-296, 'R', 568-577; 751-753, 'L', 755-759; 765-776, 'T', 778-780; 8

A:Experimental source: erythrocyte

A:Note: 885-His was also found

C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology

C:Keywords: phosphoric diester hydrolase

F:314-463/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

F:543-663/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y

Query Match 1.0%; Score 12; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 QDMTQPLSHYFI 333

DB 312 QDMTQPLSHYFI 323

RESULT 6

A28822

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - bovine

N:Alternate names: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta; ph

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 22-Jun-1999

A:Accession: A28822; A39236

R:Katan, M.; Kriz, R.W.; Totty, N.; Philip, R.; Meldrum, E.; Aldape, R.A.; Knopf, J.L.

Cell 54, 171-177, 1988

A:Title: Determination of the primary structure of PLC-154 demonstrates diversity of

A:Reference number: A28822; MUID:88270496; PMID:2455601

A:Accession: A28822

A:Molecule type: mRNA

A:Residues: 1-1216 <KAT>

A:Cross-references: GB:003137; NID:q163521; PIDN:AAA30702.1; PID:q163522

R:Ryu, S.H.; Kim, U.H.; Wahl, M.I.; Brown, A.B.; Carpenter, G.; Huang, K.P.; Rhee, S.

J. Biol. Chem. 265, 17941-17945, 1990
 A>Title: Feedback regulation of phospholipase C-beta by protein kinase C.
 A:Reference number: A39236; MUID:91009263; PMID:2211670
 A:Accession: A39236
 A:Molecule type: protein
 A:Residues: 879-889 <RTU>
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology
 C:Keywords: phosphoprotein; phosphoric diester hydrolase
 F:318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:539-659/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom
 F:887/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #statu\$ experimenta

Query Match 1.0%; Score 12; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 7
 A28821
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - rat
 N:Alternate names: triphosphoinositide phosphodiesterase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 22-Jun-1999
 C:Accession: A28821
 R:Sun, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A>Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MUID:88270495; PMID:3390863
 A:Accession: A28821
 A:Molecule type: mRNA
 A:Residues: 1-1216 <SUN>
 A:Cross-references: GB:M20636; GB:J03136; NID:9206217; PIDN:AAA41885.1; PID:9206218
 A:Experimental source: brain
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatidylodiesterase domain y homology
 C:Keywords: phosphoprotein; phosphoric diester hydrolase
 F:318-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:539-659/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y hom

Query Match 1.0%; Score 12; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 8
 T42440
 phospholipase C homolog - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 03-Dec-1999 #sequence-revision 03-Dec-1999 #text-change 02-Sep-2000
 C:Accession: T42440
 R:Shibamoto, M.; Kariya, K.; Liao, Y.; Hu, C.D.; Watari, Y.; Goshima, M.; Shima, F.; Ka
 J. Biol. Chem. 273, 6218-6222, 1998
 A>Title: Identification of PLC210, a Caenorhabditis elegans phospholipase C, as a putati
 A:Reference number: 222164; MUID:98165800; PMID:9497345
 A:Accession: T42440
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1898 <SHI>
 A:Cross-references: EMBL:AF044576; NID:92957269; PIDN:AA038963.1; PID:92957270
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homolo
 F:912-1058/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x ho

Query Match 0.9%; Score 11; DB 2; Length 1898;
 Best Local Similarity 100.0%; Pred. No. 0.085;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 410 PVILSTENHCS 420
 DB 998 PVILSTENHCS 1008

RESULT 9
 T21581
 hypothetical protein F31B12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 02-Sep-2000
 C:Accession: T21581
 R:Kershaw, J.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z19444
 A:Accession: T21581
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1922 <WIL>
 A:Cross-references: EMBL:Z50740; PIDN:CAA90606.1; GSPDB:GN00028; CESP:F31B12.1
 A:Experimental source: clone F31B12
 C:Genetics:
 A:Gene: CESP:F31B12.1
 A:Map position: X
 A:Introns: 44/1; 137/3; 207/3; 305/1; 347/1; 425/3; 486/3; 536/3; 593/1; 619/2; 708/1
 3; 1724/3; 1847/3
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom
 F:940-1086/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

Query Match 0.9%; Score 11; DB 2; Length 1922;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 410 PVILSTENHCS 420
 DB 1026 PVILSTENHCS 1036

RESULT 10
 B28821
 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-1 - rat
 N:Alternate names: phosphoinositidase C; phospholipase C-delta-1; triphosphoinositide
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 02-Jun-2000
 C:Accession: B28821; I55942
 R:Sun, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
 Cell 54, 161-169, 1988
 A>Title: Cloning and sequence of multiple forms of phospholipase C.
 A:Reference number: A90899; MUID:88270495; PMID:3390863
 A:Accession: B28821
 A:Molecule type: mRNA
 A:Residues: 1-756 <SUN>
 A:Cross-references: GB:M20637; GB:J03136; NID:9206219; PIDN:AAA41886.1; PID:9206220
 A:Experimental source: brain
 R:Tagiawa, H.; Tanase, H.; Nojima, H.
 J. Hypertens. 9, 997-1004, 1991
 A>Title: Phospholipase C-delta gene of the spontaneously hypertensive rat harbors pol
 A:Reference number: I55942; MUID:92098966; PMID:1684614
 A:Accession: I55942
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411, 'M', 'A13-422', 'S', '424-462', 'D', '464-626', 'A', '628', 'K', '630-667', 'A', '669-756
 A:Cross-references: GB:S74591; NID:9241276
 A:Note: this translation is not annotated in Genbank entry S74591, release 113.0
 C:Comment: The products of hydrolysis, diacylglycerol and D-myo-inositol 1,4,5-tripho
 C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x homolo
 C:Keywords: duplication; EF hand; lipid degradation; phosphoric diester hydrolase; si
 F:19-128/Domain: pleckstrin repeat homology <PLK>
 F:140-172/Domain: calmodulin repeat homology <EF1>
 F:176-208/Domain: calmodulin repeat homology <EF2>

F:296-440/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:491-612/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:614-724/Domain: protein kinase C C2 region homology <KC2>

Query Match 0.8%; Score 10; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGCGGYLKP 732
DB 596 NGCGGYLKP 605

RESULT 11

A44165
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - slime mold (D
N; Alternate names: phosphoinositide-specific phospholipase C
C; Species: Dictyostelium discoideum
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C; Accession: A44165

R; Drayer, A.L.; Van Haastert, P.J.
J. Biol. Chem. 267, 18387-18392, 1992
A; Title: Molecular cloning and expression of a phosphoinositide-specific phospholipase C
A; Reference number: A44165; MIMD:92406741; PMID:1326523

A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-801 <DRA>

A; Cross-references: GB:M95783; NID:q167846; PIDN:AAA33235.1; PID:167847
A; Note: sequence extracted from NCBI backbone (NCBI:113302)

C; Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1; 1-phos
phosphodiesterase domain Y homology; calmodulin repeat homology; pleckstrin repeat homol
C; Keywords: EF hand; phosphoprotein; phosphoric diester hydrolase
F:324-465/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:538-656/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
F:558-769/Domain: protein kinase C C2 region homology <KC2>

Query Match 0.8%; Score 10; DB 1; Length 801;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 723 NGCGGYLKP 732
DB 640 NGCGGYLKP 649

RESULT 12
T33374
hypothetical protein K10F12.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
C; Accession: T33374

R; Wohlmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid K10F12.
A; Reference number: Z21157

A; Accession: T33374
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-895 <WOB>

A; Cross-references: EMBL:AF025462; PIDN:AB71005.1; GSPDB:GN00021; CESP:K10F12.3
A; Experimental source: strain Bristol N2; clone K10F12
C; Genetics:

A; Gene: CESP:K10F12.3
A; Map position: 3
A; Introns: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 62
C; Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
sphodiesterase domain Y homology
F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 0.8%; Score 10; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTOPLSHY 331
DB 300 QDMTOPLSHY 309

RESULT 15

QY 723 NGCGGYLKP 732
DB 631 NGCGGYLKP 640

RESULT 13

T27376
hypothetical protein Y75B12B.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C; Accession: T27376

R; White, S.
submitted to the EMBL Data Library, October 1998
A; Reference number: Z20360
A; Accession: T27376
A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA
A; Residues: 1-896 <WIT>

A; Cross-references: EMBL:AL032663; PIDN:CAA21765.1; GSPDB:GN00023; CESP:Y75B12B.6
A; Experimental source: clone Y75B12B
C; Genetics:

A; Gene: CESP:Y75B12B.6
A; Map position: 5
A; Introns: 21/3; 54/3; 115/3; 163/2; 189/3; 223/2; 273/1; 325/1; 642/2; 674/3; 783/1;
C; Superfamily: squid 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-pho
sphodiesterase domain Y homology
F:306-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 0.8%; Score 10; DB 2; Length 896;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 YPVIISIEH 418
DB 401 YPVIISIEH 410

RESULT 14
I54390
phosphoinositide-specific phospholipase C (EC 3.1.4.-) epsilon - human
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: I54390

R; Kohno, T.; Otsuka, T.; Takano, H.; Yamamoto, T.; Hamaguchi, M.; Terada, M.; Yokota,
Hum. Mol. Genet. 4, 667-674, 1995
A; Title: Identification of a novel phospholipase C family gene at chromosome 2q33 th
A; Reference number: I54390; MIMD:95359973; PMID:7633416

A; Accession: I54390
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-997 <RES>

A; Cross-references: GB:M42108; NID:9780121; PIDN:BA07688.1; PID:9780122
C; Genetics:

A; Gene: GDB:PLCE; PLC-L
A; Cross-references: GDB:699207; OMIM:600597
A; Map position: 2q33-2q33
C; Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinosito
domain Y homology
C; Keywords: phosphoric diester hydrolase
F:302-444/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X
F:486-606/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y

Query Match 0.8%; Score 10; DB 1; Length 997;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTOPLSHY 331
DB 300 QDMTOPLSHY 309

RESULT 15

S62358
 Inositol 1,4,5-trisphosphate-binding protein, 130K - rat
 N:Alternate names: phospholipase C delta 1 homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: S62358; S69328
 R:Kanematsu, T.; Misumi, Y.; Watanabe, Y.; Ozaki, S.; Koga, T.; Iwanaga, S.; Ikehara, Y.
 Biochem. J. 313, 319-325, 1996
 A:Title: A new inositol 1,4,5-trisphosphate binding protein similar to phospholipase C-delta
 A:Reference number: S62358; MUID:96132642; PMID:8546702
 A:Accession: S62358
 A:Molecule type: mRNA
 A:Residues: 1-1096 <KAN1>
 A:Cross-references: EMBL:D45920; NID:G1183843; PIDN:BAA08351.1; PID:G1183844
 A:Accession: S69328
 A:Molecule type: protein
 A:Residues: 172-191; 228-242; 1024-1034 <KAN2>
 C:Superfamily: human phosphoinositide-specific phospholipase C; 1-phosphatidylinositol-4-domain X homolog
 F:401-543/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog
 F:585-705/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

Query Match 0.8%; Score 10; DB 1; Length 1096;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTQPLSHY 331
 |||||
 DB 399 QDMTQPLSHY 408

Search completed: March 28, 2003, 14:06:00
 Job time : 60 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:53:20 / Search time 29 Seconds
(without alignments)
1726.273 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPTAGPLPGPALPPEDPG.....ALPWHCLRGTLPLWLAACP 1207

Scoring table: OLIGO
Gapop 60.0, Gapept 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	324	26.8	425	Y450_HUMAN	075038 homo sapien
2	12	1.0	1181	P1B2_HUMAN	000722 homo sapien
3	12	1.0	1216	P1B1_BOVIN	P10894 bos taurus
4	12	1.0	1216	P1B1_HUMAN	09a66 homo sapien
5	12	1.0	1216	P1B1_RAT	P10687 ratu
6	10	0.8	756	P1D1_RAT	P10688 ratu
7	10	0.8	801	P1RA_DICDI	002158 dictyosteli
8	9	0.7	1095	P1PA_DROME	P13217 drosophila
9	9	0.7	1175	P1B4_HUMAN	015147 homo sapien
10	9	0.7	1175	P1B4_RAT	09a07 ratu
11	9	0.7	1290	P1G1_HUMAN	P19174 homo sapien
12	9	0.7	1290	P1G1_RAT	P10686 ratu
13	9	0.7	1291	P1G1_BOVIN	P08487 bos taurus
14	9	0.7	3122	DPOX_MOUSE	061493 mus musculu
15	8	0.7	243	LPSB_LYPTI	003975 lytechinus
16	8	0.7	321	LPSB_LYPTI	P09485 lytechinus
17	8	0.7	543	UBIR_YERPE	08zami lyserinla pe
18	8	0.7	544	UBIR_YERPE	09xv94 vibrio chol
19	8	0.7	581	HEM1_STRCO	09xw15 streptomyce
20	8	0.7	695	P1D1_BOVIN	P10895 bos taurus
21	8	0.7	725	YJ76_YEAST	P47144 saccharomyc
22	8	0.7	756	P1D1_HUMAN	P51178 homo sapien
23	8	0.7	1038	YK03_YEAST	P36097 saccharomyc
24	8	0.7	1234	P1P3_HUMAN	P51432 mus musculu
25	8	0.7	1234	P1P3_MOUSE	P16885 homo sapien
26	8	0.7	1232	P1G2_HUMAN	P24135 ratu
27	8	0.7	1265	P1G2_RAT	09j104 mus musculu
28	8	0.7	1567	FMN2_MOUSE	09x115 thermotoga
29	7	0.6	110	YE42_THEMA	052106 actinobact
30	7	0.6	116	MERT_ACTA	051769 pseudomonas
31	7	0.6	116	MERT_PSEFL	P04336 salmonella
32	7	0.6	116	MERT_SALTI	P41482 autographa
33	7	0.6	122	Y102_NPVAC	

34	7	0.6	137	1	HOLD_ECOLI	P28632 escherichia
35	7	0.6	141	1	GLBI_PHESE	P11740 pheretima s
36	7	0.6	146	1	RBFA_RHIO	Q98B17 rhizobium 1
37	7	0.6	163	1	PFDS_YEAST	Q04493 saccharomyc
38	7	0.6	170	1	ING_SIGHI	Q9xxx2 sigmondon hl
39	7	0.6	207	1	P1G1_MOUSE	Q62077 mus musculu
40	7	0.6	207	1	RERC_ARATH	Q9xw17 arabidopsis
41	7	0.6	250	1	PSA2_YEAST	P23639 saccharomyc
42	7	0.6	259	1	YCB0_YEAST	P25594 saccharomyc
43	7	0.6	264	1	YCB0_ANAPL	Q42296 anas platyr
44	7	0.6	264	1	APAL_CHICK	P08250 gallus gall
45	7	0.6	264	1	APAL_CORUA	P32918 coturnix co

ALIGNMENTS

RESULT 1
Y450_HUMAN STANDARD; PRT; 425 AA.

AC 075038;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0450.
GN KIAA0450.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98116662; PubMed=945484;
RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
RA Nakajima D., Nomura N., Ohara O.;
RT Characterization of cDNA clones in size-fractionated cDNA libraries
RT from human brain.*;
RL DNA Res. 4:345-349(1997).

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CC or send an email to license@isb-sib.ch).

CC EMBL: AB007919; BAA32295.1; -;
DR Hypothetical protein.
SQ SEQUENCE 425 AA; 43842 MW; 2A6D733CA149E665 CRC64;

Query Match 26.8%; Score 324; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 324; Conservative 0;

QY	884	YKALGLKGLFGRPGSLDSHAAGRPAPRSVSQRLRTASAPTSQKGRGPEL	943
DB	102	VKALGLKGLFGRPGSLDSHAAGRPAPRSVSQRLRTASAPTSQKGRGPEL	161
QY	944	VIGTRDTGSKCAVDVVPVPGPGAPAPAPAOBPGSGSPGKAPAAVAEKSPVRYPPRL	1003
DB	162	VIGTRDTGSKCAVDVVPVPGPGAPAPAPAOBPGSGSPGKAPAAVAEKSPVRYPPRL	221
QY	1004	DGPGPMATCKKCVVGSAGVNTGGLREPPSPGPASROAATROPPARADSGAPC	1063
DB	222	DGPGPMATCKKCVVGSAGVNTGGLREPPSPGPASROAATROPPARADSGAPC	281
QY	1064	CGIDPFAHIGRSREAPKRGAMRGPGSGSSSDSSPDSGIPERSRPMEGACRQPG	1123
DB	282	CGIDPFAHIGRSREAPKRGAMRGPGSGSSSDSSPDSGIPERSRPMEGACRQPG	341
QY	1124	ALDGENSALFPAOKLEIRSKSPFSGAKPLPCVVLPHAPGMAGRSPAAASAMTVSPRV	1183

DB 342 ALGEMSALEFAOKLEIRKSPMPSACKPLIPCVLPHAPCMAGPGSPAASAMTVSPRV 401
 QY 1184 LVVALYPMHCRGTLLPWLACGP 1207
 402 LVVALYPMHCRGTLLPWLACGP 425

RESULT 2
 PIB2_HUMAN
 ID PIB2_HUMAN STANDARD; PRT; 1181 AA.
 AC 000722;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 2
 DE (EC 3.1.4.11) (PLC-beta-2) (Phospholipase C-beta-2).
 GN PLCB2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92355553; PubMed=1644792;

RA Park D., Jhon D.-Y., Kriz R., Knopf J., Rhee S.G.;
 RT Cloning, sequencing, expression, and Gq-independent activation of
 RT phospholipase C-beta 2."

RL J. Biol. Chem. 267:16048-16055(1992).

CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS.

CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA-2 IS
 CC MOST EFFECTIVELY MEDIATED BY ONE G-PROTEIN ALPHA SUBUNIT,
 CC ALPHA-16.

CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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CC EMBL; M95678; AAA36453.1; -
 CC FIR; A43346; A43346.
 CC HSP; P10688; IDJX.
 CC Genew; HGNC:9055; PLCB2.
 CC MIM; 604114; -

CC InterPro: IPR000008; C2
 CC InterPro: IPR001192; PI_PLC.
 CC InterPro: IPR000909; PI_PLC_Xdom.
 CC InterPro: IPR001711; PI_PLC_Y.

CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC PRINTS; PR00390; PHPLIPASEC.
 CC ProDom; PD001202; PI_PLC_Y; 1.

CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCYC; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS50004; C2_DOMAIN_2; 1.
 CC PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 CC PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Transducer; Calcium.

FT DOMAIN 312 463 DOMAIN X (BY SIMILARITY).
 FT DOMAIN 542 658 DOMAIN Y (BY SIMILARITY).
 FT ACT_SITE 665 763 C2 DOMAIN.
 FT ACT_SITE 327 327 BY SIMILARITY.
 FT ACT_SITE 374 374 BY SIMILARITY.
 SQ SEQUENCE 1181 AA; 133679 MW; 7A6889F204D17FNA CRC64;
 Query Match 1.0%; Score 12; DB 1; Length 1181;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FNNACCOMVALN 705
 DB 616 FNNACCOMVALN 627

RESULT 3
 PIB1_BOVIN

ID PIB1_BOVIN STANDARD; PRT; 1216 AA.
 AC P10894;

DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).
 GN PLCB1.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=88270496; PubMed=2455601;
 RA Katan M., Kriz R.W., Totty N., Philip R., Meldrum E., Aldape R.A.,
 RA Knopf J.L., Parker P.J.;

RT "Determination of the primary structure of PLC-154 demonstrates
 RT diversity of phospholipid-specific phospholipase C activities."

RL Cell 54:171-177(1988).

CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS.

CC -1- CATALYTIC ACTIVITY: 1-phosphatidy1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.

CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.

CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----

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 CC or send an email to license@isb-sib.ch).

CC EMBL; J03137; AAA30702.1; -
 CC FIR; A28822; A28822.
 CC HSP; P10688; IDJX.
 CC Genew; HGNC:9055; PLCB2.
 CC MIM; 604114; -

CC InterPro: IPR000008; C2
 CC InterPro: IPR001192; PI_PLC.
 CC InterPro: IPR000909; PI_PLC_Xdom.
 CC InterPro: IPR001711; PI_PLC_Y.

CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC PRINTS; PR00390; PHPLIPASEC.
 CC ProDom; PD001202; PI_PLC_Y; 1.

CC SMART; SM00239; C2; 1.
 CC SMART; SM00148; PLCYC; 1.
 CC SMART; SM00149; PLCYC; 1.
 CC PROSITE; PS50004; C2_DOMAIN_2; 1.
 CC PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
 CC PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 CC PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
 CC Hydrolase; Lipid degradation; Transducer; Calcium.

CC Hydrolase; Lipid degradation; Transducer; Calcium.

DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; P550004; C2.DDOMAIN.2; 1.
 DR PROSITE; P550007; PIP2C_XDOMAIN; 1.
 DR PROSITE; P550008; PIP2C_YDOMAIN; 1.
 DR Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467 DOMAIN X.
 FT DOMAIN 540 656 DOMAIN Y.
 FT ACT_SITE 663 761 C2.DDOMAIN.
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT ACT_SITE 378 378 BY SIMILARITY.
 FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 1216 AA; 138714 MW; BEF809177F1B7ABD CRC64;

Query Match 1.0%; Score 12; DB 1; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FNNAGCGNVALN 705
 |||||
 DB 614 FNNAGCGNVALN 625

RESULT 4
 ID P1B1_HUMAN STANDARD; PRT; 1216 AA.
 AC Q9N066; Q9N065; Q9N089; Q9NTH4; O60325; Q9H4H2; Q9B0W2; Q9UJP6;
 AC Q9UW26;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).
 GN PLCB1 OR KIA0581.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE-Brain;
 RA PubMed-11118617;
 RA Carlasole A., Sala C., Roncarati R., Formenti E., Terstappen G.C.;
 RT Cloning and characterization of the human phosphoinositide-specific
 RT phospholipase C-beta 1 (PLCbetal).
 RL Biochim. Biophys. Acta 1517:63-72(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE-2025428; PubMed-10760467;
 RA Peruzzi D., Calabrese G., Faenza I., Manzoli L., Matteucci A.,
 RA Giannarino F., Billi A.M., Stupia L., Palca G., Cocco L.;
 RT Identification and chromosomal localisation by fluorescence in situ
 RT hybridisation of human gene of phosphoinositide-specific phospholipase
 RT C beta 1.
 RL Biochim. Biophys. Acta 1484:175-182(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21638749; PubMed-11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jackson K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Lehtsaalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT The DNA sequence and comparative analysis of human chromosome 20.;
 RL Nature 414:865-871(2001).
 RN [4]
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).
 RC TISSUE-Testis;
 RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).
 RC TISSUE-Brain;
 RX MEDLINE-98290545; PubMed-9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.;
 RL DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DICYCLIGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidy-1-D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC
 DR EMBL; AJ278313; CAB98142.1; -
 DR EMBL; AJ278314; CAB98143.1; -
 DR EMBL; AY004175; AAF6613.1; -
 DR EMBL; AL031683; CAC16181.1; -
 DR EMBL; AL031683; CAC34366.1; -
 DR EMBL; AL050315; CAB56498.1; -
 DR EMBL; AL049632; CAB46663.1; -
 DR EMBL; AL137267; CAB70666.1; -
 DR EMBL; AB011153; BAA25507.1; -
 DR HSSP; P10688; 1DX.
 DR Genew; HGNC:15917; PLCB1.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_xdom.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 2
 DR Pfam; PF00387; PI_PLC_Y; 3.
 DR Pfam; PF00388; PI_PLC_X; 2.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.

DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2 DOMAIN 2; 1.
 DR PROSITE; PS50007; PIPIC_X DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium;
 Alternative splicing.
 FT DOMAIN 316 467
 FT DOMAIN 540 656
 FT DOMAIN 663 761
 FT ACT_SITE 331 331
 FT ACT_SITE 378 378
 FT MOD_RES 887 887
 FT VARSPIC 1142 1216

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 5
 P1BL_RAT STANDARD; PRT; 1216 AA.
 AC P10687;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC-154).
 GN PLCB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86270495; PubMed=3390863;
 RA Suh P.-G., Ryu S.-H., Moon K.-H., Rhee S.-G.;
 RT Cloning and sequence of multiple forms of phospholipase C.;
 RL Cell 54:161-169(1988).
 RN [2]
 RP ACTIVITY, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
 RA MEDLINE=93203266; PubMed=8454637;
 RA Zhou D.-Y., Lee H.-H., Park D., Lee C.-W., Lee K.-H., Yoo O.-J.,
 RA Rhee S.-G.;
 RT Cloning, sequencing, purification, and Gq-dependent activation of
 RT phospholipase C-beta 3.;
 RL J. Biol. Chem. 268:6654-6661(1993).
 CC - FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE

CC C ENZYMES.
 CC -1 CATALYTIC ACTIVITY: 1-phosphatidy1-ID-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1 COFACTOR: Calcium.
 CC -1 SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
 CC -1 TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
 CC parotid gland, liver, uterus, lung, heart, adrenal gland and
 CC ovary. Not detected in spleen, pancreas, intestine, thymus or
 CC kidney.
 CC -1 MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.
 CC -1 SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1 SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 CC -----
 CC EMBL; M20636; AAA4185.1; -;
 CC PIR; A28821; A28821.
 CC HSSP; P10688; 1DX.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR001192; PI_PLC.
 CC InterPro; IPR000909; PI_PLC_Xdom.
 CC InterPro; IPR001711; PI_PLC_Y.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF00387; PI-PLC-Y; 1.
 CC Pfam; PF00388; PI-PLC-X; 1.
 CC PRINTS; PR00390; PPHPLIPASEC.
 CC PRODOM; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR PROSITE; PS50004; C2 DOMAIN 2; 1.
 DR PROSITE; PS50007; PIPIC_X DOMAIN; 1.
 DR PROSITE; PS50008; PIPIC_Y DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium.
 FT DOMAIN 316 467
 FT DOMAIN 540 656
 FT DOMAIN 663 761
 FT ACT_SITE 331 331
 FT ACT_SITE 378 378
 FT MOD_RES 887 887
 FT SEQUENCE 1216 AA; 138344 MW; 92F23691781F788B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
 DB 614 FWNAGCOMVALN 625

RESULT 6
 P1DL_RAT STANDARD; PRT; 756 AA.
 AC P10688; O9QVD3; O9QVD4; O9QVD5;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-II).
 GN PLCD1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

ON NCBI_TaxID=101116;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=68270495; PubMed=3390863;
 RT Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Cloning and sequence of multiple forms of phospholipase C.;"
 RL Cell 54:161-169(1988).
 RN [2]
 RP SEQUENCE OF 50-57; 128-140 AND 728-738.
 RC TISSUE=Brain
 RX MEDLINE=92202192; PubMed=1313009;
 RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
 RA Iwanaga S., Hirata M.;
 RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
 cytosol.;"
 RL J Biol. Chem. 267:6518-6525(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 12-130.
 RX MEDLINE=96107342; PubMed=8521504;
 RA Ferguson K.M., Lemon M.A., Schlessinger J., Sigler P.B.;
 RT "Structure of the high affinity complex of inositol trisphosphate
 with a phospholipase C pleckstrin homology domain.;"
 RL Cell 83:1037-1046(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 205-756.
 RX MEDLINE=96378790; PubMed=8784353;
 RA Grobler J.A., Essen L.-O., Williams R.L., Hurley J.H.;
 RT "C2 domain conformational changes in phospholipase C-delta 1.;"
 RL Nat. Struct. Biol. 3:788-795(1996).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 133-756.
 RX MEDLINE=96186808; PubMed=8602259;
 RA Essen L.-O., Persic O., Cheung R., Katan M., Williams R.L.;
 RT "Crystal structure of a mammalian phosphoinositide-specific
 phospholipase C delta.;"
 RL Nature 380:595-602(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 133-756.
 RX MEDLINE=9715812; PubMed=9062102;
 RA Essen L.-O., Persic O., Lynch D.E., Katan M., Williams R.L.;
 RT "A ternary metal binding site in the C2 domain of phosphoinositide-
 specific phospholipase C-delta 1.;"
 RL Biochemistry 36:2753-2762(1997).
 RL [1]
 RP FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 ACTIVATED BY PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL: M20637; AAA41886.1; -.
 DR PIR: B28821; B28821.
 DR PDB: IDJG: 07-JUL-97.
 DR PDB: IDJH: 07-JUL-97.
 DR PDB: IDJI: 07-JUL-97.
 DR PDB: IDJM: 23-JUL-97.
 DR PDB: IDJX: 07-JUL-97.
 DR PDB: IDJY: 07-JUL-97.

CC		MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC		DIACTYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC	-I-	FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
RT	J. Biol. Chem.	267:18387-18392(1992).
RT		phospholipase C of Dictyostelium discoideum."
RA	Drayer A.L., van Haastert P.J.;	"Molecular cloning and expression of a phosphoinositide-specific
RA	MEDLINE-92406741; PubMed-1326523;	
RC	STRAIN-NC-4;	
RP	SEQUENCE FROM N.A.	
RN	[1]	
OX	NCBI_Taxid=44689;	
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.	
GN	PtPA OR PLC.	
OS	Dictyostelium discoideum (slime mold).	
DT	01-OCT-1993 (Rel. 27, Created)	
DT	01-OCT-1993 (Rel. 27, Last annotation update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	
DE	(EC 3.1.4.11) (PLC) (Phosphoinositide-specific phospholipase C).	
OY	723 NGCGYVLKP 732	
DB	596 NGCGYVLPK 605	
SO	SEQUENCE	756 AA; 85962 MW; E33F213ACB1E9F9 CRC64;
FT	ACT_SITE	356
FT	ACT_SITE	311
FT	DOMAIN	630 720
FT	DOMAIN	492 609
FT	CA_BIND	189 200
FT	CA_BIND	153 164
FT	DOMAIN	21 130
KW	Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;	
DR	PRINTS: PR00390; PPHILPASEC.	
DR	PRINTS: PR00360; C2DOMAIN.	
DR	PIfam; PF00388; PI-PLC-X; 1.	
DR	PIfam; PF00388; PI-PLC-Y; 1.	
DR	PIfam; PF00169; PH; 1.	
DR	PIfam; PF00169; C2; 1.	
DR	SMART: SM00239; C2; 1.	
DR	SMART: SM00239; PH; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	PROSITE: PS00018; EF_HAND; 2.	
DR	PROSITE: PS50003; RH_DOMAIN; 1.	
DR	PROSITE: PS50004; C2_DOMAIN; 2.	
DR	PROSITE: PS50007; PIPIC_X_DOMAIN; 1.	
DR	PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.	
DR	3D-structure.	
FT	ACT_SITE	356
FT	ACT_SITE	311
FT	DOMAIN	630 720
FT	DOMAIN	492 609
FT	CA_BIND	189 200
FT	CA_BIND	153 164
FT	DOMAIN	21 130
KW	Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;	
DR	PRINTS: PR00390; PPHILPASEC.	
DR	PRINTS: PR00360; C2DOMAIN.	
DR	PIfam; PF00388; PI-PLC-X; 1.	
DR	PIfam; PF00388; PI-PLC-Y; 1.	
DR	PIfam; PF00169; PH; 1.	
DR	PIfam; PF00169; C2; 1.	
DR	SMART: SM00239; C2; 1.	
DR	SMART: SM00239; PH; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	PROSITE: PS00018; EF_HAND; 2.	
DR	PROSITE: PS50003; RH_DOMAIN; 1.	
DR	PROSITE: PS50004; C2_DOMAIN; 2.	
DR	PROSITE: PS50007; PIPIC_X_DOMAIN; 1.	
DR	PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.	
DR	3D-structure.	
FT	ACT_SITE	356
FT	ACT_SITE	311
FT	DOMAIN	630 720
FT	DOMAIN	492 609
FT	CA_BIND	189 200
FT	CA_BIND	153 164
FT	DOMAIN	21 130
KW	Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;	
DR	PRINTS: PR00390; PPHILPASEC.	
DR	PRINTS: PR00360; C2DOMAIN.	
DR	PIfam; PF00388; PI-PLC-X; 1.	
DR	PIfam; PF00388; PI-PLC-Y; 1.	
DR	PIfam; PF00169; PH; 1.	
DR	PIfam; PF00169; C2; 1.	
DR	SMART: SM00239; C2; 1.	
DR	SMART: SM00239; PH; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	PROSITE: PS00018; EF_HAND; 2.	
DR	PROSITE: PS50003; RH_DOMAIN; 1.	
DR	PROSITE: PS50004; C2_DOMAIN; 2.	
DR	PROSITE: PS50007; PIPIC_X_DOMAIN; 1.	
DR	PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.	
DR	3D-structure.	
FT	ACT_SITE	356
FT	ACT_SITE	311
FT	DOMAIN	630 720
FT	DOMAIN	492 609
FT	CA_BIND	189 200
FT	CA_BIND	153 164
FT	DOMAIN	21 130
KW	Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;	
DR	PRINTS: PR00390; PPHILPASEC.	
DR	PRINTS: PR00360; C2DOMAIN.	
DR	PIfam; PF00388; PI-PLC-X; 1.	
DR	PIfam; PF00388; PI-PLC-Y; 1.	
DR	PIfam; PF00169; PH; 1.	
DR	PIfam; PF00169; C2; 1.	
DR	SMART: SM00239; C2; 1.	
DR	SMART: SM00239; PH; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	SMART: SM00149; PLCC; 1.	
DR	PROSITE: PS00018; EF_HAND; 2.	
DR	PROSITE: PS50003; RH_DOMAIN; 1.	
DR	PROSITE: PS50004; C2_DOMAIN; 2.	
DR	PROSITE: PS50007; PIPIC_X_DOMAIN; 1.	
DR	PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.	
DR	3D-structure.	
FT	ACT_SITE	356
FT	ACT_SITE	311
FT	DOMAIN	630 720
FT	DOMAIN	492 609
FT	CA_BIND	189 200
FT	CA_BIND	153 164
FT	DOMAIN	21 130
KW	Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;	
DR		

```

CC CC C ENZYMES.
CC CC -I- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC CC diacylglycerol.
CC CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES; INCREASE IN
CC CC EXPRESSION IN THE CULMINATING FRUITING BODY AND DURING
CC CC STARVATION.
CC CC -I- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC CC -I- SIMILARITY: CONTRAINS 1 C2 DOMAIN.
CC CC -I- SIMILARITY: CONTRAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
CC CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
CC CC
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CC CC -----
CC CC DR EMBL, M95783; AAA33235.1; -.
CC CC DR PIR: A44165; A44165.
CC CC DR HSSP: P10688; 1DIX.
CC CC DR D1CYD0: DD05034; p1pA.
CC CC DR InterPro: IPR000008; C2.
CC CC DR InterPro: IPR002048; EF-hand.
CC CC DR InterPro: IPR001192; PL_PLC.
CC CC DR InterPro: IPR000909; PL_PLC_Xdom.
CC CC DR InterPro: IPR001711; PL_PLC_Y.
CC CC DR pfam: PF00168; C2; 1.
CC CC DR pfam: PF00387; PL_PLC_Y; 1.
CC CC DR pfam: PF00388; PL_PLC-X; 1.
CC CC DR PRINTS: PR00360; C2DOMAIN.
CC CC DR PRINTS: PR00390; PHPLIPASEC.
CC CC DR Prodom: PD001202; PL_PLC_Y; 1.
CC CC DR SMART: SM00239; C2; 1.
CC CC DR SMART: SM00149; PLCXG; 1.
CC CC DR SMART: SM00149; PLCY; 1.
CC CC DR PROSITE: PS00018; EF_HAND; 1.
CC CC DR PROSITE: PS50004; C2_DOMAIN_2; 1.
CC CC DR PROSITE: PS50007; PLIP_X_DOMAIN; 1.
CC CC DR PROSITE: PS50008; PLIP_Y_DOMAIN; 1.
CC CC KW Hydroxylase; lipid degradation; Transducer; Calcium-binding;
CC CC phosphorylation.
CC CC
CC CC FT DOMAIN 322 464 DOMAIN X.
CC CC FT DOMAIN 542 652 DOMAIN Y.
CC CC FT DOMAIN 661 765 C2 DOMAIN.
CC CC FT CA_BIND 490 501 EF_HAND (POTENTIAL).
CC CC FT ACT_SITE 337 337 BY SIMILARITY.
CC CC FT ACT_SITE 382 382 BY SIMILARITY.
CC CC FT MOD_RES 524 524 PHOSPHORYLATION (POTENTIAL).
CC CC FT MOD_RES 531 531 PHOSPHORYLATION (BY PKA AND PKG)
CC CC (POTENTIAL).
CC CC
CC CC SQ SEQUENCE 801 AA; 91280 MW; D84FA8C829812D09 CRC64;
CC CC
CC CC Query Match 0.88; Score 10; DB 1; Length 801;
CC CC Best Local Similarity 100.0%; Pred. No. 0.21;
CC CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC
CC CC QY 723 NGGCGYVLRK 732
CC CC |||||
CC CC Db 640 NGGCGYVLRK 649
CC CC
CC CC RESULT 8
CC CC PIPA_DROME
CC CC ID PIPA_DROME STANDARD; PRT; 1095 AA.
CC CC AC P13217;
CC CC DT 01-JAN-1990 (Rel. 13, Created)
CC CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC CC DE 1-phosphatidyl-1inositol-4,5-bisphosphate phosphodiesterase

```

(EC 3.1.4.11) (Phosphoinositide-specific phospholipase C).
DE NORPA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
XX NCBI_TaxID=7227;
[1]
RN
RP
RX MEDLINE=68311074; PubMed=2457447;
RA Bloomquist B.T., Shortridge R.D., Schneuwly S., Perdew M.H.,
RT Montell C., Steller H., Rubin G., Pak W.L.;
RT "Isolation of a putative phospholipase C gene of Drosophila, norpa,
RL and its role in phototransduction.";
Cell 54:723-733(1988).
CC
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DICACYGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1-D-myo-inositol 4,5-
CC bisphosphate + H(2O) = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC

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Query Match	Similarity	0.74;	Score	9;	DB	1;	Length	1095;	
Best Local	Similarity	100.0%;	Pred.	No.	2.9;				
Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	694	FWNAGCOMV	702						
Db	624	FWNAGCOMV	632						
RESULT	9								
PIB4_HUMAN									
ID	PIB4_HUMAN	STANDARD;		PRT;	1175	AA.			

RP SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN-Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=93343926; PubMed=7688223;
 RA Kim M.J., Bahk Y.Y., Min D.S., Lee S.J., Ryu S.H., Suh P.G.;
 RT "Cloning of cDNA encoding rat phospholipase C-beta 4, a new member of
 RL the phospholipase C.";
 RN Biochem. Biophys. Res. Commun. 194:706-712(1993).
 RP [3]
 RP SEQUENCE OF 447-1175 FROM N.A. (ISOFORM C).
 RC TISSUE=Brain;
 RX MEDLINE=99132015; PubMed=9913434;
 RA Adamski F.M., Timms K.M., Shieh B.H.;
 RT "A unique isoform of phospholipase C-beta4 highly expressed in the
 RL cerebellum and eye.";
 CC Biochim. Biophys. Acta 1444:55-60(1999).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMS. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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 CC -----
 DR EMBL: L15556; AAK13557.1; -
 DR EMBL: U57836; AAD10403.1; -
 DR EMBL: AF031370; AAC98145.1; -
 DR EMBL: AF027571; AAC24984.1; -
 DR HSSP: P10688; IDJX.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_Xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; BPHPLIPASFC.
 DR Prodom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00238; C2; 1.
 DR SMART: SM00148; PLCX; 1.
 DR SMART: SM00149; PLCY; 1.
 DR PROSITE: PS50004; C2 DOMAIN 2; 1.
 DR PROSITE: PS50007; PIPLC_X DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 FT DOMAIN 313 463
 FT DOMAIN 565 681
 FT DOMAIN 786 828
 FT ACT SITE 328 328
 FT ACT SITE 375 375
 FT VAASPLIC 1013 1022
 FT VAASPLIC 1023 1175
 FT VAASPLIC 1154 1175
 FT CONFLICT 255 255
 FT CONFLICT 308 308
 FT CONFLICT 417 417
 C) L -> M (IN REF. 2).
 R -> A (IN REF. 2).
 Q -> E (IN REF. 2).

FT CONFLICT 470 470 E -> K (IN REF. 2).
 FT CONFLICT 504 504 A -> AA (IN REF. 1).
 FT CONFLICT 545 546 EQ -> DE (IN REF. 2).
 FT CONFLICT 734 734 I -> L (IN REF. 2).
 FT CONFLICT 741 741 R -> H (IN REF. 2).
 FT CONFLICT 764 764 L -> M (IN REF. 2).
 FT CONFLICT 776 776 D -> N (IN REF. 2).
 FT CONFLICT 828 828 F -> L (IN REF. 1).
 FT CONFLICT 843 843 S -> Y (IN REF. 2).
 FT CONFLICT 852 852 L -> M (IN REF. 3).
 FT CONFLICT 916 916 Q -> T (IN REF. 3).
 FT CONFLICT 1024 1024 W -> C (IN REF. 3).
 FT CONFLICT 1043 1043 L -> M (IN REF. 3).
 FT CONFLICT 1057 1057 A -> V (IN REF. 3).
 FT CONFLICT 1067 1067 L -> V (IN REF. 3).
 FT CONFLICT 1084 1084 S -> C (IN REF. 3).
 SQ SEQUENCE 1175 AA; 134496 MW; 7379C6BB95BBCECD CRC64;
 Query Match 0.78; Score 9; DB 1; Length 1175;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 694 FWNACQMV 702
 Db 639 FWNACQMV 647
 DB 639 FWNACQMV 647
 RESULT 11
 PIGL HUMAN
 ID PIGL HUMAN STANDARD; PRT; 1290 AA.
 AC P19174;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-II)
 DE
 GN PLCG1 OR PLCI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RP TISSUE=Vein, and Brain;
 RX MEDLINE=90355993; PubMed=2167438;
 RA Burgess W.H., Dionne C.A., Kaplow J.M., Mudd R., Friesel R.,
 RA Zilberstein A., Schlesinger J., Jaye M.;
 RT "Characterization and cDNA cloning of phospholipase C-gamma, a major
 RT substrate for heparin-binding growth factor 1 (acidic fibroblast
 RT growth factor)-activated tyrosine kinase.";
 RL Mol. Cell. Biol. 10:4770-4777(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2163749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babage A.K., Bagdley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Ellington A.G., Gough J., Headman R., Dhami P.D., Dunn M.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights K., Latrod G.K., Lawlor S.,
 RA Levenslaiho M.H., Levertha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachle L.J., McIay K., McKerrry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.D.C.F., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tyman A.C., Vaidin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [3]
 RP STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=93208890; PubMed=7681365;
 RA Kohda D., Hatanaka H., Oda M., Mandiyan V., Ullrich A.,
 RA Schlessinger J., Inagaki F.;
 RT "Solution structure of the SH3 domain of phospholipase C-gamma.";
 RL Cell 72:953-960(1993).
 CC -1- FUNCTION: PLC-GAMMA IS A MAJOR SUBSTRATE FOR HEPARIN-BINDING
 CC GROWTH FACTOR 1 (ACIDIC FIBROBLAST GROWTH FACTOR)-ACTIVATED
 CC TYROSINE KINASE.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL: M34667; AAA36452.1; -;
 DR EMBL: AL022394; CAAL8537.1; -;
 DR PIR: A36466; A36466.
 DR PDB: 2HSF; 3I-AUG-94.
 DR PDB: 1HSQ; 3I-AUG-94.
 DR Genew; HGNC:9065; PLCG1.
 DR MIM; 172420; -;
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PL-PLC.
 DR InterPro: IPR000909; PL-PLC_xdom.
 DR InterPro: IPR001711; PL-PLC_Y.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 2.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00169; PH; 2.
 DR Pfam: PF00387; PI-PLC-Y; 1.
 DR Pfam: PF00388; PI-PLC-X; 1.
 DR PRINTS: PR00390; PHPHLIPASEC.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRODOM: PD000066; SH3; 1.
 DR PRODOM: PD000093; SH2; 2.
 DR PRODOM: PD001202; PL-PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00233; PH; 2.
 DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS50001; SH2; 2.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PROSITE: PS50004; C2_DOMAIN; 2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 DR HydroLase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KW Repeat; Calcium-binding; Phosphorylation; 3D-structure; Polymorphism.
 FT DOMAIN 1
 FT CA_BIND 165 176 EF-HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT DOMAIN 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 813 813 I -> T (IN DBSNP:753381).
 FT /FTID-VAR 011908.
 SQ SEQUENCE 1290 AA; 148531 MW; AE05ABE2A18EDDAC CRC64;

DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR SMART: SM00252; SH2; 2.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS50001; SH2; 2.
 DR PROSITE: PS50002; SH3; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 2.
 DR PROSITE: PS50004; C2_DOMAIN; 2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 KW HydroLase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 KW Repeat; Calcium-binding; Phosphorylation; 3D-structure; Polymorphism.
 FT DOMAIN 1
 FT CA_BIND 165 176 EF-HAND (POTENTIAL).
 FT DOMAIN 320 464 DOMAIN X.
 FT DOMAIN 489 523 PH 2 (FIRST PART).
 FT DOMAIN 550 657 SH2 1.
 FT DOMAIN 668 756 SH2 2.
 FT DOMAIN 791 851 SH3.
 FT DOMAIN 895 931 PH 2 (SECOND PART).
 FT DOMAIN 953 1070 DOMAIN Y.
 FT DOMAIN 1075 1177 C2 DOMAIN.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 783 783 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1253 1253 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 813 813 I -> T (IN DBSNP:753381).
 FT /FTID-VAR 011908.
 SQ SEQUENCE 1290 AA; 148531 MW; AE05ABE2A18EDDAC CRC64;

Query Match 0.7%; Score 9; DB 1; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 408 EXPVILSTE 416
 DB 406 EXPVILSTE 414

RESULT 12
 PIGL_RAT STANDARD; PRT: 1290 AA.
 AC PI0586;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1
 DE (EC 3.1.4.11) (PLC-gamma-1) (Phospholipase C-gamma-1) (PLC-11)
 DE (PLC-148).
 GN PLCG1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289733; PubMed=2840660;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 RT "Inositol phospholipid-specific phospholipase C: complete cDNA and
 RT protein sequences and sequence homology to tyrosine kinase-related
 RT oncogene products.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5419-5423(1988).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -1- COFACTOR: Calcium.
 CC -1- PTM: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2

SQL	SEQUENCE	1290 AA;	148547 MW;	BB3240C27972CE3B CRC64;
	Query Match		0.7%;	Score 9;
	Best Local Similarity		100.0%;	Pred. No. 3.3;
	Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;
QY	408 EYPVLSIE 416			
Db	406 EYPVLSIE 414			
	RESULT 13			
	PIGL_BOVIN	STANDARD;	PRT;	1291 AA.
AC	PIGL_BOVIN			
DT	P08487;			
DT	01-AUG-1988 (rel. 08, Created)			
DT	01-AUG-1988 (rel. 08, Last sequence update)			
DE	15-JUN-2002 (rel. 41, Last annotation update)			
DE	1-phosphatidyl-inositol-4,5-bisphosphate phosphodiesterase gamma 1			
DE	(EC 3.1.4.11) (PI3C-gamma-1) (Phospholipase C-gamma-1) (PLC-11)			
DE	(PLC-148).			
GN	PLCG1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RA	MEDLINE=86156963; Pubmed=2831461;			
RA	Stahl M.L., Ferenz C.R., Kelleher K.L., Kriz R.W., Knopf J.L.;			
RT	"Sequence similarity of phospholipase C with the non-catalytic region			
RT	of src.";			
RL	Nature 332:269-272(1988).			
RL	[2]			
RP	PHOSPHORYLATION SITES.			
RP	MEDLINE=90154080; Pubmed=1689310;			
RA	Kim J.W., Sim S.S., Kim U.H., Nishibe S., Whal M.I., Carpenter G.,			
RA	Rhee S.G.;			
RT	"Tyrosine residues in bovine phospholipase C-gamma phosphorylated by			
RT	the epidermal growth factor receptor in vitro.";			
RL	J. Biol. Chem. 265:3940-3943(1990).			
RL	[3]			
RP	PHOSPHORYLATION SITES.			
RP	MEDLINE=90154081; Pubmed=1689311;			
RA	Whal M.I., Nishibe S., Kim J.W., Kim H.K., Rhee S.G., Carpenter G.;			
RA	"Identification of two epidermal growth factor-sensitive tyrosine			
RT	phosphorylation sites of phospholipase C-gamma in intact HSC-1			
RT	cells.";			
RL	J. Biol. Chem. 265:3944-3948(1990).			
RL	[4]			
RP	PHOSPHORYLATION SITES.			
RP	MEDLINE=91208680; Pubmed=1708307;			
RA	Kim H.K., Kim J.W., Zilberstein A., Margolis B., Kim J.G.,			
RA	Schlessinger J., Rhee S.G.;			
RT	"PDGF stimulation of inositol phospholipid hydrolysis requires			
RT	PLC-gamma 1 phosphorylation on tyrosine residues 783 and 1254.";			
RL	Cell 65:435-441(1991).			
RL	[5]			
RP	STRUCTURE BY NMR OF 663-759.			
RP	MEDLINE=94236690; Pubmed=8181064;			
RA	Pascal S.M., Singer A.U., Gish G., Yamazaki T., Shoelson S.E.,			
RA	Pawson T., Kay L.E., Forman-Kay J.D.;			
RT	"Nuclear magnetic resonance structure of an SH2 domain of			
RT	phospholipase C-gamma 1 complexed with a high affinity binding			
RT	peptide.";			
RL	Cell 77:461-472(1994).			
CC	-1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES			
CC	DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS			
CC	MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE			
CC	C ENZYMS.			
CC	-1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-			
CC	bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +			

CC diacylglycerol.
 CC -1- CORFACTOR: Calcium.
 CC -1- PTA: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-GAMMA 1 AND 2
 CC INVOLVES THEIR PHOSPHORYLATION BY TYROSINE KINASES IN RESPONSE
 CC TO LIGATION OF A VARIETY OF GROWTH FACTOR RECEPTORS AND IMMUNE
 CC SYSTEM RECEPTORS.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PH DOMAINS. THE SECOND ONE IS IN TWO
 CC PARTS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y00301; CA68406.1; -.
 CC PIR: S00666; S00666.
 CC PDB: 2PLD; 26-JAN-95.
 CC PDB: 2PLE; 26-JAN-95.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001849; PH.
 CC InterPro: IPR001192; PL_PLC.
 CC InterPro: IPR000909; PL_PLC_Xdom.
 CC InterPro: IPR001711; PL_PLC_Y.
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR001452; SH3.
 CC Pfam: PF00017; SH2; 2.
 CC Pfam: PF00018; SH3; 1.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00169; PH; 2.
 CC Pfam: PF00387; PI-PLC-X; 1.
 CC Pfam: PF00388; PI-PLC-Y; 1.
 CC PRINTS: PR00390; PHPLIPASEC.
 CC PRINTS: PR00401; SH2DOMAIN.
 CC PRINTS: PR00452; SH3DOMAIN.
 CC ProDom: PD000066; SH3; 1.
 CC ProDom: PD000093; SH2; 2.
 CC ProDom: PD001202; PL_PLC_Y; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00233; PH; 2.
 CC SMART: SM00148; PLCYC; 1.
 CC SMART: SM00149; PLCYC; 1.
 CC SMART: SM00252; SH2; 2.
 CC SMART: SM00326; SH3; 1.
 CC PROSITE: PS00018; EF_HAND; 1.
 CC PROSITE: PS0001; SH2; 2.
 CC PROSITE: PS0002; SH3; 1.
 CC PROSITE: PS0003; PH_DOMAIN; 2.
 CC PROSITE: PS0004; C2_DOMAIN; 2; 1.
 CC PROSITE: PS0007; PIPLC_X_DOMAIN; 1.
 CC PROSITE: PS0008; PIPLC_Y_DOMAIN; 1.
 CC Hydroxylase; Lipid degradation; Transducer; SH2 domain; SH3 domain;
 CC Repeat; Calcium-binding; Phosphorylation; 3D-structure.
 CC CA_BIND 165 176 EF_HAND (POTENTIAL).
 CC DOMAIN 27 142 PH 1.
 CC DOMAIN 165 176 EF_HAND (POTENTIAL).
 CC DOMAIN 320 464 PH 2 (FIRST PART).
 CC DOMAIN 489 523 PH 2 (FIRST PART).
 CC DOMAIN 550 657 SH2 1.
 CC DOMAIN 668 756 SH2 2.
 CC DOMAIN 791 851 SH3.
 CC DOMAIN 895 931 PH 2 (SECOND PART).
 CC DOMAIN 953 1070 DOMAIN Y.
 CC DOMAIN 1075 1177 C2 DOMAIN.
 CC ACT_SITE 335 335 BY SIMILARITY.

FT ACT_SITE 380 380 BY SIMILARITY.
 FT MOD_RES 771 771 PHOSPHORYLATION.
 FT MOD_RES 783 783 PHOSPHORYLATION.
 FT MOD_RES 1254 1254 PHOSPHORYLATION.
 SO SEQUENCE 1291 AA; 148312 MW; 9F31CTDAA3FEBA77 CMC64;
 Query Match 0.78; Score 9; DB 1; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 408 EYPYLSTE 416
 Db 406 EYPYLSTE 414
 RESULT 14
 ID DPOZ_MOUSE STANDARD; PRT; 3122 AA.
 AC 061493; 09QWX6; 09JMD6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase zeta catalytic subunit (Ec 2.7.7.7) (Seizure related
 DE protein 4).
 GN REV3L OR POLZ OR SEZ4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/Ola; TISSUE-Testis;
 RX MEDLINE-99202265; PubMed-10102037;
 RA Van Sloun P.P.H., Romeijn R.J., Eiken J.C.J.;
 RT "Molecular cloning, expression and chromosomal localisation of the
 RT mouse Rev3l gene, encoding the catalytic subunit of polymerase zeta.";
 RL Molec. Cell. Res. 433:109-116(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kajiwara K.;
 RT "Molecular analyses of Sez4 encoding murine homologue of yeast REV3 in
 RT brain neurons.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 2368-3122 FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-Embryonic brain;
 RX MEDLINE-96216731; PubMed-8645260;
 RA Kajiwara K., Nagawawa H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
 RA Sugaya E.;
 RT "Molecular characterization of seizure-related genes isolated by
 RT differential screening.";
 RL Biochem. Biophys. Res. Commun. 219:795-799(1996).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 CC + [DNA](n).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF083464; AAC98785.1; -.
 CC EMBL: AB031049; BAA90768.1; -.
 CC EMBL: D78644; BAA11461.1; -.
 CC MGD: MGI:1337131; Rev3l.
 CC InterPro: IPR002064; DNA_POL_B.
 CC InterPro: IPR004578; POL2.
 CC Pfam: PF00136; DNA_POL_B; 2.
 CC Pfam: PF03104; DNA_POL_B_exo; 2.

PRINTS; PRO0106; DNAPOLB.
 DR SMART; SM00486; POLB; 1.
 DR TIGRFAMS; TIGR00592; POL2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
 DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
 FT ZN_FING 3034 3049
 FT ZN_FING 3078 3096
 FT CONFLICT 92 92
 FT CONFLICT 294 294
 FT CONFLICT 578 578
 FT CONFLICT 609 609
 FT CONFLICT 1278 1278
 FT CONFLICT 1298 1298
 FT CONFLICT 1416 1416
 FT CONFLICT 1848 1848
 FT CONFLICT 2368 2368
 FT CONFLICT 3122 AA; 350654 MW; A39846CAF7365B48 CRC64;
 SQ SEQUENCE

Query Match 0.7%; Score 9; DB 1; Length 3122;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 SSPDSPGIP 1108
 DB 2109 SSPDSPGIP 2117

RESULT 15
 LPSB_LYTP1
 ID LPSB_LYTP1 STANDARD; PRT; 243 AA.
 AC 603975;

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calcium-binding protein LPS1-beta (fragment).
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidae; Euechinoidae; Echinacea; Temnopneuroidea; Tokopneustidae;
 OC Lytechinus.
 OC NCBI_TaxID-7653;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Sperm;
 RX MEDLINE-91244831; PubMed-2037596;
 RA Xiang M., Ge T., Tomlinson C.R., Klein W.H.;
 RT Structure and promoter activity of the LPS1 genes of Lytechinus
 pictus. Duplicated exons account for LPS1 proteins with eight calcium
 binding domains.";
 RL J. Biol. Chem. 266:10524-10533(1991).
 CC 1- FUNCTION: CALCIUM-BINDING PROTEIN INVOLVED IN LARVAL DEVELOPMENT
 AND METAMORPHOSIS. LIKELY TO FUNCTION AS CALCIUM BUFFERS
 MEDIATING THE TRANSPORT OF CALCIUM FROM THE SEA WATER TO THE
 BLASTOCOEL WHERE CALCIUM IS REQUIRED FOR SKELETON FORMATION.
 CC 2- TISSUE SPECIFICITY: ABORAL ECTODERM, A SQUAMOUS EPITHELIUM
 COVERING THE SURFACE OF THE LATE STAGE EMBRYO AND LARVA.
 CC 3- DEVELOPMENTAL STAGE: ACTIVATED EARLY IN DEVELOPMENT IN ABORAL
 ECTODERM CELLS.
 CC 4- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 MORE SPECIFICALLY TO SPECS.

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CC EMBL; M62848; AAA30004.1; ALT_SEQ.
 DR HSSP; P02593; ICMG.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 6.

DR PRODOM; PD000012; EF-hand; 3.
 DR SMART; SM00054; EFh; 5.
 DR PROSITE; PS00018; EF_HAND; 6.
 DR Calcium-binding; Repeat.
 FT REPEAT 1 150
 FT REPEAT 151 >243
 FT CA_BIND 29 40
 FT CA_BIND 60 71
 FT CA_BIND 98 109
 FT CA_BIND 134 145
 FT CA_BIND 167 178
 FT CA_BIND 204 215
 FT NON_TER 243
 FT SEQUENCE 243 AA; 27504 MW; 505B2BB070F7ED62 CRC64;
 SQ SEQUENCE

Query Match 0.7%; Score 8; DB 1; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 DKNDGSL 185
 DB 167 DKNDGSL 174

Search completed: March 28, 2003, 14:02:59
 Job time : 35 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 13:59:00 ; Search time 112 Seconds

(without alignments)
2220.526 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPPRAGLPALPPEDPG.....ALPWHCLRGTLPLWLAGCP 1207

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SPREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp Unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriophage.*
- 17: sp_archaeal.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	45.6	656	4	Q8TEH5 homo sapien
2	286	23.7	716	4	Q8WUS6 homo sapien
3	23	1.9	466	4	Q9H9U2 homo sapien
4	23	1.9	787	4	Q9UP73 homo sapien
5	12	1.0	447	11	Q9CUC1 mus musculu
6	12	1.0	639	4	Q9H8H5 homo sapien
7	12	1.0	738	5	Q97037 hydra magn
8	12	1.0	762	4	Q9BRC7 homo sapien
9	12	1.0	772	6	Q8SPR7 sus scrofa
10	12	1.0	1012	5	Q97035 hydra magn
11	12	1.0	1183	11	Q89040 rattus norv
12	12	1.0	1210	13	Q92137 xenopus lae
13	12	1.0	1211	13	Q91086 melagris lae
14	11	0.9	32	3	P78708 neosporea
15	11	0.9	632	11	Q9JYM2 mus musculu
16	11	0.9	806	4	Q9H9X8 homo sapien

17	11	0.9	1103	4	Q9UHV3	Q9UHV3 homo sapien
18	11	0.9	1355	5	Q97033	Q97033 ephydactyl
19	11	0.9	1609	4	Q9P212	Q9P212 homo sapien
20	11	0.9	1895	5	Q9TV12	Q9TV12 caenorhabd
21	11	0.9	1898	5	Q9TV12	Q9TV12 caenorhabd
22	11	0.9	1994	4	Q9HC53	Q9HC53 homo sapien
23	11	0.9	2281	11	Q99P84	Q99P84 homo sapien
24	11	0.9	2303	4	Q9H8X6	Q9H8X6 homo sapien
25	10	0.8	756	11	Q9Z1B4	Q9Z1B4 mus musculu
26	10	0.8	756	11	Q8R3B1	Q8R3B1 mus musculu
27	10	0.8	771	11	Q63693	Q63693 rattus norv
28	10	0.8	772	11	Q62711	Q62711 rattus norv
29	10	0.8	895	5	Q17232	Q17232 caenorhabd
30	10	0.8	896	5	Q9XWB7	Q9XWB7 caenorhabd
31	10	0.8	997	4	Q15111	Q15111 homo sapien
32	10	0.8	1096	11	Q62688	Q62688 rattus norv
33	10	0.7	118	6	Q951V4	Q951V4 macaca fasc
34	9	0.7	427	17	Q9H166	Q9H166 thermoplas
35	9	0.7	505	5	Q97337	Q97337 paracentrot
36	9	0.7	596	10	Q49950	Q49950 solanum tub
37	9	0.7	613	4	Q96FL6	Q96FL6 homo sapien
38	9	0.7	673	6	Q95LH9	Q95LH9 oryctolagus
39	9	0.7	725	5	Q96101	Q96101 trypanosoma
40	9	0.7	725	5	Q9TZN8	Q9TZN8 trypanosoma
41	9	0.7	757	4	Q8TE37	Q8TE37 homo sapien
42	9	0.7	779	5	Q9U121	Q9U121 leishmania
43	9	0.7	789	4	Q8TEC1	Q8TEC1 homo sapien
44	9	0.7	884	2	Q9X2W8	Q9X2W8 rhodospirill
45	9	0.7	1010	13	Q9YHU7	Q9YHU7 xenopus lae

ALIGNMENTS

RESULT 1	Q8TEH5	PRELIMINARY:	PRT:	656 AA.
AC	Q8TEH5	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
GN	FLJ00222 protein (Fragment).			
OS	FLJ00222.			
OC	Human sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SPLEEN;			
RA	Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;			
RT	"The nucleotide sequence of a long cDNA clone isolated from human spleen."			
RL	Submitted (Jan-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AK074149; BAB84975.1; ..			
FT	NON_TER			
SQ	SEQUENCE 656 AA: 70138 MW; 1E65D386AB07F1DA CRC64;			
Query Match	45.6%; Score 550; DB 4; Length 656;			
Best Local Similarity	99.8%; Pred. No. 0;			
Matches 650; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	557	ESGEDAGASRRNGRLVVGSSFSRRKKGSLKRAASVEEGDEGDSPGGOSRGATROKRTM	616	
DB	6	ESGEDAGASRRNGRLVVGSSFSRRKKGSLKRAASVEEGDEGDSPGGOSRGATROKRTM	65	
QY	617	KLSRALSDLVKTKTSVATDIEEAASSWQVSSFSSTKQHOLLOKPAQYLRFNQOISR	676	
DB	66	KLSRALSDLVKTKTSVATDIEEAASSWQVSSFSSTKQHOLLOKPAQYLRFNQOISR	125	
QY	677	IYSSIRVDSNNPQPFNAGCOMVALNYQSEGRMLQINRAKFSANGGCGVTLKPGCMC	736	
DB	126	IYSSIRVDSNNPQPFNAGCOMVALNYQSEGRMLQINRAKFSANGGCGVTLKPGCMC	185	

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QY 737 QGVENPNSDEPLPGOLKKOLVLRITISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDC 736
DB 186 QGVENPNSDEPLPGOLKKOLVLRITISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDC 245
QY 797 SREOTRVVDNGFNPTWEETLVFVWMPETALVRELVWMDHPDPIGRDPIGORTLAFSSMMP 856
DB 246 SREOTRVVDNGFNPTWEETLVFVWMPETALVRELVWMDHPDPIGRDPIGORTLAFSSMMP 305
QY 857 GYRHYVLEGEWEASIFVHVAVSDISGVKQALGLKGLFNGPKRGSIDSHAAARPPARPS 916
DB 306 GYRHYVLEGEWEASIFVHVAVSDISGVKQALGLKGLFNGPKRGSIDSHAAARPPARPS 365
QY 917 VSQRLRTASAPTKSKQPKRGRGPELVLTGRDTSKGVADVVPGPAPAPAOEGP 976
DB 366 VSQRLRTASAPTKSKQPKRGRGPELVLTGRDTSKGVADVVPGPAPAPAOEGP 425
QY 977 GSGSPRKAAPAAVAEKPVPVRRPVLDGPGPAGMAATCKCYVSGCAGVNTGLOREP 1036
DB 426 GSGSPRKAAPAAVAEKPVPVRRPVLDGPGPAGMAATCKCYVSGCAGVNTGLOREP 485
QY 1037 PSPGPASQAARQOPARADSLGAPCCGLDPAIRGSRREARPKPGAMROGSGSGSMS 1096
DB 486 PSPGPASQAARQOPARADSLGAPCCGLDPAIRGSRREARPKPGAMROGSGSGSMS 545
QY 1097 SDSSSPSPGIPERSPPWPGACRQPGALOGEMSALFAQRLKEIRKSPMFSAGKPLPC 1156
DB 546 SDSSSPSPGIPERSPPWPGACRQPGALOGEMSALFAQRLKEIRKSPMFSAGKPLPC 605
QY 1157 VLPFHAGMGPGSPAASAMTVSPRYLVYALYPWHCKRGITLLPWLACGP 1207
DB 606 VLPFHAGMGPGSPAASAMTVSPRYLVYALYPWHCKRGITLLPWLACGP 656

RESULT 2
Q8WUS6 PRELIMINARY: PRT: 716 AA.
ID Q8WUS6:
AC Q8WUS6:
DB 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
*RA Strausberg R.;
RL Submitted (DCC-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL: BC019679; ANH19679.1; -
DR InterPro: IPR000008; C2.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00387; PI_PLC_Y; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRODOM: PD001202; PI_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 716 AA; 75724 MW; 148244B142852AB0 CRC64;

Query Match 23.7%; Score 286; DB 4; Length 716;
Best Local Similarity 100.0%; Pred. No. 5.2e-292;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 757 VLRITISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDCSREOTRVVDNGFNPTWEET 816
DB 61 VLRITISGOOLPKPRDSMLGRGETIDPEVEVEITIGLPVDCSREOTRVVDNGFNPTWEET 120
QY 817 LVFVWMPETALVRELVWMDHPDPIGRDPIGORTLAFSSMMPGYRHYVLEGEWEASIFVVA 876
DB 121 LVFVWMPETALVRELVWMDHPDPIGRDPIGORTLAFSSMMPGYRHYVLEGEWEASIFVVA 180
QY 877 VSDISGVKQALGLKGLFNGPKRGSIDSHAAARPPARPSVQRLRTASAPTKSKQPG 936
DB 181 VSDISGVKQALGLKGLFNGPKRGSIDSHAAARPPARPSVQRLRTASAPTKSKQPG 240
QY 937 RRGPELVLTGRDTSKGVADVVPGPAPAPAOEGP 982
DB 241 RRGPELVLTGRDTSKGVADVVPGPAPAPAOEGP 286

RESULT 3
Q9H9U2 PRELIMINARY: PRT: 466 AA.
ID Q9H9U2:
AC Q9H9U2:
DB 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CDNA FLJ12548 f1s, clone NT2RM4000657, weakly similar to
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
DE (EC 3.1.4.11).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirata S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL: AK022610; BAB14129.1; -
DR HSP: P10688; I03H.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00387; PI_PLC_Y; 1.
DR PRINTS: PR00390; PPHPLIPASEC.
DR PRODOM: PD001202; PI_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00149; PLCYC; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 466 AA; 52711 MW; 070CD43363C772ED CRC64;

Query Match 1.9%; Score 23; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 697 ACCGWAALMYOSEGRMLQINRAKFSANGCGGVYLRPGCMCGVFPNPNSEDPLPGOLKKOL 756
DB 1 ACCGWAALMYOSEGRMLQINRAKFSANGCGGVYLRPGCMCGVFPNPNSEDPLPGOLKKOL 60

Query Match 23.7%; Score 286; DB 4; Length 716;
Best Local Similarity 100.0%; Pred. No. 5.2e-292;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
Q9UP73 PRELIMINARY: PRT: 787 AA.
ID Q9UP73:
AC Q9UP73:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE KIAA1069 protein (Fragment).
GN KIAA1069.

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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
 Tanaka A., Kohani H., Nomura N., Ohara O.,
 RT Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB028992; BAB3021.1;
 DR HSSP: P10688; IDH.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
 FT NON-TER 1
 SO SEQUENCE 787 AA; 89169 MW; 2EFC0355E4C8DC8D CRC64;

Query Match 1.9%; Score 23; DB 4; Length 787;
 Best Local Similarity 100.0%; Pred. No. 1.3e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 VHMPEALVRLVMDHPDGRDF 843
 DB 584 VHMPEALVRLVMDHPDGRDF 606

RESULT 5
 O99CUC1 PRELIMINARY; PRT; 447 AA.
 AC O99CUC1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 DE clone:4933427D11, full insert sequence (fragment).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
 Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldi M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hornann M., Hume D.A., Kamya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK01945; BAB30513.1;
 DR HSSP: P10688; IOAS.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR Pfam: PF00036; efhand; 3.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR SMART: SM0054; EFh; 3.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00148; PLCXC; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 FT NON-TER 447
 SO SEQUENCE 447 AA; 51990 MW; 7B81156D3DCFA1C CRC64;

Query Match 1.0%; Score 12; DB 11; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SSHNTYLVGDQL 346
 DB 303 SSHNTYLVGDQL 314

RESULT 6
 Q9H8H5 PRELIMINARY; PRT; 639 AA.
 AC Q9H8H5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE cDNA FLJ13627 f1s, clone PLACE1011046, highly similar to
 DE 1-phosphatidylinositol-4,5-bisphosphate phospholipase beta 1
 DE (EC 3.1.4.11) (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Ito T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 Tanase T., Nomura Y., Jogai S., Komai F., Hara K., Takeuchi K.,
 Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.,
 RT "NEO human cDNA sequencing project."
 RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AK021689; BAB16641.1;
 DR EMBL: AK021689; BAB16641.1;
 DR HSSP: P10688; IDH.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR000909; PI_PLC_xdom.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00388; PI_PLC-X; 1.
 DR Pfam: PF00387; PI_PLC-Y; 1.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR PRODOM: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.

DR PROSITE: PS50007; PIPIC_X DOMAIN: 1.
DR PROSITE: PS50008; PIPIC_Y DOMAIN: 1.
FT NON TER 639 639
SQ SEQUENCE 639 AA; 72530 MW; 23EEFE24EAE1A185 CRC64;
Query Match 1.0%; Score 12; DB 4; Length 639;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 694 FNNAGCCQVVALN 705
DB 191 FNNAGCCQVVALN 202
RESULT 7
ID 097037; PRELIMINARY; PRT; 738 AA.
AC 097037;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PIC-delTAH.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Koyanagi M., Ono K., Suga H., Iwabe N., Miyata T.;
RT "Phospholipase C cDNAs from sponge and hydra: Antiquity of genes
involved in the inositol phospholipid signaling pathway."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB017513; BAA76278.1; -
DR HSP: P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00388; PI-PIC-X; 1.
DR Pfam: PF00387; PI-PIC-Y; 1.
DR PRINTS: PR00390; PPHLIPASEC.
DR ProDom: PD001202; PI_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00149; PLCXG; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50007; PIPIC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.
SQ SEQUENCE 738 AA; 84469 MW; 058120C26A618A6 CRC64;
Query Match 1.0%; Score 12; DB 5; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TLTSKILFKDVI 396
DB 361 TLTSKILFKDVI 372
RESULT 8
ID 09BRC7; PRELIMINARY; PRT; 762 AA.
AC 09BRC7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 87.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006355; AA06355.1; -
DR HSP: P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00388; PI-PIC-X; 1.
DR Pfam: PF00387; PI-PIC-Y; 1.
DR PRINTS: PR00390; PPHLIPASEC.
DR ProDom: PD001202; PI_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00054; EFh; 3.
DR SMART: SM00233; PH; 1.
DR SMART: SM00149; PLCXG; 1.
DR SMART: SM00148; PLCXG; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50018; EF_HAND; UNKNOWN_2.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS50007; PIPIC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPIC_Y_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 762 AA; 87585 MW; 544AB5CE2AEAE3EF CRC64;
Query Match 1.0%; Score 12; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 SSHNTYLVGDQL 346
DB 303 SSHNTYLVGDQL 314
RESULT 9
ID 08SPR7; PRELIMINARY; PRT; 772 AA.
AC 08SPR7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase C delta 4.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF498759; AAM18122.1; -
SQ SEQUENCE 772 AA; 88075 MW; 86E5706A74247548 CRC64;
Query Match 1.0%; Score 12; DB 5; Length 772;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 SSHNTYLVGDQL 346
DB 310 SSHNTYLVGDQL 321
RESULT 10

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097035
ID 097035 PRELIMINARY; PRT; 1012 AA.
AC 097035:
DT 01-MAR-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE PLC-betaH1.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Koyanagi M., Ono K., Suga H., Iwabe N., Miyata T.;
RT "Phospholipase C cDNAs from sponge and hydra: Antiquity of genes
involved in the inositol phospholipid signaling pathway.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017511; BAA/6276.1; -.
DR HSSP; P10688; 1DX.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1012 AA; 116186 MW; BD7CF51F96A23118 CRC64;

Query Match 1.0%; Score 12; DB 5; Length 1012;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWMAGCOMVALN 705
DB 609 FWMAGCOMVALN 620

RESULT 11
ID 089040 PRELIMINARY; PRT; 1183 AA.
AC 089040:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Phospholipase C beta 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GUSTATORY;
RA Roessler P., Kroner C., Freitag J., Noe J., Breer H.;
RT "Identification of a phospholipase C beta subtype in rat taste
cells.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011035; CAA09465.1; -.
DR HSSP; P10688; 1OAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.

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DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1183 AA; 134882 MW; BA3AD63FE074A18C CRC64;

Query Match 1.0%; Score 12; DB 11; Length 1183;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWMAGCOMVALN 705
DB 624 FWMAGCOMVALN 635

RESULT 12
ID 092137 PRELIMINARY; PRT; 1210 AA.
AC 092137:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Phospholipase C beta type (EC 3.1.4.3) (LIPOPHOSPHODIESTERASE 1)
DE (lecithinase C) (Clostridium welchii alpha-toxin) (Clostridium
DE OEDEMATENS beta- and gamma-toxins).
GN PLC1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93388545; PubMed=8397190;
RA Ma H.W., Biltzer R.D., Healy E., Premont R.T., Landau E.M.,
RA Iyengar R.;
RT "Receptor-evoked Cl- current in Xenopus oocytes is mediated through a
RT beta-type phospholipase C. Cloning of a new form of the enzyme.";
RL J. Biol. Chem. 268:19915-19918(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Rawlings N.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O = 1,2-
CC DIALCYLGLYCEROL + CHOLINE PHOSPHATE.
CC -1- COFACTOR: ZINC.
DR EMBL; L20816; AAA03065.1; -.
DR EMBL; Y15901; CAA75861.1; -.
DR HSSP; P10688; 1OAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_Xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00390; PPHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase.
SQ SEQUENCE 1210 AA; 138649 MW; E414CF70EC0F56DC CRC64;

Query Match 1.0%; Score 12; DB 13; Length 1210;

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Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FMNACOMVALN 705
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DB 650 FMNACOMVALN 661

RESULT 13

ID 091086 PRELIMINARY; PRT: 1211 AA.

AC 091086;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phospholipase C beta.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=96257751; PubMed=8687401;
RX Waldo G.L., Paterson A., Boyer J.L., Nicholas R.A., Harden T.K.;
RT "Molecular cloning, expression and regulatory activity of G alpha 11-
erythrocytes";
RT Biochem. J. 316:559-568(1996).
EMBL: U49431; AAC60011.1; -
DR HSSP; P10688; 10AS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00388; PI_PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y.1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00149; PLCYC; 1.
DR SMART; PS0004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1211 AA; 139061 MW; 4E96A10C6AFDB5A CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 13; Length 1211;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 QDMTQPLSHYFI 333
|||||
DB 312 QDMTQPLSHYFI 323

RESULT 14

ID P78708 PRELIMINARY; PRT: 32 AA.

AC P78708;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phosphoinositide-specific phospholipase C (Fragment).
GN NCPLC-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]

RP SEQUENCE FROM N.A.
RX TISSUE=MYCELIIUM;
RC MEDLINE=97306430; PubMed=9163731;

RA Jung O.J., Lee E.J., Kim J.W., Chung Y.R., Lee C.-W.;
RT "Identification of putative phosphoinositide-specific phospholipase C
genes in filamentous fungi";
RT Mol. Cells 7:192-199(1997).
EMBL: U65687; AAB39567.1; -
DR HSSP; P10688; 10X.
DR InterPro: IPR000909; PI_PLC_Xdom.
DR Pfam: PF00388; PI_PLC-X; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3570 MW; 18FA4E795C0A2PD9 CRC64;

Query Match
Best Local Similarity 0.9%; Score 11; DB 3; Length 32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GRCYEVDCMD 372
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DB 22 GRCYEVDCMD 32

RESULT 15

ID 09JMK2 PRELIMINARY; PRT: 622 AA.

AC 09JMK2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Phospholipase C-like protein (Fragment).
GN PCEI OR 4933403A2IRK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.

RA MEDLINE=20581708; PubMed=11146508;
RX Tidhar A., Reichenstein M., Cohen D., Faerman A., Copeland N.G.,
RT Gilbert D.J., Jenkins N.A., Shani M.;
RT "A novel transgenic marker for migrating limb muscle precursors and
for vascular smooth muscle cells";
RT Dev. Dyn. 220:60-73(2001).
EMBL: AF233885; AAF4208.1; -
DR HSSP; P10688; 10X.
DR MGD; MGI:1921305; Pcel.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR001711; PI_PLC_Y.
DR InterPro: IPR000159; RA_domain.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00387; PI_PLC-Y; 1.
DR Pfam: PF00788; RA; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y.1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00149; PLCYC; 1.
DR SMART; SM00314; RA; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 622 AA; 69951 MW; 523525661DFED363 CRC64;

Query Match
Best Local Similarity 0.9%; Score 11; DB 11; Length 622;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 ANGCGGYLKP 732
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DB 152 ANGCGGYLKP 162

Search completed: March 28, 2003, 14:04:58

Mon Mar 31 11:07:15 2003

us-09-927-112-2.oligo.rspt

Page 7

Job time : 118 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 14:02:31 ; Search time 31 Seconds
(without alignments)
1145.596 Million cell updates/sec

Title: US-09-927-112-2

Sequence: 1 MAPPRAGPLGPALPPEDPG.....ALYWHCLRGTLPLWLAGCP 1207

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Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 - 3: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
 - 4: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
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 - 6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	10	0.8	744	4	US-09-738-884-5
2	9	0.7	736	4	US-09-738-884-2
3	9	0.7	1230	1	US-08-138-641-2
4	9	0.7	1230	1	US-08-138-133-2
5	8	0.7	177	2	US-08-850-910A-18
6	8	0.7	335	4	US-09-222-938A-4
7	8	0.7	744	4	US-09-738-884-4
8	7	0.6	131	1	US-08-664-596B-18
9	7	0.6	137	1	US-08-279-058B-38
10	7	0.6	137	1	US-08-828-323-38
11	7	0.6	171	5	PCT-US95-04910-12
12	7	0.6	180	2	US-08-924-759-24
13	7	0.6	180	3	US-09-248-335-24
14	7	0.6	224	4	US-09-228-986-130
15	7	0.6	237	1	US-08-750-532-18
16	7	0.6	244	4	US-08-936-165A-379
17	7	0.6	267	4	US-08-818-112-142
18	7	0.6	267	4	US-08-818-111-137
19	7	0.6	267	4	US-09-056-556-142
20	7	0.6	267	4	US-09-072-596-137
21	7	0.6	272	4	US-09-189-637A-311
22	7	0.6	285	4	US-09-327-681-6
23	7	0.6	293	4	US-09-069-023-20
24	7	0.6	325	4	US-09-108-020-49
25	7	0.6	357	1	US-08-638-911A-37
26	7	0.6	357	4	US-09-149-476-755
27	7	0.6	376	1	US-08-279-590A-2

28	7	0.6	376	2	US-08-910-092-2	Sequence 2, App1
29	7	0.6	394	4	US-09-218-197-2	Sequence 2, App1
30	7	0.6	399	4	US-09-120-772-2	Sequence 2, App1
31	7	0.6	412	4	US-09-445-472-1	Sequence 1, App1
32	7	0.6	425	4	US-09-247-155-99	Sequence 99, App1
33	7	0.6	448	1	US-08-570-157-3	Sequence 3, App1
34	7	0.6	448	4	US-09-076-510-3	Sequence 3, App1
35	7	0.6	455	4	US-09-240-639-10	Sequence 10, App1
36	7	0.6	462	4	US-08-068-395A-1	Sequence 1, App1
37	7	0.6	485	1	US-08-165-241-1	Sequence 1, App1
38	7	0.6	485	1	US-08-464-365-1	Sequence 3, App1
39	7	0.6	505	1	US-08-068-395A-3	Sequence 3, App1
40	7	0.6	505	1	US-08-464-365-3	Sequence 3, App1
41	7	0.6	505	4	US-09-509-902A-11	Sequence 11, App1
42	7	0.6	522	4	US-08-894-818B-3	Sequence 4, App1
43	7	0.6	522	4	US-09-445-472-4	Sequence 4, App1
44	7	0.6	543	4	US-09-535-008-63	Sequence 63, App1
45	7	0.6	577	2	US-08-852-153-4	Sequence 4, App1

ALIGNMENTS

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RESULT 1
US-09-738-884-5
; Sequence 5, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GIEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-738-884-5

Query Match      0.8%; Score 10; DB 4; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      723 NGGCGVLPK 732
DB      585 NGGCGVLPK 594

RESULT 2
US-09-738-884-2
; Sequence 2, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GIEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; FILE REFERENCE: CLO00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Human
US-09-738-884-2

Query Match      0.7%; Score 9; DB 4; Length 736;

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Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 LVKGGKLP 471
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DB 425 LVKGGKLP 433

RESULT 3

US-08-138-641-2
Sequence 2, Application US/08138641
Patent No. 5474921

GENERAL INFORMATION:

APPLICANT: Koblán, Kenneth S.
APPLICANT: Pomplano, David L.
TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,641
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-138-641-2

Query Match 0.7%; Score 9; DB 1; Length 1290;
Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 408 EYVILSIE 416
|||||||
DB 406 EYVILSIE 414

RESULT 4

US-08-138-133-2
Sequence 2, Application US/08138133
Patent No. 5519163

GENERAL INFORMATION:

APPLICANT: GIBBS, JACKSON B.
APPLICANT: KOBLAN, KENNETH S.
APPLICANT: MACLEOD, ANGUS M.
APPLICANT: MERCHANT, KEVIN J.
TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
TITLE OF INVENTION: PHOSPHOLIPASE C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: U.S.A.
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,133
FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MUTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-138-133-2

Query Match 0.7%; Score 9; DB 1; Length 1290;
Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 408 EYVILSIE 416
|||||||
DB 406 EYVILSIE 414

RESULT 5

US-08-850-910A-18
Sequence 18, Application US/08850910A
Patent No. 5948761

GENERAL INFORMATION:

APPLICANT: SELHAMER, J.J.
APPLICANT: SCARBROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENT PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROENSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988

APPLICATION NUMBER: 07/2200,363
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-850-910A-18

Query Match	0.7%	Score 8;	DB 2;	Length 177;
Best Local Similarity	100.0%	Pred. No. 8.9;		
Matches	8;	Conservative	0;	Mismatches
			0;	Gaps
				0;

QY	932	SQKPGRRG	939
Db	152	SQKPGRRG	159

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RESULT 6
US-09-222-938A-4
: Sequence 4, Application US/09222938A
: Patent No. 6437108
: GENERAL INFORMATION:
: APPLICANT: Youngman, Philip
: APPLICANT: Fitez, Christian
: APPLICANT: Murphy, Christopher
: APPLICANT: Guzman, Luz-Maria
: TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
: FILE REFERENCE: 07334/060001
: CURRENT APPLICATION NUMBER: US/09/222,938A
: CURRENT FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 102
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 335
: TYPE: PRT
: ORGANISM: Streptococcus pneumoniae
US-09-222-938A-4

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Query Match	0.78	Score 8	DB 4	Length 335
Similarity	100.0%	Pred. No. 16		
Best Local				
Matches	0	Mismatches	0	Gaps 0

QY	154	SDEDSLAR	161
Db	90	SDEDSLAR	97

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RESULT 7
US-09-738-884-4
; Sequence 4, Application US/09738884
; Patent No. 6391606
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL00849
; CURRENT APPLICATION NUMBER: US/09/738,884
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0

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; SEQ ID NO 4
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Cricetus griseus
US-09-738-884-4

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Query Match	0.7%	Score 8	DB 4	Length 744
Best Local Similarity	100.0%	Pred. No. 35		
Matches	8	Conservative	0	Indels 0; Gaps 0;

Qy	761	ISGQQLPK	768
Db	625	ISGQQLPK	632

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Query Match	0.64	Score 7	DB 1	Length 131
Best Local Similarity	100.0%	Pred. No. 70		
Matches 7	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1096	SSDSSSP	1102
Db	119	SSDSSSP	125

RESULT 9

US-08-279-058B-38
; Sequence 38, Application US/08279058B
; Patent No. 5668004
; GENERAL INFORMATION:
; APPLICANT: Michael E. O'Donnell
; TITLE OF INVENTION: DNA POLYMERASE III
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,058B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yamwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: CRF D-1056CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-279-058B-38

Query Match 0.6%; Score 7; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1122 PGALOG 1128
Db 22 PGALOG 28

RESULT 10
US-08-828-323-38
; Sequence 38, Application US/08828323A
; Patent No. 6413753
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael
; TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME
; FILE REFERENCE: 19603/10214
; CURRENT APPLICATION NUMBER: US/08/828,323A
; CURRENT FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-828-323-38

Query Match 0.6%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1122 PGALOG 1128
Db 22 PGALOG 28

RESULT 11
PCT-US95-04910-12
; Sequence 12, Application PC/TUS9504910
; GENERAL INFORMATION:
; APPLICANT: The Government of the United
; APPLICANT: States of America as represented
; APPLICANT: by the Secretary, Department of
; APPLICANT: Health and Human Services
; TITLE OF INVENTION: ISOLATION AND
; TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL PRIMATE T-CELL
; TITLE OF INVENTION: LYMPHOTROPIC VIRUS AND THE USE OF THIS VIRUS
; TITLE OF INVENTION: OR COMPONENTS THEREOF IN DIAGNOSTIC ASSAYS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04910
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/231,526
; FILING DATE: 22-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAM S. FEILER
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4125PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acids
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
PCT-US95-04910-12

Query Match 0.6%; Score 7; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 160 ARROTR 166
Db 4 ARROTR 10

RESULT 12
US-08-924-759-24
; Sequence 24, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET

CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,759
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1128
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: MAIZE
IMMEDIATE SOURCE:
LIBRARY: CSL.PK0059.E2
US-08-924-759-24

Query Match
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 887 ALGKGL 893
|||||
Db 24 ALGKGL 30

RESULT 13
US-09-248-335-24
Sequence 24, Application US/09248335
Patent No. 6096504
GENERAL INFORMATION:
APPLICANT: MCCONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 24
LENGTH: 180
TYPE: PRT
ORGANISM: maize
US-09-248-335-24

Query Match
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 887 ALGKGL 893
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Db 24 ALGKGL 30

RESULT 14

US-09-228-986-130
Sequence 130, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Neuenhulzen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 130
LENGTH: 224
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-228-986-130

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1096 SSDSSP 1102
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Db 202 SSDSSP 208

RESULT 15
US-08-750-532-18
Sequence 18, Application US/08750532
Patent No. 5736339
GENERAL INFORMATION:
APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,532
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/130236
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITTA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-532-18

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Query Match          0.6%  Score 7;  DB 1;  Length 237;
Best Local Similarity 100.0%  Pred. No. 1.2e+02;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 1169 GSPAAAS 1175
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Db 133 GSPAAAS 139

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Search completed: March 28, 2003, 14:12:10
 Job time : 33 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 14:05:06 ; Search time 38 Seconds
(without alignments)
1865.249 Million cell updates/sec

Title: US-09-927-112-2

Perfect score: 1207
Sequence: 1 MAPPTAGPLPGPALPDPEDPG.....ALYPMHCLRGTLPLWLACGP 1207

Scoring table:
Gapop 60.0, Gapext 60.0

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Word size: 0

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications-AA:

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7: /cgn2_6/ptodata/1/pubpaa/PCRTS_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	100.0	1207	US-09-927-112-2	Sequence 2, Appli
2	324	26.8	325	US-09-927-112-10	Sequence 10, Appli
3	14	1.2	1054	US-09-828-447-11	Sequence 11, Appli
4	13	1.1	119	US-09-764-868-637	Sequence 637, App
5	13	1.1	119	US-09-955-999-84	Sequence 84, Appli
6	12	1.0	102	US-09-822-635-7	Sequence 7, Appli
7	12	1.0	119	US-09-800-971-9	Sequence 9, Appli
8	12	1.0	128	US-09-800-971-8	Sequence 8, Appli
9	12	1.0	128	US-09-927-112-8	Sequence 8, Appli
10	12	1.0	128	US-09-908-664-11	Sequence 11, Appli
11	12	1.0	128	US-09-908-664-20	Sequence 20, Appli
12	12	1.0	340	US-09-835-996A-19	Sequence 19, Appli
13	12	1.0	567	US-09-835-996A-8	Sequence 8, Appli
14	12	1.0	762	US-09-804-969-15	Sequence 15, Appli
15	12	1.0	762	US-09-908-664-2	Sequence 2, Appli
16	11	0.9	119	US-09-908-664-15	Sequence 15, Appli
17	11	0.9	128	US-09-908-664-23	Sequence 23, Appli
18	11	0.9	1809	US-09-823-635-2	Sequence 2, Appli
19	10	0.8	92	US-09-927-112-16	Sequence 16, Appli

20	10	0.8	182	US-09-800-971-7	Sequence 7, Appli
21	10	0.8	201	US-09-867-550-1334	Sequence 1334, Ap
22	10	0.8	628	US-09-828-447-12	Sequence 12, Appli
23	10	0.8	744	US-10-096-961-5	Sequence 5, Appli
24	9	0.7	736	US-10-096-961-2	Sequence 2, Appli
25	9	0.7	736	US-09-800-971-2	Sequence 2, Appli
26	8	0.7	48	US-09-864-761-42929	Sequence 42929, A
27	8	0.7	63	US-09-908-664-17	Sequence 17, Appli
28	8	0.7	158	US-09-764-870-377	Sequence 377, App
29	8	0.7	158	US-09-764-860-342	Sequence 342, App
30	8	0.7	158	US-09-927-112-11	Sequence 11, Appli
31	8	0.7	170	US-09-908-664-11	Sequence 13, Appli
32	8	0.7	191	US-09-908-664-22	Sequence 22, Appli
33	8	0.7	335	US-09-815-242-13433	Sequence 13433, A
34	8	0.7	335	US-09-815-242-13658	Sequence 13658, A
35	8	0.7	384	US-09-738-626-6924	Sequence 6924, Ap
36	8	0.7	608	US-09-908-664-5	Sequence 5, Appli
37	8	0.7	744	US-10-096-961-4	Sequence 4, Appli
38	8	0.7	875	US-09-548-933-15	Sequence 15, Appli
39	8	0.7	1567	US-09-835-232-2	Sequence 2, Appli
40	7	0.6	51	US-09-864-761-48515	Sequence 48515, A
41	7	0.6	71	US-09-764-877-1515	Sequence 1515, Ap
42	7	0.6	83	US-09-050-010-7	Sequence 7, Appli
43	7	0.6	93	US-09-764-869-676	Sequence 676, App
44	7	0.6	104	US-09-864-761-39244	Sequence 39244, A
45	7	0.6	113	US-09-738-626-4430	Sequence 4430, Ap

ALIGNMENTS

RESULT 1
US-09-927-112-2
Sequence 2, Application US/09927112
Patent No. US20020106774A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32544, a novel human phospholipase C and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 38155-20048.00
CURRENT APPLICATION NUMBER: US/09/927,112
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/246,808
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1207
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-112-2

Query Match 100.0%; Score 1207; DB 10; Length 1207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPTAGPLPGPALPDPEDPGDPESRKLFLSANILPVYERKMGAMOBGMVYKLRGSGK 60
DB 1 MAPPTAGPLPGPALPDPEDPGDPESRKLFLSANILPVYERKMGAMOBGMVYKLRGSGK 60
QY 1 YRFTYLDHRSCTIWRSRKNEKAKISIDSTOEVSEGRSEVORYPDGSFDPNCFSI 120
DB 1 YRFTYLDHRSCTIWRSRKNEKAKISIDSTOEVSEGRSEVORYPDGSFDPNCFSI 120
QY 61 LVRFYLDHRSCTIWRSRKNEKAKISIDSTOEVSEGRSEVORYPDGSFDPNCFSI 120
DB 61 LVRFYLDHRSCTIWRSRKNEKAKISIDSTOEVSEGRSEVORYPDGSFDPNCFSI 120
QY 121 YGSHRESIDLVSTSEVARTWTGLRYLMAGISDEDSIARORTRDWLKOTFDEADKN 180
DB 121 YGSHRESIDLVSTSEVARTWTGLRYLMAGISDEDSIARORTRDWLKOTFDEADKN 180
QY 121 YGSHRESIDLVSTSEVARTWTGLRYLMAGISDEDSIARORTRDWLKOTFDEADKN 180
DB 121 YGSHRESIDLVSTSEVARTWTGLRYLMAGISDEDSIARORTRDWLKOTFDEADKN 180
QY 181 GDSGISGEVYDOLKLNVLNPLPROVKOMFREADTDHOGTIGFEFCATFKKMSSTRDL 240
DB 181 GDSGISGEVYDOLKLNVLNPLPROVKOMFREADTDHOGTIGFEFCATFKKMSSTRDL 240

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QY 241 YLLMLTYSNKHDLDAASLORFLOVEOKMAGVTLSECCDIIIEQEPENKSKGLGIDG 300
DB 241 YLLMLTYSNKHDLDAASLORFLOVEOKMAGVTLSECCDIIIEQEPENKSKGLGIDG 300
QY 301 FTNTRSPADIDFPEHHNHVODMTOPLSHYFTTSSNTYTVBDQMSOSRVDYMAVIO 360
DB 301 FTNTRSPADIDFPEHHNHVODMTOPLSHYFTTSSNTYTVBDQMSOSRVDYMAVIO 360
QY 361 AGRCVCEVDCWDGPHDEPIVHHGTYLTKILPFVDIETINKYAFINKEYVILISNHCS 420
DB 361 AGRCVCEVDCWDGPHDEPIVHHGTYLTKILPFVDIETINKYAFINKEYVILISNHCS 420
QY 421 VIOOKMAOYLTDILGDKLDLSSVSEDAATLPSPOLMKGLIYKGRKILPANISEDABEG 480
DB 421 VIOOKMAOYLTDILGDKLDLSSVSEDAATLPSPOLMKGLIYKGRKILPANISEDABEG 480
QY 481 EVSEDESDADIEDDCKLNDASTNRKRVENAKRKLDLSIKRSKIRDCEDPNFESVTL 540
DB 481 EVSEDESDADIEDDCKLNDASTNRKRVENAKRKLDLSIKRSKIRDCEDPNFESVTL 540
QY 541 SPFGKLGKRSKAEDEYSEGDAGASRRNGRLVYGSFRRKKKSKLKAASVEEGEGOD 600
DB 541 SPFGKLGKRSKAEDEYSEGDAGASRRNGRLVYGSFRRKKKSKLKAASVEEGEGOD 600
QY 601 SPFGGSRGATROKTKTKLSALSDLYKTKSVATHDIEEPAASSWQVSSFSETKAHQIIO 660
DB 601 SPFGGSRGATROKTKTKLSALSDLYKTKSVATHDIEEPAASSWQVSSFSETKAHQIIO 660
QY 661 OKRAQGLRFENQOOLSRITSSYRVDSNTNPOEFMNAQOMALNOSGRLQOLNRAF 720
DB 661 OKRAQGLRFENQOOLSRITSSYRVDSNTNPOEFMNAQOMALNOSGRLQOLNRAF 720
QY 721 SANGCGGYVLKPGCMQGVFNPNSDPLPGOLKKOLVILIIISGOOLPKPRDSMLGDRGI 780
DB 721 SANGCGGYVLKPGCMQGVFNPNSDPLPGOLKKOLVILIIISGOOLPKPRDSMLGDRGI 780
QY 781 IDPFVEVEIILGPDVDCSRQOTRYVDNGFNPMTEETLVYMHMPELALYRFLVMDHDPIC 840
DB 781 IDPFVEVEIILGPDVDCSRQOTRYVDNGFNPMTEETLVYMHMPELALYRFLVMDHDPIC 840
QY 841 RDEIGORTLAFSSMPGRYHYVLEGEAEASIFVHAVSDISGRVQALGLKGLRGRPP 900
DB 841 RDEIGORTLAFSSMPGRYHYVLEGEAEASIFVHAVSDISGRVQALGLKGLRGRPP 900
QY 901 GSIDSHAAARRPARBSVSRILIRTAASAPTKSQKPGRRGFPPELVLTGTRDTGSKVADVV 960
DB 901 GSIDSHAAARRPARBSVSRILIRTAASAPTKSQKPGRRGFPPELVLTGTRDTGSKVADVV 960
QY 961 PPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPLYRVPRVLDGPGAPGMAATCMKCV 1020
DB 961 PPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPLYRVPRVLDGPGAPGMAATCMKCV 1020
QY 1021 GSCAGVNTGGLQREPRPSPBPASROAIIROQPARADSLGAPCCGLDHPHAIPIGRREAPK 1080
DB 1021 GSCAGVNTGGLQREPRPSPBPASROAIIROQPARADSLGAPCCGLDHPHAIPIGRREAPK 1080
QY 1081 GPGANROGPGSSGSSSSSPDSCPIERBRPMPREGACROGAIQGMASLPAOKLEET 1140
DB 1081 GPGANROGPGSSGSSSSSPDSCPIERBRPMPREGACROGAIQGMASLPAOKLEET 1140
QY 1141 RSKSPMSAGKRPILPCVYLPHAPGAGGSPAAASAMTVSRVLVLAALYWHCLRGTL 1200
DB 1141 RSKSPMSAGKRPILPCVYLPHAPGAGGSPAAASAMTVSRVLVLAALYWHCLRGTL 1200
QY 1201 PMLACGP 1207
DB 1201 PMLACGP 1207

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; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-10

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Query Match 26.8%; Score 324; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.2e-310;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 884 VKOALGLKGLRGPKEPSIDSHAAGRPAPRSYQILKRTASAPTKSQKPGRRGPEL 943
DB 2 VKOALGLKGLRGPKEPSIDSHAAGRPAPRSYQILKRTASAPTKSQKPGRRGPEL 943
QY 944 VLGRDTGSKGVADVYPPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPLYRVPRV 1003
DB 62 VLGRDTGSKGVADVYPPGPGAPAPAPAOEGPSSPGKAPAAVAEKSPLYRVPRV 1003
QY 1004 DGPBGAAATCMKCVYSGCAGVNTGGLQREPRPSPBPASROAIIROQPARADSLGAPC 1063
DB 122 DGPBGAAATCMKCVYSGCAGVNTGGLQREPRPSPBPASROAIIROQPARADSLGAPC 1063
QY 1064 GGLDHPHAIPIGRREAPKPGAPGAMROGPGSSGSSSSSPDSCPIERBRPMPREGACROG 1123
DB 182 GGLDHPHAIPIGRREAPKPGAPGAMROGPGSSGSSSSSPDSCPIERBRPMPREGACROG 1123
QY 1124 ALQGMASLPAOKLEETIRSKSPMSAGKRPILPCVYLPHAPGAGGSPAAASAMTVSPRV 1183
DB 242 ALQGMASLPAOKLEETIRSKSPMSAGKRPILPCVYLPHAPGAGGSPAAASAMTVSPRV 1183
QY 1184 LVVALYPMHCLRGTLDPMLACGP 1207
DB 302 LVVALYPMHCLRGTLDPMLACGP 325

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RESULT 3
US-09-828-447-11
; Sequence 11, Application US/09828447
; Patent No. US20020069432A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
; FILE REFERENCE: 16313-0037
; CURRENT APPLICATION NUMBER: US/09/828,447
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1054
; TYPE: PRT

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; ORGANISM: Physcomitrella patens
US-09-828-447-11

Query Match
Best Local Similarity 1.2%; Score 14; DB 10; Length 1054;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 VHODMTQPLSHYFI 333
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Db 104 VHODMTQPLSHYFI 117

RESULT 4
US-09-764-868-637
; Sequence 637, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-637

Query Match
Best Local Similarity 1.1%; Score 13; DB 9; Length 119;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YLMAGISDEDSLA 160
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Db 53 YLMAGISDEDSLA 65

RESULT 5
US-09-955-999-84
; Sequence 84, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; FILE REFERENCE: PT086P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-955-999-84

Query Match
Best Local Similarity 1.1%; Score 13; DB 9; Length 119;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YLMAGISDEDSLA 160
|||||
Db 53 YLMAGISDEDSLA 65

RESULT 6
US-09-822-635-7
; Sequence 7, Application US/09822635
; Patent No. US20010039331A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; TITLE OF INVENTION: 16836, A NOVEL HUMAN PHOSPHOLIPASE C AND
; FILE REFERENCE: 10448-035001
; CURRENT APPLICATION NUMBER: US/09/822,635
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,921
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-822-635-7

Query Match
Best Local Similarity 1.0%; Score 12; DB 10; Length 102;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 FWNAGCOMVALN 705
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Db 53 FWNAGCOMVALN 64

RESULT 7
US-09-800-971-9
; Sequence 9, Application US/09800971
; Patent No. US20020098577A1
; GENERAL INFORMATION:
; APPLICANT: Rachel A. Meyers
; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
; FILE REFERENCE: 10448-023001
; CURRENT APPLICATION NUMBER: US/09/800,971
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,453
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/188,032
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
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US-09-800-971-9

Query Match 1.0%; Score 12; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 77 FWNAGCOMVALN 88

RESULT 8

US-09-800-971-8
; Sequence 8, Application US/09800971
; Patent No. US20020098577A1
; GENERAL INFORMATION:
; APPLICANT: Rachel A. Meyers
; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C
; FILE REFERENCE: 10448-023001
; CURRENT APPLICATION NUMBER: US/09/800,971
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,453
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/188,032
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-800-971-8

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 9

US-09-927-112-8
; Sequence 8, Application US/09927112
; Patent No. US20020106774A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Sllios-Santiago, Immaculada
; TITLE OF INVENTION: 32544, a novel human phospholipase C and
; FILE REFERENCE: 38155-20048.00
; CURRENT APPLICATION NUMBER: US/09/927,112
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/246,808
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-927-112-8

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 10

US-09-908-664-11
; Sequence 11, Application US/09908664
; Patent No. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-908-664-11

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 694 FWNAGCOMVALN 705
Db 79 FWNAGCOMVALN 90

RESULT 11

US-09-908-664-20
; Sequence 20, Application US/09908664
; Patent No. US20020115178A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-908-664-20

Query Match 1.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 FNNAGCQWALN 90

RESULT 12

US-09-835-996A-19
; Sequence 19, Application US/09835996A
; Patent No. US20020142953A1

GENERAL INFORMATION:

APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Montgomery, Julie
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje
APPLICANT: Ren, Feiyan
APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-19

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QY 335 SSHNTYLVGDOL 346
Db 303 SSHNTYLVGDOL 314

RESULT 13

US-09-835-996A-8
; Sequence 8, Application US/09835996A
; Patent No. US20020142953A1

GENERAL INFORMATION:

APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
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APPLICANT: Zhou, Ping
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APPLICANT: Drmanac, Radoje
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APPLICANT: Qian, Xiaohong
APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM

FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-8

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QY 335 SSHNTYLVGDOL 346
Db 303 SSHNTYLVGDOL 314

RESULT 14

US-09-804-969-15
; Sequence 15, Application US/09804969
; Patent No. US20020081595A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi
APPLICANT: Nepomniachy, Boris
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Abuln, Alejandro
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020081595A1 Human Phospholipases and Polynucleotides
; FILE REFERENCE: LEX-0148-USA
; CURRENT APPLICATION NUMBER: US/09/804,969
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,885
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 60/189,693
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 762
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-804-969-15

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 303 SSHNTYLVGDOL 314

RESULT 15

US-09-908-664-2
; Sequence 2, Application US/09908664
; Patent No. US20020115178A1


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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Tsai, Fong Yin
; TITLE OF INVENTION: 16816 AND 16839, NOVEL HUMAN
; TITLE OF INVENTION: PHOSPHOLIPASE C MOLECULES AND USES THEREFOR
; FILE REFERENCE: 38155-20022.00
; CURRENT APPLICATION NUMBER: US/09/908,664
; PRIOR APPLICATION NUMBER: US 60/218,675
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-908-664-2

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Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 335 SSHNTYLVGDQL 346
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Db 303 SSHNTYLVGDQL 314

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Search completed: March 28, 2003, 14:14:22
Job time : 41 secs